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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶: C12N 15/12, C07K 14/47, A61K 38/17,

(11) International Publication Number:

WO 98/45436

C12N 15/12, C07K 14/47, A01K 58/17, C12N 15/10, C12Q 1/68

(43) International Publication Date:

15 October 1998 (15.10,98)

(21) International Application Number:

PCT/US98/06955

A2

(22) International Filing Date:

10 April 1998 (10.04.98)

(30) Priority Data:

08/838,821

10 April 1997 (10.04.97)

US

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Published

Without international search report and to be republished upon receipt of that report.

(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

(57) Abstract

Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.

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PCT/US98/06955 WO 98/45436

SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

FIELD OF THE INVENTION

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The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed in vivo, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they 20 were transcribed.

Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the nonsecreted "chaff", wasting effort and resources in the process.

Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted

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proteins, namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

SUMMARY OF THE INVENTION

The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEO ID NO:17, SEO ID NO:18, SEO ID NO:19, SEO ID NO:20, SEO ID NO:21, SEO ID NO:22, SEO ID NO:23, SEO ID NO:24, SEO ID NO:25, SEO ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,

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or a complement of said sequence.

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In other embodiments, the present invention provides an isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

SEO ID NO:1, SEO ID NO:2, SEO ID NO:3, SEO ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEO ID NO:82, SEO ID NO:83, SEO ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ

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or a complement of said sequence.

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In further embodiments, the present invention provides an isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ

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ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ 1D NO:56, SEQ 1D NO:57, SEQ 1D NO:58, SEQ 1D NO:59, SEQ 1D NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109. SEO ID NO:110, SEO ID NO:111, SEO ID NO:112, SEO ID NO:113, SEO ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ-ID-NO:156, SEQ-ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

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30 or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

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or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described polynucleotides.

DETAILED DESCRIPTION

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each SEQ ID NO: in the Sequence Listing.

15 <u>Table 2</u>

5

10

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

	i	BV31	18	CB302	35	BZ83 · ·	52	CD244
	2	BV34	19	CB318	36	BZ87	53	CD265
20	3	BV37	20	CB321	37	CB15	54	BT217
	4	BV45	21	CB96	38	CB2	55	BV278
	5	BV8	22	CB98	39	CB44	56	BV280
	6	BV93	23	BZ42 -	40	CCII	57	BV282
	7	BV99	24	BZ53	41	CC182	58	BV285
25	8	CB100	25	BZ56	42	CC298	59	BV286
	9	CB107	26	BZ6	43	CC310	60	BV291
	10	CB110	27	BZ607	44	CC323	61	BV295
	11	CB114	28	BZ61	45	CC332	62	BW389
	12	CB118	29	BZ62	46	CC335	63	BX135
30	13	CB123	30	BZ641	47	CC338	64	BX141
	14	CB129	31	BZ644	48	CC41	65	BX148
	15	CB137	32	BZ72	49	CC52	66	BZ1
	16	CB239	33	BZ74	50	CD107	67	BZ16
	17	CB259	34	BZ82	51	CD205	68	BZ187

	69	BZ19	103	CE159	137	CH315	171	CC194
	70	BZ205	104	CE2	138	CH325	172	CC198
	71	BZ222	105	CE347	139	BZ568	173	CC199
	72	BZ230	106	CE36	140	BZ578	174	CC205
5	73	BZ234	107	CE40	141	BZ588	175	CC215
	74	BZ244	108	CE87	142	BZ597	176	CC253
	75	BZ269	109	CG1	143	BZ598	177	CC258
	76	BZ280	110	CG44	144	CH637	178	CC259
•	77	BZ288	111	CG60	145	CH644	179	CC265
10	78	BZ304	112	CG68	146	CH699	180	CC288
	79	BZ328	113	BP202	147	C1240	181	CC95
	80	BZ331	114	BP242	148	CI247	182	CC96
•	81	BP646	115	BP243	149	CJI	· 183	CD311
	82	BP652	116	BZ444	150	CJ19	184	CD323
15	83	BP656	117	BZ453	151	CJ24	185	CH338
	84	BP666	118	CC233	152	CJ27	186	CH355
	85	BP667	119	CC242	153	CJ3	187	CH377
	86	BP674	120	CC247	154	CJ37	188	CH421
	87	BP695	121	CC344	155	CJ42	189	CH425
20	88	BP705	122	CC346	156	CJ44	190	CH522
	89	BP713	123	CC351	157	CJ49	191	CH541
	90	BP720	124	CC359	158	CJ50	192	CH555
	91	BP750	125	CC364	159	CJ55	193	CH558
	92	BP754	126	CC365	160	CJ6	194	CH582
25	93	BW143	127	CC374	161	CJ76	195	CH595
	94	BR307	128	CE303	162	CJ77	196	CH720
	95	BR309	129	CE328	163	CJ84	197	CH723
	96	BR312	130	CG199	164	C186 ·	198	CH724
	97	BR318	131	CG209	165	CJ91	199	CH735
30	9.8	CB187	132	CG210	166	CCIII	200	CH742
	99	CB190	133	CG350	167	CC118	201	CI126
	100	CB204	134	CG354	168	CC120	202	CI129
	101	CB213	Í35	CG426	-169	CC126	203	CI133
	102	CE120	136	CH303	170	CC130	204	CI181

	205	C1229	239	CG160	273	C1395	307	CJ397
	206	C125	240	CG175	274	C1407	308	CJ400
	207	C152	241	CG176	275	CI411	309	CJ404
	208	C184	242	CG180	276	C1437	310	CJ415
5	209	CI91	243	CG279	277	C1443	311	CJ420
	210	BP163	244	CG292	278	C1444	312	CJ424
	211	BP175	245	CG300	279	C1459	313	CJ434
	212	BP199	246	CG301	280	C1480	314	CJ454
	213	BP272	247	CG314	281	C1490	315	CJ457
10	214	BP284	248	CG315	282	C1492	316	CJ481
	215	BP294	249	CG324	283	C1493	317	CJ493
	216	BP299	250	CG336	284	C1510	318	CJ501
	217	BP300	251	CG99	285	CI522	319	CJ514
	218	BP306	252	CH143	286	CI534	320	CJ539
15	219	BP311	253	CH207	287	CI542	321	CJ540
	220	BP312	254	CH224	288	C1560	322	CJ549
	221	BP327	255	CH227	289	CI561	323	CJ551
	222	BP345	256	CH245	290	CI583	324	CK126
	223	BP368	257	CH246	291	C1586	325	CK151
20	224	BP467	258	CH27	292	CJ145	326	CK181
	225	BP468	259	СН30	293	CJ149	327	CK201
	226	BR375	260	CH4	294	CJ160	328	CK213
	227	BR390	261	CH64	295	CJ164	329	CK218
	228	BR408	262	CH78	296	CJ168	330	CK234
25	229	BR418	263	CH85	297	CJ176	331	CK37
	230	BY66	264	CH87	298	CJ183	332	CK48
	231	CF118	265	CN320	299	CJ194	333	CL104
	232	CF127	266	CN343	300	CJ206	334	CL110
	233	CF22	267	CN344	301	CJ230	335	CL122
30	234	CF235	268	CN395	302	CJ237	336	CL132
	235	CG109	269	CN423	303	CJ257	337	CL147
	236	CG131	270	C1363	304	CJ265	338	CL152
	237	CG153	271	C1386	305	CJ378	339	CL181
	238	CG158	272	CI392	306	CJ389	340	CL182

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	342	CL469	376	CN532	410	CO48	444	CO153
	343	CL470	377	CN552	411	CO444	445	CO145
	344	CL481	378	CN593	412	CO431	446	CO140
5	345	CL493	379	CN619	413	CO391	447	CO139
	346	CM12	380	CN621	414	CO384	448	CO128
	347	CM178	381	CN667	415	CO36	449	CO1254
	348	CM188	382	CN703	416	CO351	450	CO1247
	349	CM194	383	CN718	417	CO337	451	CO1232
10	350	CM246	384	CN729	418	CO327	452	CO1224
	351	CM251	385	CN835	419	CO315	453	CO1223
	352	CM54	386	CN896	420	CO304	454	CO1206
	353	CM62	387	CO933	421	CO270	455	CO1198
	354	CN140	388	CO924	422	CO268	456	CO1196
15	355	CN171	389	CO908	423	CO264	457	CO1194
	356	CN173	390	CO900	424	CO261	458	CO1187
	357	CN238	391	CO889	425	CO257	459	CO1180
	358	CN29	392	CO888	426	CO253	460	CO1178
	359	CN291	393	CO874	427	CO25	461	CO1175
20	360	CN304	394	CO851	428	CO246	462	CO117
	361	CN327	395	CO83	429	CO244	463	CO1168
	362	CN49	396	CO821	430	CO240	464	CO1164
	363	CN50	397	CO806	431	CO228	465	CO1162
	364	CN54	398	CO798	432	CO223	466	CO1161
25	365	CN65	399	CO79	433	CO222	467	CO1159
	366	CJ305	400	CO71	434	CO209	468	CO1153
	367	CJ316	401	CO7	435	CO205	469	CO1151
	368	CJ317	402	CO69	436	CO204	470	CO1137
	369	CJ336	403	CO66	437	CO20	471	CO1123
30	370	CJ347	404	CO639	438	CO197	472	CO1076
	371	CJ360	405	CO638	439	CO185	473	CO1072
	372	CJ365	406	CO625	440	CO170	474	CO1026
	373	CJ366	407	CO62	441	CO17	475	CO1000
	374	CN483	408	CO602	442	CO163	476	CN755

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	478	CN709	512	CR1186	546	CR641	580	CO474
	479	CO975	513	CR1190	547	CT729	581	CO480
	480	CO990	514	CR329	548	CN922	582	CO500
5	481	CP280	515	CR354	549	CN934	583	CO519
	482	CP283	516	CR377	550	CN951	584	CO522
	483	CP287	517	CR390	551	CN952	585	CO526
	484	CP289	518	CR392	552	CN980	586	CO559
	485	CP294	519	CR422	553	CPIII	587	CO595
10	486	CP304	520	CR423	554	CP147	588	CO605
	487	CP307	21د	CR466	555	CU13	589	CO618
	488	CP311	522	CR477	556	CP251	590	CO629
	489	CP313	523	CR478	557	CP258	591	CO643
	490	CP314	524	CR482	558	CP33	592	CO653
15	491	CP328	525	CR491	559	CP41	593	CO661
	492	CP352	526	CR494	560	CP91	594	CO667
	493	CQ286	527	CR502	561	CP92	595	CO695
	494	CQ294	528	CR506	562	CQ160	596	CO696
	495	CQ304	529	CR513	563	CQ165	597	CO707
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	497	CQ331	531	CR515	565	CQ30	599	CO718
	498	CQ333	532	CR527	566	CR100	600	CO720
	499	CR1116	533	CR529	567	CR178	601	CO722
	500	CR1118	534	CR537	568	CR184	602	CO736
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	502	CR1127	536	CR540	570	CR335	604	CO767
	503	CR1135	537	CR541	571	CR4	605	CP116
	504	CR1141	538	CR545	572	CR61	606	CP151
	505	CR1142	539	CR587	573	CR93	607	CI293
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	507 ⁻	CR1147	541	CR593	575	CO310	609	C1298
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	509	CR1156	543	CR611	577	CO387	611	CU2
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	614	CU39	648	CR726	682	CT738	716	CS524
	615	CU40	649	CR733	683	CT726	717	CS534
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	618	DA155	652	CR839	686	CT702	720	CT143
	619	DA16	653	CR872	687	CT693	721	CT149
	620	DA165	654	CR890	688	СТ677	722	CT156
	621	DA170	655	CR916	689	CT658	723	CT159
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	623	DA223	657	CR930	691	CT636	725	CT188
	624	DA224	658	CR936	692	CT631	726	CT189
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	626	DA227	660	CT747	694	CT611	728	CT193
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	629	DA244	663	CT649	697	CT583	731	CT207
	630	DA246	664	CT624	698	CS224	732	CT220
	631	DA274	665	CT564	699	CS255	733	CT223
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	633	DA490	667	CT864	701	CS271	735	CT227
	634	DA495	668	CT857	702	CS278	736	CT24
	635	DA496	669	CT852	- 703	CS284	737	CT254
	636	DA504	670	CT838	704	CS296	738	CT256
25	637	DA505	671	CT808	705	CS297	739	CT258
	638	DA507	672	CT807	706	CS317	740	CT271
	639	DA516	673	CT797	707	CS319	741	CT275
	640	DA529	674	CT791	708	CS322	742	CT28
	641	DA84	675	CT785	709	CS353	743	CT284
30	642	CR1003	676	CT783	710	CS366	744	CT293
	643	CR1013	677	CT780	711	CS471	745	CO1020
	644	CR1044	678	CT771	712	CS475	746	CO1043
	645	CR1056	679	CT754	713	CS485	747	CO1067
	646	CR1063	680	CT750	714	CS516	748	CO1069

	749	CO1080	783	DB257	817	CW1617	851	CT384
	750	CO1081	784	DB343	818	CW1632	852	CT392
	751	CO1094	785	DB415	819	CW1636	853	CT394
	752	CO956	786	DB53	820	CW1640	854	CT415
5	753	CO973	787	DB85	821	CW169	855	CT421
	754	CJ471	788	CW1000	822	CW172	856	CT423
	755	CJ472	789	CW1038	823	CW173	857	CT434
	756	CJ475	790	CW1087	824	CW175	858	CT440
	757	CJ483	791	CW1100	825	CV123	859	CT443
10	758	CJ484	792	CW1109	826	CV156	860	CT450
	759	CJ485	793	CW1112	827	CV160	861	CT453
	760	CJ486	794	CW115	828	CV192	862	CT457
	761	CJ488	795	CW1150	829	CV203	863	CT466
	762	CJ496	796	CW1155	830	CV215	864	CT474
15	763	CJ497	797	CW1177	831	CV227	865	CT475
	764	CJ498	798	CW1195	832	CV263	866	CT479
	765	CJ507	799	CW1200	·833	CV275	867	CT489
	766	CJ508	800	CW1201	834	CV305	868	CT51
	767	CJ519	801	CW1214	835	CV328	869	CT519
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	769	CJ521	803	CW1230	837	CV394	871	CT526
	770	CJ522	804	CW1233	838	CV410	872	CT536
-	771	CJ534	805	CW1272	839	CV416	873	CT541
	772	CJ536	806	CW1292	840	CV461	874	CT547
25	773	CJ543	807	CW1306	841	CV493	87 5	CT550
	774	CJ544	808	CW1311	842	CV501	876	CT559
	775	CJ547	809	CW1314	843	СТЗ	877	CT562
	776	CK53	810	CW1334	844	CT314	878	DE36
	777	CK7	811	CW1365	845	CT317	879	DE37
30	778	CK70	812	CW1372	846	CT320	880	DE4
	779	CL49	813	CW149	847	CT326	881	DE42
	780	CL63	814	CW152	848	CT340	882	DE63
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	782	DB208	816	CW1611	850	CT358	884	DE83

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	886	DE105	920	CS773	954	CW795	988	DA348
	887	DE110	921	CS776	955	CW802	989	DA373
	888	DE114	922	CW222	956	CW823	990	DA388
5	889	DE117	923	CW224	957	CW835	991	DA389
	890	DE119	924	CW226	958	CZ115	992	DA390
	891	DE91	925	CW232	959	CZ122	993	DA391
	892	DE95	926	CW254	960	CZ186	994	DA414
	893	DE96	927	CW272	961	CZ214	995	DA428
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	895	CW424	929	CW313	963	CZ251	997	DA451
	896	CW457	930	CW314	964	CZ268	998	CW1458
	897	CW485	931	CW347	965	CZ270	999	CW1475
	898	CS383	932	CW354	966	CZ278	1000	CW1481
15	899	CS384	933	CW363	967	CZ291	1001	CW1506
	900	CS399	934	CW374	968	CZ320	1002	CW1510
	901	CS405	935	CW382	969	CZ326	1003	CW1543
	902	CS409	936	CW383	970	CZ362	1004	CW1550
	903	CS431	937	CW386	971	CW1414	1005	CW1552
20	904	CS438	938	CW388	972	CW1440	1006	CZ372
	905	CS454	939	CW512	973	CE209	1007	CZ374
	906	CS588	940	CW517	974	CE216	1008	CW902
	907	CS629	941	CW53	975	CE232	1009	CW922
	908	CS636	942	CW554	976	CE242	1010	CW924
25	909	CS637	943	CW585	977	CF193	1011	CW976
	910	CS638	944	CW618	978	CH776	1012	CW979
	911	CS645	945	CE197	979	CW1381	1013	CW984
	912	CS679	946	CW662	980	CW1389	1014	CW998
	913	CS682	947	CW675	981	CW1399	1015	CZI
30	914	CS734	948	CW691	982	CZ653	1016	CW753
	915	CS743	949	CW707	983	CZ681	1017	CW759
	916	CS752	950	CW735	984	CZ711	1018	CW800
	917	CS756	951	CW762	985	CZ719	1019	CW891
	918	CS765	952	CW768	986	DA306	1020	CW960

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	1023	DF1117	1057	CW1682	1091	DH1213	1125	DF494
	1024	DF1125	1058	DF814	1092	DH190	1126	DF499
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	1026	DF14	1060	DF842	1094	D1207	1128	DF706
	1027	DF163	1061	DG1	1095	DI216	1129	DF713
	1028	DF174	1062	DG17	1096	D1243	1130	DF727
	1029	DF175	1063	DG174	1097	DI248	1131	DF737
10	1030	DF180	1064	DG256	1098	DI261	1132	DF756
	1031	DF185	1065	DG26	1099	DF1005	1133	DF757
	1032	DF201	1066	DG266	1100	DF1009	1134	DF762
	1033	DF202	1067	DG326	1101	DF1010	1135	DF776
	1034	DF203	1068	DG327	1102	DF102	1136	DF777
1 5	1035	DF206	1069	DG329	1103	DF1050	1137	DF780
	1036	DF219	1070	DG330	1104	DF1062	1138	DF783
	1037	DF230	1071	DG331	1105	DF1063	1139	DG12
	1038	DF232	1072	DG44	1106	DF1084	1140	DG121
	1039	DF239	1073	DG65	1107	DF153	1141	DG128
20	1040	DF244	1074	DG69	1108	DF218	1142	DG141
	1041	DF259	1075	DG7	1109	DF251	1143	DG149
	1042	DF266	1076	DG71	1110	DF280	1144	DH28
	1043	DF46	1077	DG76	1111	DF286	1145	DH303
	1044	DF65	1078	DG82	1112	DF316	1146	DH318
25	1045	DF69	1079	DH1086	1113	DF317	1147	DH322
	1046	DB145	1080	DH1098	1114	DF343	1148	DH340
	1047	DB150	1081	DH1135	1115	DF347	1149	DH371
	1048	DB159	1082	DH1145	1116	DF370	1150	DH40
	1049	DB174	1083	DH1153	1117	DF382	1151	DH401
30	1050	DB180	1084	DH1182	1118	DF396	1152	DH432
	1051	CYI	1085	DH1185	1119	DF428	1153	DH451
	1052	CY11	1086	DH1190	1120	DF453	1154	DH496
	1053	CY3	1087	DH1191	1121	DF457	1155	DH502
	1054	CY9	1088	DH1201	1122	DF460	1156	DH529

	1157	DH66	1191	DF915	1225	DH1357	1259	D1501
	1158	DF518	1192	DF948	1226	DH145	1260	D1504
	1159	DF521	1193	DF950	1227	DH999	1261	DKIII
	1160	DF538	1194	DF956	1228	DI160	1262	DK113
5	1161	DF543	1195	DF966	1229	DI386	1263	DK120
	1162	DF545	1196	DF968	1230	D1391	1264	DK122
	1163	DF547	1197	DF971	1231	DI435	1265	DK126
	1164	DF568	1198	DF973	1232	D1448	1266	DK134
	1165	DF587	1199	DF979	1233	DI454	1267	DK136
10	1166	DF589	1200	DF984	1234	DJ109	1268	DK150
	1167	DF591	1201	DF989	1235	DJ146	1269	DK160
	1168	DF601	1202	DH1257	1236	DJ167	1270	DK170
	1169	DF606	1203	DH1308	1237	DF1065	1271	DK182
	1170	DF62	1204	DH1314	1238	DI387	1272	DK185
15	1171	DF620	1205	DI341	1239	D1393	1273	DK197
	1172	DF625	1206	DH1265	1240	D1403	1274	DK206
	1173	DF648	1207	D1349	1241	DI430	1275	DK219
	1174	DF657	1208	DI355	1242	DI438 ·	1276	DK223
	1175	DF659	1209	DI362	1243	DJ2	1277	DK227
20	1176	DF661	1210	D1366	1244	DJ188	1278	DK229
	1177	DF662	1211	DI508	1245	DJ238	1279	DK230
	1178	DF670	1212	DI516	1246	DJ259	1280	DK243
	1179	DF674	1213	D1518	1247	DK64	1281	DK264
	1180	DF682	1214	DF1066	1248	DK70	1282	DK268
25	1181	DF688	1215	DF1069	1249	DK81	1283	DK31
	1182	DF810	1216	DG279	1250	DK84	1284	DK39
	1183	DF823	1217	DH1010	1251	DI462	1285	DK93
	1184	DF835	1218	DH1013	1252	D1466	1286	DL101
	1185	DF860	1219	DH1044	1253	DI474	1287	DL110
30	1186	DF877	1220	DH1045	1254	DI475	1288	DL116
	1187	DF883	1221	DH1073	1255	DI479	1289	DL132
	1188	DF895	1222	DH1078	1256	D1480	1290	DL63
	1189	DF909	1223	DH1340	1257	DI482	1291	DL82
	1190	DF910	1224	DH1349	1258	DI500	1292	DL95

	1293	DL99	1327	DL491	1361	DL547	1395	DO181
	1294	DJ332	1328	DL495	1362	DL550	1396	DO419
	1295	DJ362	1329	DL498	1363	DL551	1397	DO424
	1296	DK290	1330	DL504	1364	DL601	1398	DO440
5	1297	DK321	1331	DM118	1365	DL604	1399	DO447
	1298	DK324	1332	DM122	1366	DL605	1400	DO568
	1299	DK329	1333	DM126	1367	DL607	1401	DO575
	1300	DK357	1334	DM128	1368	DL608	1402	DO589
	1301	DK360	1335	DM130	1369	DL616	1403	DO610
10	1302	DL141	1336	DM147	1370	DL619	1404	DO715
	1303	DL146	1337	DM169	1371	DL620	1405	DO722
	1304	DL162	1338	DM26	1372	DL634	1406	DO737
	1305	DL163	1339	DM404	1373	DM194	-1407	DO742
	1306	DL169	1340	DM406	1374	DM197	1408	DO755
15	1307	DL181	1341	DM407	1375	DM221	1409	DO765
	1308	DL185	1342	DM420	1376	DM248	1410	DO797
	1309	DL218	1343	DM425	1377	DM250	1411	DO836
	1310	DL220	1344	DM435	1378	DM262	1412	DO884
	1311	DL248	1345	DM445	1379	DM265	1413	DO896
20	1312	DL289	1346	DM449	1380	DM272	1414	CZ549
	1313	DL290	1347	DM459	1381	DM278	1415	CZ598
	1314	DL291	1348	DM462	1382	DM293	1416	DT431
	1315	DL316	1349	DM469	1383	DM303	1417	DT443
	1316	DL320	1350	DM482	1384	DM340	1418	DT446
25	1317	DL321	1351	DM6	1385	DM360	1419	DT449
	1318	DL425	1352	DM94	1386	DM365	1420	DT450
	1319	DL426	1353	DJ279	1387	DM522	1421	DT455
	1320	DL427	1354	DJ284	1388	DM533	1422	DT458
	1321	DL439	1355	DJ299	1389	DM542	1423	DN106
30	1322	DL440	1356	DJ319	1390	DM87	1424	DN153
	1323	DL444	1357	DJ323	1391	DN124	1425	DN176
	1324	DL457	1358	DL531	. 1392	DN144	1426	DT530
	1325	DL463	1359	DL535	1393	DN147	1427	DT534
	1326	DL466	1360	DL543	1394	DN167	1428	DT535

	1429	DT544	1463	DWI	1497	BK5
	1430	DT563	1464	DW389	1498	BK504
	1431	DT584	1465	DW398	1499	BK513
	1432	DT590	1466	DW654	1500	BK517
5	1433	DT596	1467	DW659		
	1434	DT597	1468	DW665		
	1435	DT598	1469	DW694		
	1436	DT640	1470	DW705		
	1437	DT655	1471	DW716		
10	1438	DT674	1472	DW749		
	1439	DT719	1473	DW761		
	1440	DT734	1474	DW765		·
	1441	DT779	1475	DW771	٠.	
	1442	DT801	1476	DW78		
15	1443	DT802	1477	DW780		
	1444	DN696	1478	BK10		
	1445	DN697	1479	BKII		
	1446	DN704	1480	BK2		
	1447	DN710	1481	BK368		
20	1448	DN711	1482	BK373		
	1449	DN714	1483	BK374		
	1450	DN721	1484	BK375		
	1451	DN722	1485	BK384		
	1452	DN732	1486	BK402		
25	1453	DN740	1487	BK410		
	1454	DN746	1488	BK415		
	1455	DN 7 47	1489	BK425		
	1456	DN753	1490	BK427		
	1457	DN756	1491	BK436		
30	1458	DN764	1492	BK445		
	1459	DN770	1493	BK455		
	1460	DN772	1494	BK458		
	1461	DN1120	1495	BK494		
	1462	DU372	1496	BK498		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selection "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

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As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplpasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decayalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

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Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions, most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

	Stringenc y Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer	Wash Temperature and Buffer [†]
5	, A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	В	DNA:DNA	< 50	T ₈ *; 1xSSC	T _B *; 1xSSC
	С	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50	T _D *; 1xSSC	T _D *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T _F *; 1xSSC	T _F *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	н	DNA:DNA	< 50	T _H *; 4xSSC	T _H *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	< 50	T ₁ *; 4xSSC	T _J *; 4xSSC
.15	К	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50	T _L *; 2xSSC	T _L *; 2xSSC
	М	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T _N *; 6xSSC	T _N *; 6xSSC
	0	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	DNA:RNA	< 50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T _R *; 4xSSC	T _R *; 4xSSC

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²: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

[†]: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

* T_B - T_R : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m(^{\circ}C) = 2(\# \text{ of } A + T \text{ bases}) + 4(\# \text{ of } G + C \text{ bases})$. For hybrids between 18 and 49 base pairs in length, $T_m(^{\circ}C) = 81.5 + 16.6(\log [\text{Na}^+]) + 0.41(\%G+C) - (600/\text{N})$, where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

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sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

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Sepharose[®]; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

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USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as porbes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise antiprotein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

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Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ, Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

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A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

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Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

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Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term-relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigenpulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

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In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brurswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

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Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

25 <u>Hematopoiesis Regulating Activity</u>

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A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

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example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

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A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-liketissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-liketissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

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plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

15 Activin/Inhibin Activity

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A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663. 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

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A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 Receptor/Ligand Activity

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A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusioninjury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

20 Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

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Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

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ADMINISTRATION AND DOSING

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A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

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can directly signal T cells. Alternatively antibodies able to bind surface immunolgobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

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When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about $0.01~\mu g$ to about 100~mg (preferably about 0.1~ng to about 10~mg, more preferably about $0.1~\mu g$ to about 1~mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

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Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem. Soc. 85, 2149-2154 (1963); J.L. Krstenansky, et al., FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

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pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses(including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorbtion of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

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The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

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Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
ΑI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
ΑZ	Human	Colon	Caco-2 Adenocarcinoma
В	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1 or 2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
ВО	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1or2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	PeripheralBloodMononuclearCell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CI	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	SalivaryGland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	PeripheralBloodMononuclearCell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ DJ	Human	Placenta	26yrs., 1 specimen
DK DK	Human	Fetal Kidney2	Fetal Kidney
את	Fiuilian	1 Ctal Ridney2	1 otta 1210110)

DI	**	n :	27/4
DL	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61 yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE ·	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human	Lung CA	Adult Lung CA
FK	Human	Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX		Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
H	Human	Blood	PeripheralBloodMononuclearCell
11	Huillali	Dioor	i cripheralibioodivionondereal Cen

НА	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
НН	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
НО	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
ΙA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID	Human	Muscle	N/A
ΙE	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61 yrs., pool of 11
ΙΗ	Human	Muscle	N/A
П	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IP	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
Π	Human	Brain Thalamu	Adult Brain Thalamus

SEQUENCE LISTING

(1)	GENERAL	INFORMATION:
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(i) APPLICANT: Jacobs, Kenneth McCoy, John LaVallie, Edward Racie, Lisa Merberg, David Treacy, Maurice Spaulding, Vikki

Agostino, Michael
(ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS

- (iii) NUMBER OF SEQUENCES: 1500
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy Disk
 - (B) COMPUTER: IBM PC Compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
 - (B) TELEFAX: (617) 876-5851
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCC TTCATGGCCT AAGTGTTTAA ATTATAAGCT GGTGAAGTGA AATAACACAA
ATCAAGCTCA CCAATTTTAA TACTCAGCTG TTGATAAACA ACACTGAAGA GTGACATTTA
AAGTAGCATT AAGTAGCATT TGAATGACTT CCAAAAGGCT
GATCATAAAA ATCACTTCAA TCATTTCAA ATTTTACTTT AGCAGCAATG AAGTTATTTG
240

CAACCTGGGA AAACCTCGAG

GTATGACTCA GATGAACCTT CTGCTCTGTC TTGGAGTTAT TATGGTCATT TCATTTTCTG

300

320

(2) INFORMATION FOR SEQ ID NO:2:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 357 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
GAATTCGGCC TTCATGGCCT ACGAGTGGAT CTGGTTGAGA GGAAAGCAGC TAAAAATACA GGAGATGAAA GGGATCATAA CGAACATAAT GAACCATGTT CATTATGGTT CGTGGGGAGG CAGGAAAGCA CAGTATCCAG GGCATAGGCA GAAGAGCTGT CTTTCACGGG AGGAGGGAA CATATTCTAC TGCAATAAGC AAGGGCGGGG TAAGTACGGA TCGGGTACTT TGGGAACTAT GACGGTAGGG AGTTCAGGAA GTTGCTGCCT GAAGGCATAA AGGTTTTTTT TTTTTTTTTT	60 120 180 240 300 357
-	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 249 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
GAATTCTTTA TATAATTTGG ATACCTACTC ATTGTCAGTT GTATGCTTTG CAAATATCTT TCCTGACCCT TACTTACCTT TTCACTCTTA ATGGTATCTT TGATGAATCA AAAATTTTTC TTTTTTTGTT GTTTTTTGAG ACAGAGTCTT AACTCTGTCA CCCAGGCTGG AGTGCAGTGC	60 120 180 240 249
(2) INFORMATION FOR SEQ ID NO:4:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 262 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
GAATTCGGCC TTCATGGCCT AGACCTGCCT CTAGCTCCTT TCCTTCTACT CTCCTGCTCA GACCATTAGT AGGTACTTTG TTAAATAAAA AACTAGATTA ACATCAATAT TACTCCAATT TGGTATCTTT TACACTATGT ATTATACCTA CTTTCTTTTT ATTTCATTTA CAAATAGTTT AAATTACTTT ATCAACCAGC TGTATTGTTT CCCTCTTGTA AAAGTACCAT CAAGTGGGGA AAATGTATGT GGCAGTCTCG AG	60 120 180 240 262
(2) INFORMATION FOR SEQ ID NO:5:	
00	

(A) LENGTH: 250 base pairs

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
AAATTCGGCC TTCATGGCCT AATAACTTAC CCAGTCACGA ATATTTCTTC ATAGCAGCAT CAGAGTGGAC TAATACGATT ATAATTATCA TCACCTTTTG ACTGACCAAT TGATTTACAG CATTGAGTTC AATCTGTTTT TTTAAAAAAAT ATCTTCTAAA TATCAGGTGC TGTATTAGAT CTGGGGTACA AAAATGTATT TTCATTTACT CACTAATTTA CTTAAAAATT ATTTATTGAG CTACCTCGAG	60 120 180 240 250
2) INFORMATION FOR SEQ ID NO:6:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
GAATTCGGCC TTCATGGCCT AGGTGCTGGA AGTAAGCTGT GTGAACAAAT GAGACGATTC CCCTTTCTAA TGAGTTTATA TGCAATGTGG TATCTTTACC GATACATGCT CTGTCAGAAA GAAGCAGCCC ACTTCTGTCC AATAGCCAAT CCGGCTTCAG GAGCAGCAGG AGAGGCTTCG GGAACGGGAG AAGAGGCTTC AGCAGCTGC CGAGCCACAG AGCGACTTGG AGGAGCTGCA CCGAGAACAAG AGCGCACTGC AGTTGGAGAG CTCGAG	60 120 180 240 276
(2) INFORMATION FOR SEQ ID NO:7:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 284 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
GAATTCGGCC TTCATGGCCT ACTCATTCCA AAATAAAAAA AAAAATTTCC CATGATCTTA TCTAGCTTCT CTAGCAGTAC TTGTATGATT TCACCTTTCT TTCTTTATTC TTTTCTTCCA TATTTTTTTT TTTTGAGACA GGGTCTCACT CTATTGTCCA GGCTAGAGTG CAGTAGTTTG ATCATGACTC ACTCTAACCT GGACCTCCGG GGCCTAAGTA ATCTTCCCAC CTCAGCCTCT CAAGTAGCTG GGACTACAGG GATGTACCAC CATGCCTGGC TAAG	60 120 180 240 284
(2) INFORMATION FOR SEQ ID NO:8:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 394 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTGAATTCT	AGACCTGCCT	CGAGGACGCC	AGGGAAGTGA	GTTGAAAATC	TGAAAATGCG	60
GCCATGGACT	${\tt GGTTCCTGGC}$	GTTGGATTAT	GCTCATTCTT	TTTGCCTGGG	GGACCTTGCT	120
GTTTTATATA	${\tt GGTGGTCACT}$	TGGTACGAGA	TAATGACCAT	CCTGATCACT	CTAGCCGAGA	180
ACTGTCCAAG	ATTCTGGCAA	AGCTTGAACG	CTTAAAACAG	CAGAATGAAG	ACTTGAGGCG	240
AATGGCCGAA	TCTCTCCGGA	TACCAGAAGG	CCCTATTGAT	CAGGGGCCAG	CTATAGGAAG	300
AGTGCGCGTT	TTAGAAGAGC	AGCTTGTTAA	GGCCAAAGAA	CAGATTGAAA	ATTACAAGAA	360
ACAGACCAGA	AATGGTCTGG	GGAAGGATCT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGTGATGA	AAATGCTTTA	TGCTTCAACA	CTGTTGGAGG	ACACAACTGT	GTTTGCAAGC	60
CGGGCTATAC	AGGGAATGGA	ACGACATGCA	AAGCATTTTG	CAAAGATGGC	TGTAGGAATG	120
GAGGAGCCTG	TATTGCCGCT	AATGTGTGTG	CCTGCCCACA	AGGCTTCACT	GGACCCAGCT	180
GTGAAACGGA	CATTGATGAA	TGCTCTGATG	GTTTTGTTCA	ATGTGACAGT	CGTGCTAATT	240
GCATTAACCT	GCCTGGATGG	TACCACTGTG	AGTGCAGAGA	TGGCTACCAT	GACAATGGGA	300
TGTTTTCACC	AAGTGGAGAA	TCGTGTGAAG	ATATTGATGA	GTGTGGGACC	ACTCGAG	357

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCGGCC	TTCATGGCCT	ATTTCCGATC	TATGTATCTG	TACTCATACA	GCCTCATCGG	60
GCTAAACAGC	CTTCTTTTCA	GAACAGTAGA	TCACTCAACT	GGGTTTTCAA	GTGACTGTTT	120
ACCTTTCAAG	GCTGGCTTTA	TAGGTCTTGC	CTCACTGTAT	CCAGCAATCC	AAACTTTACC	180
CTATCCCAGT	CAGGACTGCA	CACCTCATAT	TGAAAGACAT	ACCTTAGAAC	CAGACTCCCC	240
AAACCTTACA	AATATCCCAC	CCTTGACTCC	CGTTCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCTAGA	CCTGCCTCGA	GCGCCACACA	GTGACTGCCG	GGTAAAGTTG	TGGAATTACG	60
TCCCTGGACT	CACCCCCTGC	CTTCCTCGCC	GAGTCCTGGC	CATAAAGGGC	CGCGCCACCA	120
CCCTGCCCTG	ACCCTCCCCA	ACTCTCCCTG	TCTCCTCTTT	CATTCTTCCC	CTCTTTCCTT	180
TTCCCTCTCT	TTCCCCACTT	CGATATGAGC	TGCTTCTTAA	CGGTATGAGA	TTATTTNACT	240
CCTTCTTCTT	CCTTTCCCTT	CCTGTCCTGC	CTGGCCTAGA	GAGGTGCCCT	GCCTGTCCCT	300
CCTGCACCCA	CCGTCCTTTT	CCAAGCATGA	ACAGTGGGAC	AGGCCCCAGG	AGATGGGTGC	360
CAGGGAGCAG	AAGGGGGAGC	CTTCAGGCCT	GGACAAAACG	AAACACCCCC	CCAAAAAAAG	420
NAAACCCACG	ACTCGAG					437

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTTCTTCTA AGT	AGATETT CETTECECAT	TAAACTAGGT	TTTCTACTGC	AAGATATTTT	60
GTGCATTGCT GTT	TTAAACC CTTTTAACAC	CGAATCATAG	CAGTCTAAGA	AGTCTTCTGA	120
ACCATCCTGG ACT	CTTGGTG TGATTTTAA	TTGTGTCTAC	AAGTTCTCTG	ACATTCTTCC	180
CACCAAGAGG TAG	AGTCTGT TTCCCCTCC	TTTGAACCTA	GGTAGGCCTT	TGTTACTGCC	240
TTGATGAATA CAA	TGAGACT CGAG				264

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATTTTTTAC	CCAAAGCTCT	GGAATTGTAC	ATTTATTTT	TAAAACTCAA	AGAGGGAAAG	60
AGCCTTGTAT	CATATGTGAA	CATTGTATCA	TAGGTAATGT	TGTACAGACC	CTTTTATACA	120
GTGATCTGTC	TTGTTCCTGC	AGCAAAAATC	CTCTATGGAC	ATAGGAGGTG	CTGTGTCCCA	180
TGCCCTCTTG	CCCTGACAGT	GTCCCATGGG	CCCCCTTCTG	CTCCCTGCCC	CCTCCCTGCT	240
ACTGCTGATG	CACTCCCCCC	CCTCGAG				267

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCGGCC	TTCATGGCCT	ATTTTTTATT	TGTTTTGTTT	TGTTTTGTGG	GGATGGGGTT	60
TTGCCGTGTT	GCCCAGGCTG	GTTTCGAATT	TTTGGGCTTA	TGCAATCCAC	CCACCTTGGC	120
CTCCCAAAGT	GCAGGGATTA	CAGGCATGAG	CCATCTTGCT	GGGCCACCTT	TTTCTTCTCT	180
TTTAACAAAT	TCAGCAATTT	TTCAGTCCCA	GAAATCTGTA	AATACATTTT	TTGTGGAAAA	240
ATACAATGGG	AATGGCATCA	AAAGATGGTT	TCTATTAGGA	ATGGGAACAG	GTAACAGTTT	300
TCCCTGCCAC	CTCAACAATC	TCGAG				329

- (2) INFORMATION FOR SEQ ID NO:15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGCTGGCAG	GCGGGCCAAA	GGTAATGAAG	CAAAGAGAGA	GGGAAAAGAC	GTGTGAAAAT	60
${\tt TGCAGAGGGG}$	${\tt GTGACCGAGG}$	GAAACACGTG	AGCGTGATAA	TGACAGAAAA	ACCACGGAAG	120
GAGCAAACCT	${\tt GGGCAGGGGG}$	TGGGAAACCC	${\tt GGGCCGTTTC}$	CAGGGAGCAC	AGGCAGACTC	180
AGAGGTAACA	CTCAAAAGCA	ACAACAGAAG	CAAGGAGGAA	GTGGGAAAAT	ATTTTTAATG	240
TGCTACAACG	AAACAGCTGC	CTGAATTCTA	TATACCCTCT	GAAAATAATC	TGCACATAAA	300
ATGGGAAAGC	TTCACCGCAG	CAGACCCCAC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCC	TTCATGGCCT	ATGCTTCTTC	CACGCACCAC	CACCACCACC	ACCACCATCA	60
TGGCCATAGC	CACGGTGGCC	TGGGGGTGCT	${\tt GCCTGATGGG}$	CAGTCCAAGC	TCCAGGCCCT	120
GCATGCCCAG	TATTGCCAAG	GACCGGGCCC	TGCCCCGCCA	CCCTACCTCC	CACCCCAGCA	180
GCCCTCTCTT	CCCCCACCTC	CCCAGCAGCC	CCCACCCTTG	CCCCACCTGG	GCTCCATTCC	240
ACCGCCTCCC	GCCTCAGCCC	CACCTGTGGG	GCCACATCGC	CACTTCCACG	CCCATGGCCC	300
AGTCCCAGGG	CCCCAACACT	ATACCTTGGG	CCGGCCAGGC	AGGGCACCCA	GACGGGGGC	360
TGGAGGACAC	CCTCAGTTTG	CTCCACATGG	CCGCCACCCC	CTGCACCAGC	CCACATCCCC	420
ACTGCCCCTG	TACAGTCCTG	CCCCCAGCA	CCCTCCAGCC	CACAAACAGG	GCCCTAAGCA	480
CTTCATCTTC	AGCCACCACC	CATCTCGAG				509

- (2) INFORMATION FOR SEQ ID NO:17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCC TTCATGGCCT AAAGATGGCG GAGAACAGCG GTCGCGCCGG CAAGAGCAGC	60
GGGAGCGGCG CGGGGAAGGG GGCGGTGTCC GCAGAGCAGG TGATTGCTGG CTTCAACCGC	120
CTTCGGCAGG AACAGCGAGG CCTGGCATCC AAAGCAGCTG AGTTGGAGAT GGAGTTGAAT	180
GAGCACAGCC TAGTGATCGA TACACTGAAG GAGGTAGATG AAACTCGTAA GTGCTACCGC	240
ATGGTTGGAG GAGTGCTGGT GGAGCGAACT GTCAAAGAGG TGCTGCCCGC TTTGGAGAAC	300
AACAAGGAGC AGATACAGAA GATCATTGAG ACACTGACAC AAGCAACTCG AG	352
(2) INFORMATION FOR SEQ ID NO:18:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 207 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
GAATTCGGCC AAAGAGGCCT AGCTAGGTTC TGAAGCTTCT GAGTTCTGCA GCCTCACCTC	60
TGAGAAAACC TCTTTGCCAC CAATACCATG AAGCTCTGCG TGACTGTCCT GTCTCTCCTC	120
GTGCTAGTAG CTGCCTTCTG CTCTCTAGCA CTCTCAGCAC CAATGGGCTC AGTCCCCCCC	180
CCCGTACACG CCTCGAGGCA GGTCGAG	207
(2) INFORMATION FOR SEQ ID NO:19:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 306 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
GAATTCGGCC TTCATGGCCT AGGCGGGACT AACACAGGGT TGTCATCTTT TCCTTTTGCC AAGAAAGAAC ATTAAAATGT ACTACCAGCA TCTGCCATCA CTAGCATTTC ATAAAAAGAG	60 120
GTTCTGTTAG CAACAGAGTA GAAACTGTAG GAAAGCATCT CAGAACAAA CTAAGTTGAA	180
TAAATTCACC TAATAAAAAT GCCTTGGTCT AGGATTCCTT TTCTTCATCA AAAGCTGCAA	240
GAGAAAGCCA CTGCTTACCT GATGCCGATT TACTGGTCAT TGGGGTGGGC AGGTTTGGTT	300
CTCGAG	306
(2) INFORMATION FOR SEQ ID NO:20:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 374 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
GGTCTCACTT GTCTCATCCT GTCGCCCAGG CTGGAATGCA GTGGTATGAT CTCAGCTCAC	60
TGCAACCTCA GCCTCCTGGG TTCAAGTGAT TATCCTGCCT CAGCCTCCAA GTANCTGGGA	120
CTATAAGCAC ACATCACCAC ACCCAGCCAA TTTTTTTGAA TTTTTAATAG GGTTTCACTA	180
TGTTGGCCAG GCTGGTTGAA CTCCTATCCT CAAGCGATCC ACCCACCTCG GCCTCCCGAA	240

	TACCTGAGCC ACCGTGCCCA GCCCATTTCA CAGTACTTTT TATTTAACCC GGGCACCATG CAATATACAG CTATTTCATT TTCCTTTTGT CTCTGTTTCT CGAG	300 360 374
(2) INFORMA	ATION FOR SEQ ID NO:21:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 306 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:21:	
AGAAGAGGTA GTCCTTCACA CAAAATTACT	GAATTCGAAA TATTGGCATA TGGTTCTTTT GGATTAGATT ATATAAAATC GAACCAGGCC CCAAGCACTC CTTTTTCTCT GCATGATACT TCTGCTTATT CTAGCTACAT GATTTATAGT CTTGCTCCCC AATATGTTAT GTATGGAAGC TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCTT AGAGATGTGA TGCAGAAGCT CCTGAAGATC AGTGTACTGT TACCCGGACG	60 120 180 240 300 306
(2) INFORM	ATION FOR SEQ ID NO:22:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 340 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:22:	
AGGTCTGGAT GTTGGAACTG AATGAAGTTA GCAGCTGGAA	ACAAAACAGG ATACCAAAGT TGAGCTGGAG ACTTACAAGC AAACTCGGCA GAAATGTACA GTGATGTGTG GAAGCAGCTA AAAGAGGAGA AGAAAGTCCG GAAAAAGAAC TGGAGTTACA AATTGGAATG AAAACCGAAA TGGAAATTGC CTGGAAAAGG ACACCACGA GAAGCAGGAC ACACTAGTTG CCCTCCGCCA GAAGTCAAAG CGATTAATTT ACAGATGTTT CACAAAGCTC AGAATGCAGA CAGCAGAAAGA ATGAAGCCAT CACGCTCGAG	60 120 180 240 300 340
(2) INFORM	ATION FOR SEQ ID NO:23:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
ATACCCAGCA	AAAGAGGCCT AGATTTTAAA TTTGTTTGAT ACCTGCTGTG TATTCCTTGC CATTGTTGCC CATATTGTTG ACATGTAGTA TGTATTTATT ACAATTATAT ATGTATCTTA TTTTTTTCAT GTATAGCATG TACAGTCACA CTCGAG	60 120 176
(2) INFORM	ATION FOR SEQ ID NO:24:	

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 414 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
GAATTCGGCC AAAGAGGCCT ATTCTTTGTC TTTTGCACAT GTTCTTTGAG TCTTAGTATC	60
TGTAACGTGG CGCTACTCTC TCTATCATGG GGGGGCATGT TTTGACATTA AATTGACTTT	120
TAAGAAAAC ATGTCACTAA CCTGAAGCTC AGCCACACA TGACTTTTAA GGTTTTATTT	180
AGACTITACT GITGITCICA TGAGAGTAGG TACAGACTGC ATAAGGITTA GAATCCCAGC	240
ATATGTCTGA AACGACGGGA CTTTCACTGT GATTTCCACC AGAGAAATTA TAGCAGAGTG	300
GCTGAGCATG TGCTCTGAGG CCAGGCCCCA GCTCTGCTGC TGACGAGCTG TGTGGTCCTG	360
GGCAGAGTGG TCTCCGAGTT CCAGTCCCTC CTCTGTAAAA TGGGCTTACT CGAG	414
(2) INFORMATION FOR SEQ ID NO:25:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 497 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
CARTERCOCCO ARRONGOT ARRONGATA COMROMANA CHOMOTERA TOTOTORACA	60
GAATTCGGCC AAAGAGGCCT AAACATATAC CTAGTCTATA CTCTCTTA TCTCTGAACA CTTTTCATCT GGAGCTATTA ATGCCCTCTA GCCTTTATTA TAATTATCAC ATATAATTAT	120
GCCTTTCTC CTCAAAATTA TCTGTTGGAG TCATCTTATA GTAGAGTCTT TACAGAACAC	180
AAAGCATTCA ATCACTTTAT TTCAGACACC AACCTTGTTT TTGATGAACA TATGTTAGTC	240
TTAAGCCATC TAAAGTAATG CTAATGTGGG ATCTTATGGA AGACTACTGG TAATACAGGA	300
AAAAAAGTGG CAAAGAAATC TGACACGTTT GGCAATTATT CCTGAGGCTC TGACCTCTCA	360
ATTGTTGAGT GTTGGAGGTC ACAGTAAACA AACCATATAA AGATCATGTT GAAAGTCAAC	420
ATTATTAATA TACCATACTT GAAGGATATG TGGTTATTGT CTCACGTGTC CATGTGAAGA	480
GACCACCGTC CCTCGAG	497
(2) INFORMATION FOR SEQ ID NO:26:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 111 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
GAATTCGGCC AAAGAGGCCT AGTTTTTGAT GAATTTGTGT TATTTACTTA TAACTAGAGT	60
TTGAATGTTT ATTGGGAAAA CTTAATCATG ATCATCTACT GGTGGCTCGA G	111
(2) INFORMATION FOR SEQ ID NO:27:	

- (A) LENGTH: 311 base pairs

(i) SEQUENCE CHARACTERISTICS:

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAATTCGGCC	AAAGAGGCCT	ATGCAATTCT	GACCAGGAAG	CTCCTCTTTA	ATTGGAAATT	60
CTTAGAAAGG	TATGGAGCAA	AGGAGATCCC	AGCAAACATT	CCGGCATCTA	CTGCTCTTGG	120
GTTTTTTCTG	TGTTGGTTTT	TTTTGTTTTG	TTTTGTTTAT	GAGATGGAGT	CTCACTCTGT	180
CGCCCAGGCT	GGAGTGCAGT	GGCGCAATCT	CAGCTCACTG	CAATCTCCAC	CTCCAGAGTT	240
CAAGTGAATA	TCCTGCCTCA	GCCTCTCAAA	CAGCTGGAAT	TACAGGTATA	CACCACCACA	300
CCGAGCTCGA	G					311

- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 597 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCGGCC AAAGAGGCCT	AAGTGCAGTG	GTGCGATTAT	AGC1 CACTGT	AGCCTCAGAA	60
TCCTGGGCTC AAGCTGTCCT	CCCACTTAGC	CTCCCAAAGT	GCTGGGACTA	CAGGCGTGTG	120
CCACGGGGCC CAGCCATTTT	TTCGAATATT	TTCAATCTGC	AGTTGTTTGA	ATCCACAGAT	180
GCAGAACCCA TTTCTAATGG	AGGGCTGACT	ATACCTTTCT	GATGACCTAA	ATATTTGTGT	240
CCACTATTGG GACACTCCTT	TCTTAGTGTC	AAGGTTTGTG	AGAAATTGAG	GGCTGTTTGA	300
TGGGCAAAGA TTTATTTATT	TATTTACTGG	CTTATCTACA	ATTGAGACAG	GGTCTCACTA	360
TGTTTCTCAG GCTAGTTCTA	ACTCCTGGGC	TGAAGCAGTC	CTCCCATCTC	AGCCTCCCAG	420
AGTGCTGGGA TTACAGGTGT	GACACACCAT	ACCCGGCAGA	GCAAAGAGTT	AAGAGTACAA	480
GACATTTGAT CATCTTGAGG	AGTATTTACT	TCAGACTGAA	ACACCACATG	AAATTCTAGA	540
GTCCAACAGA AAGTGTAATA	ATTTTTTGCT	TTTCCCTTCT	TCCGCTACAT	CCTCGAG	597

- (2) INFORMATION FOR SEQ ID NO:29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTCGGCC	AAAGAGGCCT	AATTCTAGAC	ATGCTCAGCT	TTGTGGATAC	GCGGACTTTG	60
TTGCTGCTTG	CAGTAACCTT	ATGCCTAGCA	ACATGCCAAT	CTTTACAAGA	GGAAACTGTA	120
AGAAAGGGCC	CAGCCGGAGA	TAGAGGACCA	CGTGGAGAAA	GGGGTCCACC	AGGCCCCCCA	180
GGCAGAGATG	GTGAAGATGG	TCCCACAGGC	CCTCCTGGTC	CACCTGGTCC	TCCTGGCCCC	240
CTGGTCTCGG	TGGGAACTTT	GCTGCTCAGT	ATGATGGAAA	AGGAGTTGGA	CTTGGCCCTG	300
GACCAATGGG	CTTAATGGGA	CCTAGAGGCC	CACCTGGTGC	AGCTGGAGCC	CCAGGCCCTC	360
AAGGTTTCCA	AGGACCTGCT	GGTGAGCCTG	GTGAACCTGG	TCAAACTGGT	CCTGCAGGTG	420
GTCGTGGTCC	AGCTGGCCCT	CCTGGCAAGG	CTGGTGAAGA	TGGTCACCCT	GGAAAACCCG	480
GACGACCTGG	TGAGAGAGGC	CTCGAG				506

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 324 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
GAATTCGGCC AAAGAGGCCT AGTCTGTGGT CATTTTCAAC TCTCATTTAT AGGATTCTAA AAGGGCACTA CATTACTCCA CTCCCTTATC TAAAATAAAT TTAAAATTCA TCGGAATTTG ICCAGTCCTC CATCACTGGA AAATGTACAG ATTCCTTCTC TGGAAATATC TAAAGAAAAG IACAGCTAAT GTTCCCCCAT TTCGTGTTGT TTTGTTGCTG CTTTAACTAT GAACTCATCT GGCCGGGCGC AGTGACCAAG CCGCCGGGAG CTGGGGAAGA ACGCACCGGG GCGCCGACTG GGCCAGGAGA CCAGAACACT CGAG	60 120 180 240 300 324
(2) INFORMATION FOR SEQ ID NO:31:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 245 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
GAATTCGGCC AAAGAGGCCT AGGAGCAGAT TCCTCATGGT GCTTGTTTAT TATATATATT IAATCCTGCT TGACACTTTA CCCAAGGGAG ATGGTCCCTT TTATCAGTTG AATGTTAGCA GCGTTATTTC AGAGTGTGGT GACTGGTTAG AGAAACTCAT GTACTCAACC AGCCACAGTT TCAAACAAAA TTTTTATGTG CAAAGGACAG CAACCTTCTT GTATGTTAAA CCACCAGTAC TCGAG	60 120 180 240
(2) INFORMATION FOR SEQ ID NO:32:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
GAATTCGGCC AAAGAGGCCT AGGTGCTTTG GTTTTTGCTT TTTTAGTCAT CCCCATGAGA ATAATAAACT CCATGAGGC AGCAACTTGG CTGGCCTGTG TGCCAGTGCT GGGGACATCA CTGAGAAATG AAGGCCCATT TGGCAGGCTA TTTTTGAGCA AGATTCCTGA GGCCCAATCG TTGGGTGATG AGATGGACCC GAGGTATTTC ACTCCAGCTC TCGAG	60 120 180 225
(2) INFORMATION FOR SEQ ID NO:33:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 447 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: .double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: GCCAAAGAGG CCTAGAGAGC TCTGGGGGGC AACCTGGAGG TCTGAAAAGA GGAGCCAGAG 60 AAGGTGGTAC CAGGCTTCCT GGTCAGAACC GGCCTGGAGC TCCTTCCCTT CCCCCTGGCC 120 TGAGAGGTTG CTTTTAAGTC TTCCACCCCT TGTTCCATCT GCCTGCCAAC CCATCGGAAA 180 GGAATCCACA TCATATTGGA GATGACCCCA TCAACCCCAG GGCTCCAGCA CTACCAAGTT 240 GGAATTCCAC GCCCGGGAGT GGGGTAGAGG AAGACGAGAC AGGACGAGGC AGAAAAGCAC 300 ATTTTAAAAA CCAGACAAGA TGGCTAGGCC ATCACCAACC AACGGACTTA CCTTACATTT 360 TTGTAGGTAA TTCCCCCCAA ATCTTGATTT TTTTTTTCCT CAATTATCCT TTAAAAAATA 420 AGAAAACACA TTCCAAACCC ACTCGAG 447 (2) INFORMATION FOR SEQ ID NO:34: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 402 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34: GCGATTGAAT TCTAGACCAT GCCTGCTCTG GGCCCAGCTC TTCTCCAGGC TCTCTGGGCC 60 GGGTGGGTCC TCACCCTCCA GCCCCTTCCA CCAACTGCAT TCACTCCCAA TGGCACGTAT 120 CTGCAGCACC TGGCAAGGGA CCCCACCTCA GGCACCCTCT ACCTGGGGGC TACCAACTTC 180 CTGTTCCAGC TGAGCCCTGG GCTGCAGCTG GAGGCCACAG TGTCCACCGG CCCTGTGCTA 240 GACAGCAGGG ACTGCCTGCC ACCTGTGATG CCTGATGAGT GCCCCCAGGC CCAGCCTACC 300 AACAACCCGA ATCAGCTGCT CCTGGTGAGC CCAGGGGCCCC TGGTGGTATG CGGGAGCGTG 360 CACCAGGGG TCTGTGAACA GCGGCGCCTG GGGCAGCTCG AG 402 (2) INFORMATION FOR SEQ ID NO:35: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 307 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35: GAATTCGGCC AAAGAGGCCT AGTGGAAGAT TTGGGTACTG TCTTTAATAA ATCAATCAAT 60 CGACTCTTAT TTCAAGGAGA AAGTTCTATG TTATATGTTG AAGGTGAACA GATCATATTT 120 AGAGGATATA ACAATTAGAA ATCTAGAAAA TAATTATCAC TTTTATAAAA TTTTTAGTCA 180 ACTGTACAAA TAATTACATA AAACATCAAT TAATTATGCT TAAAAATCAC TAATGTTCAT 240 AATATATAAT CACTATTTGT AATCAAAAGT TTAATTTTAT GCCAAAAAAT AAAAAATGCT 300 TACTCGA

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 324 base pairs

307

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCC	AAAGAGGCCT	ACTTCCATAA	CCGTGCTTTT	GACGTTAAAA	ATTTTAAATT	60
CAGCCTTTTG	GAGAACACTA	AGTATCTTAG	TGTGTTTTTA	CTTACTATAA	TAATATTATT	120
GACCTAGTGT	AATATTACTG	CCATATGGAC	CTCAAGGGTA	CTTTTCTGAT	AAATTTCTGT	180
TATGGTTTCA	TAATTAAACA	AAAGGATAAT	ATACAGAGTT	GTGGAGTTTT	TTTGGTTTTG	240
TTTTGTTTTG	AGATAGCCTG	GGCAACGAGT	GAAACTCTGT	CACACACACA	CACACACACA	300
CACAGACACA	CACCAAATCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCGGCT	TCATGGCCTA	CAAGAAGATG	AAGAAGATTG	TGGATGCCGT	GATCAAGTAC	60
AAGGACAGCA	GTGGACGTCA	GCTCAGCGAG	GTCTTCATCC	AGCTGCCCTC	GCGAAAGGAG	120
CTGCCCGAGT	ACTACGAGCT	CATCCGCAAG	CCCGTGGACT	TCAAGAAGAT	AAAGGAGCGC	180
ATTCGCAACC	ACAAGTACCG	CAGCCTCAAC	GACCTAGAGA	AGGACGTCAT	GCTCCTGTGC	240
CAGAACGCAC	AGACCTTCAA	CCTGGAGGGC	TCCCTGATCT	ATGAAGACTC	CATCGTCTTG	300
CAGTCGGTCT	TCACCAGCGT	GCGGCAGAAA	ATCGAGAAGG	AGGATGACAG	TGAAGGCGAG	360
GAGAGTGAGG	AGGAGGAAGA	GGGCGAGGAG	GAAGGCTCCG	AATCCGAATC	TCGGTCCAGT	420
CTCGAG						426

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCGGCC	TTCATGGCCA	ACACATAATC	CACGCTCATC	TTGCAAAGCG	CTATTTCAGG	60
CACATCATTG	GAATACAGGA	AGTAGCCCTG	CACCTGCCAG	TGAGCTCGCC	ATTCACTGAT	120
TGGAAGAGTG	ACCTGGCATC	TTGGAAATCA	TTGTGTGTCT	TCAGGAGAAT	GTGCAGTGTC	180
TTGTAACAAC	TAATTATAAT	GCAAATTAGG	GCTACATTGT	AATCTGCTTT	GTTAATGAAA	240
ATGATAAAAC	AGAATATTGA	CAAGCTAGGA	CACCTGTGGT	ATCTTTAATT	GTATCTCCTT	300
CAGAAGTTTG	CTTCTTATGG	TATAATAAAG	TATGGAAGAA	TATTGAGTAT	ATGTTTACTC	360
TGGGCCTGGG	AGAACTTAAC	TTTCTAGAGC	AGTTTGTTGA	CTTGTGTGCA	ATGGGGAGAG	420
GTACCATGAT	GACACTCACA	GGGAGCCACT	GTTCACTGAC	ACTTGGAAGG	CCCTGCCTCG	480
AG	•					482

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTGTTTGCCC	ACACCCTCCT	TGAATTTAAC	TGCCACAATC	TATCCGCAGA	TGTGTTTTGT	60
TCTGTTTCTT	${\tt GTTTTTCACT}$	AGCGTTTGCG	TTGCTTCCTC	TGAAGCCAGA	GGGTGAAAGG	120
CCCTAGCAAA	${\tt GTTAGTTATC}$	AGTCAACTGA	TGATAACTGT	GATCCTTAAA	GATGAATTCC	180
CAGCCTGAGG	TGACACACAG	AGGTTCAGCA	GACGTCTCAG	GATCTGTCAC	ATGTCATGTT	240
GCTTGGTGTG	AAGATGGAAG	AACAAAGTCC	ACATCAGTTT	CTGCTCCTTC	AAACAGTGTG	300
TCGATATGAA	ACATTGAGAT	TTGGCAGAAA	CATGTGCCTA	GTTTGCAGCA	CCAAATACTC	360
GAG						363

- (2) INFORMATION FOR SEQ ID NO:40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAATTCGGCC	TTCATGGCCT	AAAGGGATAT	TCACTCAAAT	CCCTAAGTAT	TTCAGAAACA	60
GCCTGAGAGC	AAGTCCTTGG	CTTCGCTTTC	TAGTTTTAAA	AGGCTTTTAA	CTGTTTAGTC	120
TGAGATTCCC	CTAAAAGTTC	CAGGAAAGCA	AACTCAAAAA	GAGCCTAGGT	GGTCAATCAT	180
TATTTTTGCT	GCGTTTATAT	AAATAATCAG	GCCAAGTTAA	TGAGACTAAA	CTTATTTTGC	240
AAGCAAATCA	GTCTTTGCTT	ATTTTTGGTA	GGAATGGGGG	TAAATGGAGA	GAGAGAAATT	300
ATGTTTCAGA	AGAAAACTAT	AGCACACCAA	CTCGAG			336

- (2) INFORMATION FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

r agtgggaaac	ATTATTTCAA	GACATTAGGG	ATAAGAATGC	60
r attgtttcaa	GGATTTATCA	ATACATAGAG	CAAATAATTA	120
TTATTTCTTT	ACTTTAGAAA	CAGTACAGCT	ACTTACAAAT	180
TATCTTAAAT	CTGAAGCTTC	TACCTTCCTA	AGAACAAAAC	240
				251
	r attgtttcaa r ttatttcttt	I ATTGTTTCAA GGATTTATCA I TTATTTCTTT ACTTTAGAAA	I ATTGTTTCAA GGATTTATCA ATACATAGAG I TTATTTCTTT ACTTTAGAAA CAGTACAGCT	I AGTGGGAAAC ATTATTTCAA GACATTAGGG ATAAGAATGC I ATTGTTTCAA GGATTTATCA ATACATAGAG CAAATAATTA I TTATTTCTTT ACTTTAGAAA CAGTACAGCT ACTTACAAAT I TATCTTAAAT CTGAAGCTTC TACCTTCCTA AGAACAAAAC

- (2) INFORMATION FOR SEQ ID NO:42:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42: GTTCAACCAG TTCAAATACT TTTTCAACCT CTATTTCTTA CTTCTTGCCT GCTCTCAGTT 60 TGTTCCCGAA ATGAGACTTG GTGCACTCTA TACCTACTGG GTTCCCCTGG GCTTCGTGCT 120 GGCCGTCACT GTCATCCGTG AGGCGGTGGA GGAGATCCGA TGCTACGTGC GGGACAAGGA 180 AGTCAACTCC CAGGTCTACA GCCGGCTCAC AGCACGAGGC ACAGTGAAGG TGAAGAGTTC 240 TAACATCCAA GTTGGAGCCC TCGAG 265 (2) INFORMATION FOR SEQ ID NO:43: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 437 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43: GAATTCGGCC TTCATGGCCT AAGATGATTG TGCTATTATT GTTTGCCTTG CTCTGGATGG 60 TGGAAGGAGT CTTTTCCCAG CTTCACTACA CGGTACAGGA GGAGCAGGAA CATGGCACTT 120 TCGTGGGGAA TATCGCTGAA GATCTGGGTC TGGACATTAC AAAACTTTCG GCTCGCGGGT 180 TTCAGACGGT GCCCAACTCA AGGACCCCTT ACTTAGACCT CAACCTGGAG ACAGGGGTGC 240 TGTACGTGAA CGAGAAAATA GACCGCGAAC AAATCTGCAA ACAGAGCCCC TCCTGTGTCC 300 TGCACCTGGA GGTCTTTCTG GAGAACCCCC TGGAGCTGTT CCAGGTGGAG ATCGAGGTGC 360 TGGACATTAA TGACAACCCC CCCTCTTTCC CGGAGCCAGA CCTGACGGTG GAAATCTCTG 420 AGGGCGCCAC ACTCGAG 437 (2) INFORMATION FOR SEQ ID NO:44: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 242 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44: GAATTCGGCC TTCATGGCCT AGTACCTTAA AAACTTTGGA AATAATAATA ATAATAATAA 60 ACAAAAAATA ATCCCAAACC CCGTAAGTTT AACTTTCTAT GCTTTGGCTG TTTTTGGTTT 120 ATTTTTGTT TTTTAGAAGG GGTCTCGCTC TGTCGCCCAG AATGGAGTGC AGTGGCTTAA 180 TCAGGGCTCA TTGCAGCCTC GACCTCCTTG GTTCGGGCGA TCCTCCTCCC TCCACACTCG 240 242 (2) INFORMATION FOR SEQ ID NO:45: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 264 base pairs
 - 105

(B) TYPE: nucleic acid(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AATTAAATTA	AATTAAAATC	TTTGTTACAA	ACTATGAAAA	TGAATATAAG	TAAATTTCAT	60
ATCATTTCTT	TTCTAGATTT	ATTATCTAGG	ATAGATTTGG	ATGAACTAAT	GAAAAAAGAT	120
GAACCGCCTC	TTGATTTTCC	TGATACCCTG	GAAGGATTTG	AATATGCTTT	TAATGAAAAG	180
GGACAGTTAA	GACACATAAA	AACTGGGGAA	CCATTTGTTT	TTAACTACCG	GGAAGATTTA	240
CACAGATGGA	ACCAGAAGCT	CGAG				264

- (2) INFORMATION FOR SEQ ID NO:46:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAATTCGGCC	TTCATGGCCT	AACCTGGAGA	AACTATTTAA	GTTGGATGAA	GCAAGTGCCC	60
AGCTCCTTGC	TTATAAGGAA	AAAGGCCATT	CTCAGAGTTC	ACAATTTTCC	TCTGATCAAG	120
AAATAGCTCA	TCTGCTGCCT	GAAAATGTGA	GTGCGCTCCC	AGCTACGGTG	GCAGTTGCTT	180
CTCCACATAC	CACCTCGGCT	ACTCCAAAGC	CCGCCACCCT	TCTACCCACC	AATGCTTCAG	240
TGACACCTTC	TGGGACTTCC	CAGCCACAGC	TGGCCACCAC	AGCTCCACCT	GTAACCACTG	300
TCACTTCTCA	GCCTCCCACG	ACCCTCATTT	CTACAGTTTT	TACACGGGCT	GCGGCTACAC	360
TCCAAGCAAT	GGCTACAACA	GCAGTTCTGA	CTACCACCTT	TCAGGCACCA	TAGTGACTCG	420
AG						422

- (2) INFORMATION FOR SEQ ID NO:47:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

G	AATTCGGCC	TTCATGGCCT	ACCGAAGGGC	ATCCCATCGG	TTGGGTAGGT	CATGGTTAAA	60
Α	AATCATCTC	CTTTGGTTGC	ATATTTAATT	ATTTTCCACT	ATTTTTTCCT	CACACAAAAT	120
G	ATTTTGCCC	GGTACCCTTT	TTGGGGGTGC	ACAGTCCATG	AGATGAATAT	TGAATGGGGA	180
G	ACCTGGGTT	CTAGTCTCGC	ATTTACCAGT	CAGGTTACAA	TGCGACCTTG	AGCAAGTCAC	240
T	TCACCTCCC	AGCGCCTCAG	TTTCCTCATT	GTAAGATAGG	AAAAGCCTTG	TCATTTTTAA	300
Α	TTTATTTA	TTTGCATATA	CCTCATGGCG	AACTCGAG			338

- (2) INFORMATION FOR SEQ ID NO:48:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAATTCGGCC	TTCATGGCCT	ACTATGCTCT	GCACGTGGGT	CATTTCTTAC	TGGTTTCTAA	60
AAGCCTTTCA	TTTTCTGCCT	GTACACAATA	GCCCCCTTCC	TCCATTGTTT	TTAGGATCCT	120
TTTTCCTCTT	ACCAGCTGTT	AACCTGGAAG	TATTTCTTCT	TCATCCCGAA	TCTCCCATGT	180
CCTCCCCACT	TCTATTTGTT	TCCATCCAAT	GTGGATTCAT	GATCATTTTA	TGGATTTTAA	240
ACTACTCTGG	GGCTACCCTC	GAG				263

- (2) INFORMATION FOR SEQ ID NO:49:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAATTCGGCC	TTCATGGCCT	AGAAACACAT	GTGATCTGTA	CTCATGAGAA	CCTGTAGTTA	60
ACTATACGAG	CCTTGCTGTG	CATTTTGTTT	TTATCTGAGC	CTGTCTTTCA	ATGTCCTATC	120
CCTTGAGAGA	ACTGAGGGCT	GAGAACCAAG	CTTTCCGAAG	CGGTCTGAGT	GTCAGCGGTG	180
GTAGTGGTCT	CTGGAGAAAA	GAATGGAGAC	AGGATAGGAC	TTGGAGAAGA	GTGAGTCATT	240
GTTACCCAGA	AACCCTGGAG	AACACTGGAC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:50:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGGCGTTCTC	ACGCCCGCAA	CAATTCCTGA	GTAGGGCCTT	GCTTGAGTTC	TTCGGAAAGT	60
CTCATCCACC	CCCACATCGC	CTCTTTAGGA	AGTCACTTAA	TGTTGGGCTT	CATTATTCCC	120
ACATCCCTTT	CCTTACTACT	TGCCTGCACT	TCTTGAGAAA	AAGACTGCAG	AAAGGAGAGG	180
TGGGGCTTTC	AGTAGAAACA	AGCAAACCGC	AGGTCCCTGT	GGGGGGACTC	TCCAGGAAGA	240
AGGGTAATTT	CCTGCCTCCT	TAAATTGGCT	GCTACTGTCA	GTTATTTTGC	TCCCAACCCC	300
AGAGCTTCAC	TTGCTCCTTC	ACTTCCCAGT	TCCGCAAGAA	CCGTGGGCGA	CAGTTATGGA	360
GAAGCGTCTG	CAGGAGGCTC	AGCTGTACAA	GGAGGAAGGG	AACCAGCGCT	ACCGGGAAGG	420
GAAGTACCGA	GATGCTGTGA	GTAGGTACCA	TCGAGCTCTG	CTTCAGCTGC	GGGGTCTGGA	480
TCCGAGTCTG	CCCTCTCCGT	TACCTAATCT	CGGACCTCAG	GGCCCGGCCC	TCACGCCTGA	540
ACGACCTGCC	TCGAG					555

- (2) INFORMATION FOR SEQ ID NO:51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGAAGATGG	ACTGCTCTGG	GGCCCATGTG	CAAGTGACCT	GTGCCAAGCT	CATCTCCAGG	60
ACAGGCCACC	TGATGAAGCT	TCTCAGTGGG	CAGCAGGAAG	TAAAGGCATC	CAAGATAGAA	120
TGGGATACGG	ACCAATGGAA	GATTGAGAAC	TACATTAATG	AGAGCACAGA	AGCCCAGAGT	180
GAACAGAAAG	AGAAGTCGCT	TGAGCTCAAA	AAAGAAGTTC	CAGGATATGG	CTATACTGAC	240
AAACTCATCT	TGGCATTAAT	TGTTACTGGA	ATACTAACGA	TTTTGATTAT	ACTTTTCTGC	300
CTCATTGTGA	TATGTTGTCA	CCGAAGGTCA	TTACAAGAAG	ATGAAGAAGG	ATCACTCGAG	360

- (2) INFORMATION FOR SEQ ID NO:52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 621 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAATTCGGCC	TTCATGGCCT	AGCTCCTGCG	TAAAGGAGCA	TGAGAGCGTG	GGAGTTTTGC	60
AGTGGCCGTG	GGGTTCTTCG	TCGCGTCTCG	GTCGGGCGTC	GCTTTCTGCA	GCTCCTGTCA	120
GGGAGCGCGA	GGCCTGTTAT	TAACCGCGGA	GCGCTTTGTC	ACGAANTCCC	TGTGGCGTCT	180
TGAAGAAGGC	ATTCCCCACC	CGCCAAATGG	CGTCCATGCC	CCCGACGCCC	GAGGCCCAGG	240
AGAGTCGAGG	TACCTTTTTC	GTCCAAGTTT	ATNGCTGCTT	TCGGTCTCTG	CCTGACCCCN	300
TCCTTTGGAG	GAGAGTTGGG	CATGCCTGTT	GTGGTAGGAG	TGCTCNTGAG	CCCCAAATAG	360
CCCTTTGACC	AAGTGTTCTT	CGTTCCAAGA	CCACACACAT	AATGGTTTAC	CAACTTCNTT	420
CTTTCAGAAC	TACCAACTGG	GAGCAGGGAC	CTGTGGAGGA	ATCTCTGAGA	GAGTTTCTCA	480
ATGTCTTATC	TGTTTGTTTT	GTTTTGTTTG	GAGATAGGGT	CTGGCCTTGT	CGCTGGAGTG	540
TTGCTTGTCT	GGCTGGAGTG	CAGTGCTGAT	ATCATAGCTC	CGTCTGGAAC	TCAGGGAATC	600
CTTACGCCTC	AGCCTCTCGA	G				621

- (2) INFORMATION FOR SEQ ID NO:53:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAATTCGGCC	TTCATGGCCT	ACAATTTGGA	GCAAGGCTTA	GCAGAAGACG	GCGGCATGAG	60
CAGCGTGACT	CAGGAGGGCA	GACAAGCCTC	TATCCGGCTG	TGGAGGTCAC	GTCTGGGCCG	120
GGTGATGTAC	TCCATGGCAA	ACTGTCTGCT	CCTGATGAAG	GATTATGTGC	TGGCCGTGGA	180
GGCGTATCAT	TCGGTTATCA	AGTATTACCC	AGAGCAAGAG	CCCCAGCTGC	TCAGCGGCAT	240
CGGCCGGATT	TCCCTGCAGA	TTGGAGACAT	AAAAACAGCT	GAAAAGTATT	TTCAAGACGT	300
TGAGAAAGTA	ACACAGAAAT	TAGACGGACC	TCTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:54:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
•	
GAATTCGGCC AAAGAGGCCT ACATTACTGG GTTAGAAAAC AAAGAGGGAG TGCCCTGCAC ATTTTCTTTT GTGCTTTTAA ATGTTTCTTA AGTTGGAACA GGTTTCCTCG GGCCTGTTTT GACTGATTGC TGGAGTGCAT TTGATAGTTA AAAATTACTA ATTGGTTTTA TTTCCCTTCA CACTCTGCCT CCCCTATTTC CCCCAATTGA CCCTAAACCT CGAG	60 120 180 224
(2) INFORMATION FOR SEQ ID NO:55:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 249 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
GATTTAATGC ATGCTAGCAA CAGCCTTAAC TTTGGATTCA GTTATTTGAA ACACTTTTCC GGCATCTTTC CCTTTCTAAT GTTGTGGGGT GGAAACCGGA TGGCAAATCA CTGTGAGCCG GATACCTCAG CACAGTCCAC CTTGTGTGTG ACTTCACAAA TGGGGGACTT CACAAATGGG GTAACTGAAT GTTATTACTT TCAAATTTTG ACATGGAGCA TTATGATCAA GGAAATGGAG CAACTCGAG	60 120 180 240 249
(2) INFORMATION FOR SEQ ID NO:56:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 257 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
GCTGCGCCGC ACCCTGAGAG ATGGTTGGTG CCATGTGGAA GGTGATTGTT TCGCTGGTCC TGTTGATGCC TGGCCCCTGT GATGGGCTGT TTCACTCCCT ATACAGAAGT GTTTCCATGC CACCTAAGGG AGACTCAGGA CAGCCATTAT TTCTCACCCC TTACATTGAA GCTGGGAAGA TCCAAAAAGG AAGAGAATTG AGTTTGGTCG GTCCTTTCCC AGGACTGAAC ATGAAGAGTT ATGCCGGCTA CCTCGAG	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:57:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 229 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATAAATGCAT CTCGGTGGAA AAATAATCAT TTTCTTGGCA TATCTCGAG

(A) LENGTH: 257 base pairs(B) TYPE: nucleic acid

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

GAATTCTAGA CTTTGTCTCC AGAGCATTGC CTTTATAAGC AGATTGGCAC CAACAGTTCC

ATAGTTTAAC ATCTAGTTAA GCTACAAATA TAGTATAAGC ATTATTAGCA GCTGGTACTT CTGCTAGGGG TTGTAAATTC CAGGTGTTAC ACTGACCTCA ATCCAATTTA CATAATTTAC

60 120

180

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
GAATTCGGCC TTCATGGCCT ACACTGCTAT GTATGTTTTC TCCTTAATGA TGAAG AGATGATGCT AATAATAGTA GCTGATGTAC TGACTTTTAG CTGTGTGCAA AGCCA AAAATACTTT ACAAGTGTTA ACTTGTTTGA TCTTCACAAC AACCCTAAGA AGTGG ATTAAAGTAG ATTTTGGAAG ACTGATCTAT TTAATTATTA ATAGATCTGT CTCAT TTTTCCCCCA ACTCGAG	TGTTC 120 ATATT 180
(2) INFORMATION FOR SEQ ID NO:59:	•
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 223 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
GAATTCGGCC TTCATGGCCT ACGCGTCTGC TTCGGAGACC GTAAGGATAT TGATC GAGATCCCTG CTCAGAACCC CCTTCCTGTG TGGCCTGCTC TGGGCCTTTT GTGCC CGCCAGGGCC TTTTGTGCCC CAGGCGCCAG GGCTGAGGAG CCTGCAGCCA GCTTC ACCCGGCAGC ATGGGCCTGG ATAAGAACAC AGTATCACTC GAG (2) INFORMATION FOR SEQ ID NO:60:	CCCAGG 120
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 171 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
GAATTCTAGA CCTGCATGTC CCAGTGTGAA ATTTCAGCAC GGCATTTTCT GCAT ATGGCCATCC AAAGGATTCC GCTGCAGAAA TTATTGATGT GCTATTTTTG CTGT ATGCAGGCTG CTTTGGGCCC CTGGGTCACT CTTCCAAGGC TGCAACTCGA G (2) INFORMATION FOR SEQ ID NO:61:	

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 336 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
GAATTCGGCC TTCATGGCCT AAAAAGCAAA AGAAAAGTAA AAGGAAGAAA CAAGAACAAG AAAAAAGATT ATATTGATTT TAAAATCATG CAAAAACTGC AACTCTGTGT TTATATTTAC CTGTTTATGC TGATTGTTGC TGGTCCAGTG GATCTAAATG AGAACAGTGA GCAAAAAGAA AATGTGGAAA AAGAGGGGCT GTGTAATGCA TGTACTTGGA GACAAAACAC TAAATCTTCA AGAATAGAAG CCATTAAGAT ACAAATCCTC AGTAAACTTC GTCTGGAAAC AGCTCCTAAC ATCAGCAAAG ATGTTATAAG ACAACTTTTA CTCGAG (2) INFORMATION FOR SEQ ID NO:62:	60 120 180 240 300 336
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 212 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
GAATTCGGCC AAAGAGGCCT AGAAGAGCAA GCGCCATGTT GAAGCCATCA TTACCATTCA CATCCCTCTT ATTCCTGCAG CTGCCCCTGC TGGGAGTGGG GCTGAACACG ACAATTCTGA CGCCCAATGG GAATGAAGAC ACCACAGCTG ATTTCTTCCT GACCACTATG CCCACTGACT CCCTCAGTGT TTCCACTCTG CACGCTCTCG AG	60 120 180 212
(2) INFORMATION FOR SEQ ID NO:63:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 349 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
GAATTCGGCC TTCATGGTCT ATGCTACTCA GTTGGATCTA GCAGAAACAA AAGCTGAGTC TGAGCAGTTG GCGCGAGGCC TTCTGGAAGA ACAGTATTTT GAATTGACGC AAGAAAGCAA GAAAGCTGCT TCAAGAAATA GACAAGAGAT TACAGATAAA GATCACACTG TTAGTCGGCT TGAAGAAGCA AACAGCATGC TAACCAAAGA TATTGAAATA TTAAGAAGAG AGAATGAAGA GCTAACAGAG AAAATGAAGA AGGCAGAGGA AGAATATAAA CTGGAGAAGG AGGAGGAGAT CAGTAATCTT AAGGCTGCCT TTGAAAAGAA TATCAACACT AAACTCGAG	60 120 180 240 300 345
(2) INFORMATION FOR SEQ ID NO:64:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 391 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCGGGCTAGT	CATGGCGTCC	CCGTCTCGGA	GACTGCAGAC	TAAACCAGTC	ATTACTTGTT	60
TCAAGAGCGT	TCTGCTAATC	TACACTTTTA	TTTCTGGATC	ACTGGCGTTA	TCCTTCTTGC	120
AGTTGGCATT	TGGGGCAAGG	TGAGCCTGGA	GAATTACTTT	TCTCTTTTAA	ATGAGAAGGC	180
CACCAATGTC	CCCTTCGTGC	TCATTGCTAC	TGGTACCGTC	ATTATTCTTT	TGGGCACCTT	240
TGGTTGTTTT	GCTACCTGCC	GAGCTTCTGC	ATGGATGCTA	AAACTGTATG	CAATGTTTCT	300
GACTCTCGTT	TTTTTGGTCG	AACTGGTCGC	TGCCATCGTA	GGATTTGTTT	TCAGACATGA	360
GATTAAGAAC	AGCTTTAAGA	ATAATCTCGA	G			391

- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GAATTCGGCC	TTCATGGCCT	AGGGAGTCTG	AAGCAATTTC	TGAAGAAGAC	CAAAAAGAAC	60
CACAAGACGA	TGAATGAAAA	GGCATGGAAG	${\tt CGTTGGTGCA}$	CACAAATCCT	CTCTGCCCTA	120
AGCTACCTGC	ACTCCTGTGA	CCCCCCATC	ATCCATGGGA	ACCTGACCTG	TGACACCATC	180
TTCATCCAGC	ACAACGGACT	CATCAAGATT	GGCTCTGTGG	CTCCTGACAC	TATCAACAAT	240
CATGTGAAGA	CTTGTCGAGA	AGAGCAGAAG	AATCTACACT	TCTTTGCACC	AGAGTATGGA	300
GAAGTCACTA	ATGTGACAAC	AGCAGTGGAC	ATCTACTCCT	TTGGCATGTG	TGCACTGGAG	360
ATGGCAGTGC	TGGAGATTCA	GGGCAATGGA	GAGTCCTCAT	ATGTGCCACA	GGAAGCCATC	420
AGCAGTGCCA	TCCAGCTTCT	AGAAGACCCA	TTACAGAGGG	AGTTCATTCA	AAAGTGCCTG	480
C						481

- (2) INFORMATION FOR SEQ ID NO:66:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 583 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GAATTCGGCC	AAAGAGGCCT	ACGATTGAAT	TCTAGATCTG	CCCGTCTTGG	CCTCGCAAAG	60
TGCTGGGATT	ACAGGCGTGA	ACCACTGTGC	CTGGCATATT	TGTCTATTAA	TTTGCTTTTC	120
TTTAGATGTA	TTCTAGAGGG	GGGAAAATCA	GTAGAAGAAC	AGTTATGTAA	TTCTAACAAG	180
TTCTCCATGT	GTCTTGCCAT	CTNGCTTTTT	CTCATCCTAT	CAGTACTGGA	TGAGAATGTT	240
TATTTCACTG	AACTTTGCCA	AAGAGTTTCA	ACATTTTTT	${\tt GTTTAATCAT}$	AGGAGAAAA	300
GGTTTATCTT	AAAATTTTTAA	ATTTTTTTTT	AATTCTTTCA	TTACAAATGA	AGTCCCAGAA	360
GTTGTATTTG	TTTCTTTAGG	CTGTTCTTAA	TTGTTCATTG	GAACAGGCAG	GGTTTGAAGG	420
AGTGGGGATA	CTGGGAAAGC	CAGGGTGATG	AGAAAATAGG	AAAGGGGTCT	TGTCATTGGG	480
AGGCCACTAT	ACCAGTGGCC	CTTGTACCAG	GACTAATATG	GTACTTTGAA	GCTTTAAATT	540
CATTTCTTTA	TTCAATAATT	TTAGGCATCC	CAGGATACTC	GAG		583

(2) INFORMATION FOR SEQ ID NO:67: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67: GAATTCGGCC AAAGAGGCCT AGCTATCCGC TTTGCTATTT TAGTGGCATT ATCAAAATCA CTGGAAGCAC CTGTNGTAAT ATGGTCGGTT CCAAATATAA GCTCCTTGC CACTCTTCCT CCCATACTAA CATCCATTG TGCAAGCAGC TGGGCTCTAG TTTCATTCCA TCTGTCATTC TCAGGTAACA GGGACACATG TCCAAGTGTT GGCCCCCGTG GCATGATTGT AGCTTTGTTG

ATAGGCATTG CATCTTTTGT GTAATATGCA ATAATGGCAT GACCAGATTC ATGATATGCT

GTGATGGTTT TGTTTTTGTT ATCAATTTCC ACACTTCTTC TTTCAGGCCC CATTAGAATT

TTGTCTTTGG AAAACTCCAG CTCCTTCATG GTAACCATTT CTTTTCCATC AACAGCTGCT

TTTAATGCAG CCTGGTTCAC AAGATTCTCC AACTCTGCTC CGGAAAAGCC AACAGTACCT

120

180

240

300

360

420

480

(2) INFORMATION FOR SEQ ID NO:68:

CGAG

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAATTCGGCC	AAAGAGCCTA	ATTGAATTCT	AGACCGGCCT	CATCGTTCTT	TGCCTTCCTG	60
GTCACCATCT	GCTACGCTGG	AAATACATAT	${\tt TTCAGTTTTA}$	${\tt TAGCATGGAG}$	ATCCAGGACC	120
ATACAGTGAT	TTACCATTTT	GATAATTAAA	AGGAAAAAA	AAGGAAGACT	CTCACTGTAA	180
AAACAGCTGT	AGGTATAATG	TATATTCCCA	GAGAATTGTA	TTTAACTAAT	TAATGTTTTT	240
TATATTCTTA	AATTTGCTCA	CAAATTGTGG	TTTGTTACAA	TTAAACTGGA	TACTTATTTG	300
${\bf CAAAGTGTTG}$	TAGCTTATAA	TGAACTCTTA	AGTATCTTAT	TAATGTATTA	ATGTCTTCAT	360
AGATCATATT	TTCTTAGACA	ATGTTTAAAT	AGATAAATTG	CTAATATTGA	GAATGTGTCA	420
AGTTTGTAAA	CCTAACTTTT	AAGATGCCAG	AACTCGAG			458

- (2) INFORMATION FOR SEQ ID NO:69:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GAATTCGGCC	AAAGAGGCCT	ACGGCCAAAG	AGGCCTAGGT	GGTGATTGAC	CTAAGAAAAA	60
AGTGTCTTAA	ATATCTGGAT	TCTATGGGAC	AAAAGGGCCA	CAGGATCTGT	GAGATTCTCC	120
TTCAGTATTT	ACAGGATGAA	AGTAAGAACC	GCTCGAG			157

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GAATTCGGCC	AAAGAGGCCT	AGTGGACTGC	TACTTCCCTT	TAGCACTATA	TACAAACATA	60
ACTGCTACTT	CCCTTTAGCC	CAGGATCAAA	ATAATGATTC	AGTTAAAAGT	TGCTTGCCTA	120
ACAAAATTTC	AAAATATGGA	CTTCTGTGAA	TTGCTAAAAC	ACATCCTTTT	AACTAGGCAT	180
CTTTAAGTCT	ATAGTATCTT	TAAAGTTAAT	TTCAAAATTT	AGCAGAGCCT	GGAACACAAA	240
TTATTCAGGA	AATAATTCCT	GAACCTACCT	CTATCTTCAT	AAAACGTATT	GGGGCAAGAA	300
CTATTCTATT	GAATTCTAGA	CCTGACTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:71:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GAATTCGGCC	AAAGAGGCCT	ACCATCTGTC	ACTAATATCA	AAGGAGGCC	AAGGACACAG	60
CCCTGGGGGA	ACTTACCAGG	TCAACCCACA	ATGGGTGAAT	TTATAGTTTG	TTAGTTAGTG	120
GTCAGTTACC	AACTTCTCTG	TCTGTCTAAT	GCTTTGACTA	AAATGTCCAG	ATTATTTACC	180
TAGTTAACAA	AATTAAAGAA	GATTCTAAGA	CCAGTTTAGC	ATCATTTTCT	CTGAAGTCCA	240
TAATGAATGT	CTGTTAAACT	CTCGTCACTC	TTATTTAGGT	GCTTTTGGGT	CATTTGTTGT	300
AGGTTCATTC	TCCCAAATCA	ATGTCACATA	TACGTCTGTA	ACTTGTGTTA	TCAGCTTCCT	360
TCCTAGGGCT	TTAACTTCTT	TTCAGTCTTA	TAGCATTCCT	TCCATTTTCC	TTTCAGTTCA	420
CTCCAATAAA	AGCTCGACAA	ACTCCTGGGA	GCCCCTTGGT	GCTCGAG		467

- (2) INFORMATION FOR SEQ ID NO:72:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GAATTCGGCC	AAAGAGGCCT	ACGATTGAAG	TCTAGATGCA	CACATTCAGC	TTCTGTCTCA	60
GTCCTGAGAG	TGGTTGTGTT	TTATTGGCTG	ATGAGTTATT	TCCACATATC	ACATGTATAA	120
GGTATTTGAA	TGAAGGTGCT	TTGTAGTCAT	GACACACTAC	TCTTTTACTA	ATTATTAATA	180
TCTTAAGATT	ACAATTTGAG	AGGTAGAGAT	GGTATTGTTT	TTAATGGGTG	TGGGGGGTGG	240
TGATGATAGG	TATTTTTACC	CTGGTAAGTG	ACCTACTAGG	TTTTATTAAG	TGTTGCAACT	300
TGTCCAGTGT	GTGGATGGGA	TCTCGAG				327

(2) INFORMATION FOR SEQ ID NO:73:

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 206 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
GAATTCGGCC AAAGAGGCCT AGTGGTGGTA TGTATTTGAG TTCACAGTAT TTGTTTTATA GCAGTTTTGC AAGCACATAC TGTGCCACG ATTTTCCCAC ATTATTTTTA GACAAGGGAA CACAGCCATC AAAACTGATA CCATGGCCGG GCGTGGTGGT GGGTGCCTGT AGTCCCAGCT ACTTGGGAAC TCGGGACATT CTCGAG	60 120 180 206
(2) INFORMATION FOR SEQ ID NO:74:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 184 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
GAATTCGGCC AAAGAGGCCT CCACCATGCC CGGCCTCAAC GATATTGATT CTTTGGGCTG TAGTCAGTAT TGGATTATGA TCAATATTAT CACCATTTAT TTTGTTGCTC CAGTTCTTCC AGCTGTGGCC AATCCTTCAG TTGGATTCTT GTGCCCCATC AACATTCTCC ATCCTTCTC CGAG	60 120 180 184
(2) INFORMATION FOR SEQ ID NO:75:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 232 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
GAATTCGGCC AAAGAGGCCG ACTTTATTAT ACCATACATA CTATAGGTAC CTGGGCACAA GATAGGTCAG GGGGTACTGT ACCCCTATTT ACATGCTTAA TCACATCATA AGGTTGCAGG TGGTACTTGA AATCATCACT AATGAGACAG CAAATATGTT AGACTTGCTG GCCCAGCAAG CCACAGAAAT AAGGATCACC ATCTATTAGA ATAGACTGGC TTCAAACTCG AG	60 120 180 232
(2) INFORMATION FOR SEQ ID NO:76:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 330 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:76:

GAATTCGGCC	AAAGAGCCTA	CTAAAATTCC	TTGTTTTGTG	TTTTTAATAT	TCCATCGTTG	60
ATAGTTAATA	TTCTTTTNGA	GGTTTTGTTT	TAGACAAAGT	AATGTTTTTC	TGAAATGATT	120
CTAAGACAAT	TGGTCAGAAA	TAGTCTCTGC	TTGTTTGGTT	TATGTTTGGT	CAGTTGTGCT	180
TTGATTATAG	ATGGTTCCTC	ATCTGAGATT	AAAGTGGGAC	AGAACTTCAA	AAGTAAAAGG	240
GTAAATGTTC	GCTGTGATGC	TTATGTGGCA	CATGTGCTAG	TCCTTGATAG	TGGCGAGAAA	300
GATCTTAATT	GCTCAAAGGA	AGTACTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ACAGTGCATT.	ATGTTATTTT	GTTATCTCTG	CAGTAACTTT	60
TTTGTCTTAT	TTAAAGCTTC	TGAGATTATG	GATTTTTGTT	120
TTATCATTCC	TATATAGTAC	TAAGCTGTCT	ACAGAATAGT	180
TGGGAAGATC	CTAGTTTGAA	TCTTGGCTGT	GCGACTTTAA	240
CCTCAGTCAC	CTGAACTCTG	CAGTGGGGAT	CCTTATGCCT	300
TCACGAAAAT	ACGCTTGTAC	TTTGAGTTCA	GTACCTAGCC	360
GGGACAGTCA	TCACGCAGCG	CTTTGCACAC	AGCTCTCACG	420
TTTGGTAAAT	CTTTACTAGT	AAATGTTTCT	TAAAAGCATT	480
CCTCGAG				507
	TTTGTCTTAT TTATCATTCC TGGGAAGATC CCTCAGTCAC TCACGAAAAT GGGACAGTCA	TTTGTCTTAT TTAAAGCTTC TTATCATTCC TATATAGTAC TGGGAAGATC CTGAACTCTG TCACGAAAAT ACGCTTGTAC GGGACAGTCA TCACGCAGCG TTTGGTAAAT CTTTACTAGT	TTTGTCTTAT TTAAAGCTTC TGAGATTATG TTATCATTCC TATATAGTAC TAAGCTGTCT TGGGAAGATC CTAGTTTGAA TCTTGGCTGT CCTCAGTCAC CTGAACTCTG CAGTGGGGAT TCACGAAAAT ACGCTTGTAC TTTGAGTTCA GGGACAGTCA TCACGCAGCG CTTTGCACAC TTTGGTAAAT CTTTACTAGT AAATGTTTCT	ACAGTGCATT ATGTTATTTT GTTATCTCTG CAGTAACTTT TTTGTCTTAT TTAAAGCTTC TGAGATTATG GATTTTTGTT TTATCATTCC TATATAGTAC TAAGCTGTCT ACAGAATAGT TGGGAAGATC CTGAACTCTG CAGTGGGGAT CCTTATGCCT TCACGAAAAT ACGCTTGTAC TTTGAGTTCA GTACCTAGCC GGGACAGTCA TCACGCAGCG CTTTGCACAC AGCTCTCACG TTTGGTAAAT CTTTACTAGT AAATGTTTCT TAAAAGCATT CCTCGAG

- (2) INFORMATION FOR SEQ ID NO:78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GAATTCGGCC	AAAGAGGCCT	AGATTGAATC	TAACCTTTTT	GCCTCTTCCC	AAGTAGCCTA	60
TTTGAGCTAG	AACAAAACTT	TGTTAGCCAT	TTTGGGAGAG	AATAGGGAAT	CTAGAGAATG	120
AAGATCTGCC	CGACCTGCCT	CGAG				144

- (2) INFORMATION FOR SEQ ID NO:79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEO ID NO:	(xi)	SEOUENCE	DESCRIPTION:	SEO	ID	NO:7
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GAATTCGGCC	AAAGAGGCCT	AACGACGGTA	ATCAAGTTTT	GCTCCAGAAG	CATCAAGAAA	60
CTTAGCTACT	GCTTCCAAAT	CAGTACCGGT	TTCAGTTAAG	CCTTGAATAA	TACAGTCTTG	120
AAACTGAGTA	GGGTCAAACC	TCTCTTTTTC	ATCTCTTTTT	CTAGTTTTAA	AACGCTGGCC	180
TGATAGCGTT						240
AGAGGAAAGA						297

- (2) INFORMATION FOR SEQ ID NO:80:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GAATTCGGCC AAAGAGGCCT AGACTGCTGG TEGTGAACTG CTTTTCTTGT AGGTTGTAGA 60 GGCTGAAAAA GCCAATCTTA ATAGACATGA GGCTCATGTT TGCACAGTGT GCTCTCGAG 119

- (2) INFORMATION FOR SEQ ID NO:81:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GAATTCGGCC AAAGAGGCCT	ACTCAGCTGC	AAAAAAGCAT	ATTTTCTGTG	TTTCTGGACT	60
GCACTGTNGT CCTTGCCCTC	ACATAGACAC	TCAGACACCC	TCACAAACAC	AGTAGTCTAT	120
AGTTAGGATT AAAATAGGAT	CTGAACATTC	AAAAGAAAGC	TTTGGAAAAA	AAGAGCTGGC	180
TGGCCTAAAA ACCTAAATAT	ATGATGAAGA	TTGTAGGACT	GTCTTCCCAA	GCCCCATGTT	240
CATGGTGGGG CAATGGTTAT	TTGGTTATTT	TACTCAATTG	GTTACTCTCA	TTTGAAATGA	300
GGGAGGGACA TACAGAACTC	GAG				323

- (2) INFORMATION FOR SEQ ID NO:82:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCGGCC	AAAGAGGCCT	AGGCAAATCA	GAACTCTTAA	GTTGTTTCAT	CCTTATTTTA	60
TTCTTAAAAT	AAAGAATTTC	ATTTCAAATA	CGGATTAATT	TTTTTTCTGG	GAAAAAACAC	120
ACTGTAAAAC	ATAATTTTCT	ACCTTTTAAA	ACGTTTTACA	ATTTATCCCA	TCTTCTAACA	180
ACTTATCATA	CTCATACCTG	CCGAGGTTTC	TCTAAATTTG	TCCCTCCTCT	TCTTTTTCCT	240

CCATTTCCAA GGCTTAAAGA TTTTACCAAT GGTGGATAGT TTCCCCTTTC TTTTGAAGGG AGGTGTTTGG GAACCTGCTG TGGGGCCATC TGAGTTTGCT ATAGAAGCTT TGTCCAGTCC GTCAACTGAG CCGGAGATGT GGACCCGGAG CGGGCGCCC CTGCTCGAG	300 350 409
(2) INFORMATION FOR SEQ ID NO:83:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 463 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
GAATTCGGCC AAAGAGGCCT ATAAATATAT AATTGACTTA TTTATTAAAT TTAGGAGAAA AAAAAAGTTT TCCTTGACAT TCAGCTCTAT TGGATTTATT TCCATTTAAT TGCATCATGT GTTATGTCTT GGTAAACACT CCATTTCCTG TCTTGGTGGG CATCCTGTC GTGTACCTGT GCAGTACACT TTAATCATCA AGACTTCAAA GTGCTTTTGA GCTATCAAAT CTTGGGAGAG TCCCATCTAG CATCTTAATA ATTATTTTTC CAAGTTCGTT ATAATTAACT CCTTTAACCT CATCTCATTA AATCAATTTT GTATTATCAT TCTGTTGTTC TCTGGAAAGC AGCCAATTGT TCAGCTCTTG AATCAGAATT TTCAAAGACT CACCTCTCTT ACCTGGGCTT GCACATATTT GTCCTAAAGTA ATTCTCTATC CCTTAAACCT CTGAGCCCTC GAG	60 120 180 240 300 360 420 463
(2) INFORMATION FOR SEQ ID NO:84:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 316 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
GAATTCGGCC AAAGAGGCCT AATTTTGTAA AAAGGAATAT CATTCTTGA TTTTAGATCT TAGACATCAG GCACTGACAT AGAGCTTAGA TATGTTCTTA AGGTAGCTAA GCCATTTATT ATAGGATAGT CAGATAGGAT AGTTCTAGGA TTTATAGACC TTTTCAGATA CTCTTTATCC AGTGAGAGAT GACCTATTTT TATTAAAACT TGGGTTTGGT ATCTTGGAAT TGGCTTGAAA ATGATTTGTT TTTACATTGG ATGTGAACGG AAAGTTTGTA TCTCAAATGT TTTACCACCT GAAGGGACAG CTCGAG	60 120 180 240 300 316
(2) INFORMATION FOR SEQ ID NO:85:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 494 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
GTGGACATGG AAGTAGGTGA GGTTGGGGGA CCTATGAAGA AAAAAAGAGC CTTTCCACTG GGCAGTGAAG TGTGTACACA CACACTGGGG GCAGAGCAGT GTGAAAACAT TCTGCACCAG CACACAAATG ACTTTTGGCA AATCATCTNC CTGATCTGTC GGATGTTACG TCTCTGCAGA	60 120 180

ATCTGGAGAA	AACCAGAAAA	CCCAGCTTGT	TTGCCCTCAT	TTTGGCAGTT	TAATTTAGGA	240
ATCACACTGG	CTTTACATAA	ACTCTTTACC	AAAAAAACTG	TATTCTGTAT	TTTGAAGGCA	300
CAAGTTAACA	TGGGCCCAAG	GGAAGGAAGC	ATTGTATACA	ATTACATAAT	AGCTACTCTA	360
TTACTTTAAA	ACCTAATGGC	AGCCTCGGGC	AGAAAAGTCA	AAAGGGGAGA	GAAACCATTT	420
CTGTGAAATT	ATCTGATGCA	ATCATCTCTT	TGGAGACATT	GTCAGTTGAC	AATGGTTCTG	480
CTTTTTCTĆT	CGAG					494

- (2) INFORMATION FOR SEQ ID NO:86:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

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- (2) INFORMATION FOR SEQ ID NO:87:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GAATTCGGCC	AAAGAGGCCT	AGCTTATCCA	GTCTAGTAAT	TTTTTTTTTTA	TGTGTGCACA	60
GCACAAATAG	TTACAATAGT	TCCCTTTTTT	GACATCAAAT	TCAACAATAC	CTGGCATATA	120
ATTGCTAAAT	ACTGTCATCA	TTTTCATTAT	CATTATCCCC	CACATAGTCA	TAAATAAGCA	180
CACATGCTAA	TCTTCAACTC	TTCTTCTATT	ATTTGCTGCC	TTCTTACCTG	CGTTAGTGAG	240
AAAGTGCCTT	CAAATAGATT	GCCAACAGTT	ATATGGCTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:88:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAATTCGGCC	AAAGAGGCCT	AGTGCAGTAT	TCACGTGTAA	CTTTTAAGTT	TTCAGTACAG	60
					AGTATTTAGG	120
		ATGTAAGCTT				180
CTTGGATTTT	TGTACCAGAG	ATGTGCTAAA	CTGATGAAAT	ACATTGAGAA	AGTTTCCATC	240
TTATTCTTTT	ATATGGGACT	${\tt GATGATGTGT}$	GTTGGGGTAG	ACTGCTCCTG	CAGAGTTTGG	300
AAGAAGTCAC	CAGCAAAGCC	GGCCAATCTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:89:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTCGGCC	AAAGAGGCCT	AGGTTTCTAG	ACTGGAAGAA	CAAATGAATG	GCTTAAAAAC	60
	CATCTTCAAA					120
GGAACAACAG	GCCAGTATGG	AAGAGAAATT	CCACAATGAA	TTAAATGCCC	ACATAAAACT	180
TTCTAATTTG	TACAAGAGTG	CCGCTGATGA	CTCAGAAGCA	AAGAGCAATG	AACTAACCCG	240
GGCAGTAGAG	GAACTACACA	AACTTTTGAA	GGAAGACAAG	GAACGCNAGA	AAAAAGACGA	300
AGAAAAGGTG	AAGGCAGAGG	AAGAATCAAA	GAAAAAAGAA	GAGGAAGAAA	AAAAGAAACA	360
TCAAGAGGAA	GAGAGAAAGA	AGCAACTCGA	G			391

- (2) INFORMATION FOR SEQ ID NO:90:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GAATTCGGCC	AAAGAGGCCT	AGCTTCTCTG	CTTTATTTAT	TCATTTATTT	TTAATTTTTT	60
			GGAGTGTGGT			120
			GTCTTTTTAA			180
AGCTGTACGA	GTTCTGCCCC	AAATCTGCAC	TTGGGCCTCA	GGATCAGGCC	GCCTCCCCAT	240
CAATCTGGTG	GATGCCAGTT	ATAACCTTTG	CCCTGCACCC	CATCCACACT	GTAGTTCAGA	300
GAAAATCAAC	AGTCAGCAAT	CATATCACAA	GCACTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:91:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCGGCC AAAGAGGCCT ACGAGTCAGC ATCTAGACTC AGCTCCTTCT TCCCGCCTGC

CCTCACACAT GCGTGCATTC ACTCTCCTGT CCAGGCTCAT GTCCTTGTGC CCGCTTGCTG CTTTGCCTCC TTGCTTGTTT CTGACTTGCT CACCCACTCT CTGTCATTGT CTTGCTTACT CAGGCTCACC CTATCAACTC GAG	120 180 203
(2) INFORMATION FOR SEQ ID NO:92:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
GAATTCGGCC AAAGAGGCCT AGTTGAATTA TTGCCACATG TTAGGAATGT GGAAGGTTGC TTGGATAAAT GAGAAAAGAA AGAAAAGAAT GCAAGTAATG TCCTGCTGGG GTAGTGCAGT CCTCGAG	60 120 127
(2) INFORMATION FOR SEQ ID NO:93:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 179 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
GAATTCGGCC AAAGAGGCCT AGATCCCACG AATTTAGGCT CAGAAGCATC GCTCCTCTCC AGCCCTGCAG CTATTCACCA ATATCAGTCC TCGCGGCTCT CCAGGGCTCC CTGCCCTGAC CTCTTCCCTG GGTTTTCTGC CCCAGCCTCC TCCTTCCCCC CCCCCCTATA TCCCTCGAG	60 120 179
(2) INFORMATION FOR SEQ ID NO:94:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 326 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:	
GAATTCGGCC AAAGAGGCCT ACTGGAATCA CTAAACTTTG TCTCATTTT TTTCTCTCC ATCAAATATC AATTTTGGAT TCAGATCCAG TTTTTTTCTT TCAATTATTT CTGCCTTTTA AAATAATACT ACCTCCTTCC TCCCACAATT CATTTCAGCT TGTTTTAGTT CCTTGGGTTC TATATTTTTT CTTCCTAGTA TTACAATATA TGCACAAATA TTAGGTTATA AAACTTCCAA TACAACTTTT ACTGCCACTC ACAGGTTTTT CAATTGTTTT CATTTTCATG TACATTTAAA TAATGTATAT ATTAGGGATA CTCGAG	60 120 180 240 300 326
(2) INFORMATION FOR SEQ ID NO:95:	

- - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
TCCAGCTTTT ACTTTTATTG AGCAAGTATA CGTTATTTAT TTAGTCATCC ATTCATTCAT 1 TTACTCATTT ATTTATTTT TTTTCAGCTT ATTTCTGCTT TCATCTTAAT TCCTCTCTTA 1 AACTTTTTGG TATCACATTG GTTCTCCCTG ACCTCCACCA CTGTAACCTG ACTTAAGTTA AATGTTTAAT TTATTTTTT TTTTTTTTTT	60 20 80 40 40
(2) INFORMATION FOR SEQ ID NO:96:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 240 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:	
AACATCATGT TTGTGAAAGT TTCATGCATA TCGTTGCAAG TATTTGTATT TCATTCATTT CTATTGTTGT ATAATGTTAC ATTGCATGAA TATGCAGCAA TTTGTTCTAC TGTAAAAAGC 1	60 20 80
(2) INFORMATION FOR SEQ ID NO:97:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 330 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:	
TTCTTGTTTT ACTTTTCCCT ATTTTTGTTT TATACCCATC TATTCTTTTT TAGGATCTAT TCTCCACTTT TAACTTTGAG GATTCTAAAA TACTTACTTT AAAGTTATTT TTAACTTGTT CTATTTTTGT TTTTGTCAGG AGCGAATTTG CCTTTTTTAT TTGGCTGTTC TACCATGCTT	6 12 18 24 30
(2) INFORMATION FOR SEQ ID NO:98:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 279 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAATTCGGCC	TTCATGGCCT	ACTCTACTCC	AAGTAGGAAA	AGGCCAGGAG	GTCCTGTTAA	60
AGGATGCACT	CAGAGCCCGG	GCTCCCTAAC	GTATGAGAGT	GCTAACCAGC	AGGTGTAGAC	120
TTTTCAGGAG	TGAAGAATGA	GGCAGGCATT	CCAAACCTGG	ACCTTCATCA	CCTTTTGTTT	180
CATCTCAAGA	CAATTCTGAG	GGACTGTTTT	GGAGCGTGTC	TGGAAGGTGA	ACGTTGAAGA	240
AGAGTGTGGG	CTTTGATGTG	ACTCAGTTGA	ATACTCGAG			279

- (2) INFORMATION FOR SEQ ID NO:99:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAATTCTCAT	GAAACTCTCA	GCGGAAAGCT	ACAAGGAAAC	ACAGATGGTG	AAGATTAAAG	60
AGGAACCCAT	GGAGGTTGAC	ATCCAGGACT	CCCATGTCTC	GATATCACCC	AGCCGGAATG	120
TTGGCTACAG	CACTTTAATC	GGGCGAGAGA	AAACCGAACC	CTTACAGAAG	ATGCCAGAGG	180
GCAGAGTACC	CCCAGAGAGA	AACCTCTTCA	GTCAGGATAT	CTCTGTGAAA	ATGGCTTCCG	240
AGCTCCTCTT	TCAACTGTCA	GAAAAGTGA	GCAAAGAGCA	CAATCATACA	AAAGAAAACA	300
CCATCCGGAC	CAATCTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:100:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GAATTCGGCC	TTCATGGCCT	AGAGCAACAT	AGTGAGACCT	CATCTCTACA	AAAAATAAAG	60
AGAAAATTAG	TTGGGGGTGG	TGGCGTGCAC	CTATAGTCCC	AGCTACTCAG	GAGGTTGAGG	120
TGGGAGGATC	ACTTGAGCCC	AGGAGTTTGA	GGCTGCAGTG	AGCTGTGGTC	ATGCCACTGC	180
ACTCTAGCCT	GAGTGACAGA	GCAAGATCCT	GTCTCAAAAA	ATAAAGTAAA	TAAAAATAA	240
CAGTCAACAA	CAGTGATTTG	TCTTCAAGCT	GCCCTCCTCT	TCGGCTCTCA	AGGCAGTTTG	300
TGAAGTGTCT	AGGATAGGAA	TTTTCCAGAA	GGGCTTGCTC	GAG		343

- (2) INFORMATION FOR SEQ ID NO:101:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGAAGATGTG	CCAAAGTTCA	GAAAACATAA	TCTTATCTGA	TCAGATTAAA	GATCACAACT	60
CCAGTGAAGC	CAGATTTTCT	TCAAAGAATA	TTAAGGATTT	GCGATTACCA	TCAGATAATG	
TAAGCATTGA	TCAGTTTTTG	AGAAAAAGAC	ATCAACCTCA	ATTOTOTOTO	TCTGATGTTA	120
GCGAGCAAGG	CACTATTCAT	TTCCAACCTC	AIGAACCIGA	ATCIGITAGT	TCTGATGTTA	180
CCACACACAC	TOTTOLAL	TIGGAACCTC	TGACTCCATC	CGAGGTACTT	GAGTATGAAG	240
CCACAGAGAI	ICTICAGAAA	GGTAGTGGTG	ATCCTTCAGC	CAAGACTGAT	GAAGTAGTGT	300
CIGATCAAAC	AGATGACATT	CCTGGAGGAA	ATAACCCCNA	CACTCTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:102:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GAATTCGGC	C TTCATGGCCT	ACTCGCGGTC	TGTTAGTAGT	ATAGTGATGC	CAGCAGCTAG	60
GACTGGGAG	GA GATAGGAGAA	GTAGGACTGC	TGTGATTAGG	ACGGATCACA	CCAACACCCC	
CGTTTGGT	AT TGGGTTATGG	CAGGGGGGTTT	TATATTCATA	ATTCTTCTC	CGAAGAGGGG	120
GGCCCCTAR	AG ATAGAGGAGA	CACCTCCTAC	CTCTTTGATA	ATTGTTGTGA	TGAAATTGAT	180
GGCTCCAGC	C TOCONTONO	CACCIGCIAG	GIGTAAGGAG	AAGATGGTTA	GGTCTACGGA	240
CTCCCACC	G TGGGATGAGC	GGGCCAAGAT	CGATGATCCC	ACAGACTCCA	AGCCTGAGGA	300
CIGGGACAA	G CCCGAGCATA	TCCCTGACCC	TGATGCTAAG	AAGCCCGAGG	ACTGGGATGA	360
AGAGATGGA	C GGAGAGTGGG	AACCCCCAGT	GATTCAGAAC	CCTGAGTACA	AGGGTGAGTG	420
GAAGCCCCG	G CAGCGTCTCG	AG				442
						772

- (2) INFORMATION FOR SEQ ID NO:103:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

AATAAAACTA GGAAAGTGGC ATG	GAAAGTA AGTTGGAACC ATGTAAGAAA AAAAGACACA GAGCTAG GCGTGAAGTT GCTGCTCAGT TTACATGTAT	60 120
GAAGTTCTGT GTGGACTTAA GCT	CCTACTT CAGTCATTTA TTGTATGACT TGGACAAGTT	180
GCCAAACATC TCTAATATTC ATT	CATATTT GTAGGGTAAA AGGATGAGTA ATATGTATCT	240
TTAGTGTATA AAACATTTAC AGA	CAACTCG AG	272

- (2) INFORMATION FOR SEQ ID NO:104:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

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- (2) INFORMATION FOR SEQ ID NO:105:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CARMMOOGGO						
GAATTCGGCC	TTCATGGCCT	ATGAAAATTT	GGAAGAAGAA	TCCAATGAAA	GTGGTAGCCC	60
TTTTCICCOT	CTTTTTTCAAC	TTTC > T COM> >			OTOGTAGECE	60
TTTTOACCCT	GIIIIIGAAG	IIGAACCIAA	TCTCTAACGA	TAACCCAGAG	GAACATGTAC	120
TGAAGGTAAT	TCCTGAGGAT	COTTONONE	CTC > CC > C >		AAAGAGGATG	120
	I CC I ONGONI	GCTTCAGAAT	CIGAGGAGAA	GCTAGACCAA	AAAGAGGATG	180
GTTCAAAATA	CGAAACTATT	CATTTGACTG	ACCAACCAAC	C2 2 2 Cm2 2 mm	CACAATGCAT	
		o	AGGAACLAAC	CAAACTAATG	CACAATGCAT	240
CTGATAGTGA	GGTTGACCAA	GACGATGTTG	TTGAGTGGAA	ACA CCCTCCT	TCTCCATCTG	
101000000			110AGIGGAA	AGACGG IGC I	TCTCCATCTG	300
AGAGTGGGCC	TGGATCCCAA	CTCGAG				326

- (2) INFORMATION FOR SEQ ID NO:106:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAATTCGGCC T	TCATGGCCT	ATGGCAATGG	TGGTCGTGGT	CCTCCCTCCC	3 TOMOGRAPH	
CATCCTCTTC C	TCCAGGAAG	GATGCCTCTC	CCATATCCCT	0010001000	AIGNGGICT	60
TCCCCACTTT C	CCTTTCACA	CECCECICIO	GGATATGGCT	GAAGGCCTCT	GGGTGCAGCC	120
TGGCCAGTTT C	CCTTTCAGC	GICCIGATAC	GGCGGAAGAT	GATGTCCAGG	TCCCGTTTCA	180
TCTCTACTAG G	GTCCTCGTG	TGGTGCAGGA	AGCGTTCGCT	CATCTGCTGC	AGGCGGGCAT	240
TGGACAGGTT G	TTGAAGTTG	AGCAGCATCT	CATTGGTCTT	CTCAAAGCGG	TCCAGCATGT	300
TCTTCTGGGA C	AGGATGATG	GCGTTGACAT	CATCTGTGTT	CACCATGCTC	ACCATCCCCC	360
CGCAGAAGAC C	CTCGAG			a recurrence to	MOGNICCOCC	
	CICOMO					377

- (2) INFORMATION FOR SEQ ID NO:107:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GAATTCGGCC	TTCATGGCCT	ACATGACACC	ACCTGAACGT	CTCTTCCTCC	CAAGGGTGTG	60
TOTOROGRACO	CEN CN COMOC	maarra			45.0001010	00
IGGCACCACC	CIACACCICC	TCCTTCTGGG	GCTGCTGCTG	GTTCTGCTGC	CTGGGGCCCA	120

GGGGCTCCCT	GGTGTTGGCC	TCACACCTTC	AGCTGCCCAG	ACTGCCCGTC	AGCACCCCAA	180
GATGCATCTT	GCCCACAGCA	ACCTCAAACC	TGCTGCTCAC	CTCATTGGAG	ACCCCAGCAA	240
GCAGAACTCA	CTGCTCTGGA	GAGCAAACAC	GGACCGTGCC	TTCCTCCAGG	ATGGTTTCTC	300
CTTGAGCAAC	AATTCTCTCC	TGGTCCCCAC	CAGTGGCATC	TACTTCGTCT	ACTCCCAGGT	360
GGTCTTCTCT	GGGAAAGCCT	ACTCTCCCAA	GGCCACCTCC	TCCCCACTCT	ACCTGGCCCA	420
TGAGGTCCAG	CTCTTCTCCT	CCCAGTACCC	CTTCCATGTG	CCTCTCCTCA	GCTCCCAGAA	480
GATGGTGTAT	CCAGGGCTGC	AGGAACCCTG	GCTGCACTCG	ATGTACCACG	GGGCTGCGTT	540
	CAGGGAGACC	AGCTATCCAC	CCACACAGAT	GGCATCCCCC	ACGCACTCGA	600
G						601

- (2) INFORMATION FOR SEQ ID NO:108:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTCGGCC TTCATGGCCT ATTTTTTTT TTTTTATCAA AAGTTTGTTT TATTTTCAAT
ACAAGATAAA TACCATGCTT GTTACTAGTG CAGTTCTCGA G 101

- (2) INFORMATION FOR SEQ ID NO:109:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GAATTCGGCC TTCATGGC	CT ACAGAATTGG	AGGCATGATG	AAGACTCTGC	TGCTGTTTGT	60
GGGGCTGCTG CTGACCTG	GG AGAGTGGGCA	GGTCCTGGGG	GACCAGACGG	TCTCAGACAA	120
TGAGCTCCAG GAAATGTC	CA ATCAGGGAAG	TAAGTACGTC	AATAAGGAAA	TTCAAAATGC	180
TGTCAACGGG GTGAAACA	GA TAAAGACTCT	CATAGAAAA	ACAAACGAAG	AGCGCAAGAC	240
ACTGCTCAGC AACCTAGA	AG AAGCCAAGAA	CAAGAAAGAG	GATGCCCTAA	ATCACACCAC	300
GGAATCAGAG ACAAAGCT	GA AGGAGCTCCC	ACCACTCTCC	AATCACACA	MONGACCAG	
CTGGGAAGAG TGTAAGCC	CT CCCTCAAACA	AGGAGIGIGE	AATGAGACCA	IGAIGGCCCT	360
CTGGGAAGAG TGTAAGCC	CI GCCIGAAACA	GACCIGCATG	AAGTTCTACG	CACGCGTCTG	420
CAGAAGTGGC TCAGGCCT	GG TTGGCCGCCA	GCTTGAGGAG	TTCCTGAACC	AGAGCTCGCC	480
CTTCTACTTC TGGATGAA	TG GTGACACTCG	AG			512

- (2) INFORMATION FOR SEQ ID NO:110:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TTCATGGCCT	ΔΔΔΤΤΛΤΤΛΑ	ACCMG10100			
TICATOGCCI	WWITHITH	AGGTGACAGT	ACACAGGAAA	CATTACAATT	60
TCAGCTATAC	ATTTACATCA	GATTATTGGG	TOCCTATION	ででころでころかかか	120
100101010		9.111111000	TOCCIAITIO	IICAICAII:	120
AGGACAGAAT	CTGGATAGTA	TGCTTCATGG	CACTGGGATG	AAATCAGACT	180
AAAGTCAGAA	AATGGAGTAA	CCTTACCACC	10100101		
	MATONOTAA	CCTTAGCACC	AGAGGATACC	TTGCCTTTTT	240
TTGCTCAGGG	CACTGTCCAG	ATGATGCTAT	TAATAACACA	TOCATARCTA	300
CTTTCCCCNTC	AMAGAAGA		TIMITIMENCH	IGCATAACTA	300
CITIGCCATC	ATAGAAGAAG	ATGACCAGGG	AGAAACCACA	TTAGCTTCAG	360
ATATGAAGGA	TCTCATTTC	ACTOCABACA	mmomoos s s =		,
	TCTONTTTTC	MOTOCAMAGA	TTCTCCAAAA	GCCCAGCTAC	420
AGAATGTTGT	CGGACCAATT	TATGTAACCA	GTATTTCCAA	CCCACACCCC	480
•			OTATTIGEAA	CCCACACCGC	480
					485
	TCAGCTATAC AGGACAGAAT AAAGTCAGAA TTGCTCAGGG CTTTGCCATC ATATGAAGGA	TCAGCTATAC ATTTACATCA AGGACAGAAT CTGGATAGTA AAAGTCAGAA AATGGAGTAA TTGCTCAGGG CACTGTCCAG CTTTGCCATC ATAGAAGAAG ATATGAAGGA TCTGATTTTC	TCAGCTATAC ATTTACATCA GATTATTGGG AGGACAGAAT CTGGATAGTA TGCTTCATGG AAAGTCAGAA AATGGAGTAA CCTTAGCACC TTGCTCAGGG CACTGTCCAG ATGATGCTAT CTTTGCCATC ATAGAAGAAG ATGACCAGGG ATATGAAGGA TCTGATTTTC AGTGCAAAGA	TCAGCTATAC ATTTACATCA GATTATTGGG TGCCTATTTG AGGACAGAAT CTGGATAGTA TGCTTCATGG CACTGGGATG AAAGTCAGAA AATGGAGTAA CCTTAGCACC AGAGGATACC TTGCTCAGGG CACTGTCCAG ATGATGCTAT TAATAACACA CTTTGCCATC ATAGAAGAAG ATGACCAGGG AGAAACCACA ATATGAAGGA TCTGATTTTC AGTGCAAAGA TTCTCCAAAA	TTCATGGCCT AAATTATTAA AGGTGACAGT ACACAGGAAA CATTACAATT TCAGCTATAC ATTTACATCA GATTATTGGG TGCCTATTTG TTCATCATTT AGGACAGAAT CTGGATAGTA TGCTTCATGG CACTGGGATG AAATCAGACT AAAGTCAGAA AATGGAGTAA CCTTAGCACC AGAGGATACC TTGCCTTTTT TTGCTCAGGG CACTGTCCAG ATGATGCTAT TAATAACACA TGCATAACTA CTTTGCCATC ATAGAAGAAG ATGACCAGGG AGAAACCACA TTAGCTTCAG ATATGAAGGA TCTGATTTTC AGTGCAAAGA TTCTCCAAAA GCCCAGCTAC AGAATGTTGT CGGACCAATT TATGTAACCA GTATTTGCAA CCCACACCGC

- (2) INFORMATION FOR SEQ ID NO:111:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAATTCGGCC	TTCATGGCCT	ACACACATTG	TGAGCTGTAT	ACGTTAACCC	AAAGTCTGCA	60
TTCAAAGTGG	AATTATAACT	GGGCAGTGAA	TGAGTTGCTC	AGTCCATCTA	TTAACCATAC	120
TCTTTTAGGC	TTTTTTTTGC	CTCTAATTGT	TGTAATAATT	AACATTTTCC	CAGGAAGTTG	
TTTTACAGAA	GAAGGGGCCT	TAGCGGCTTT	Chacacata	CACATITICC	CAGGAAGTTG	180
GATTGACCAC	AGCACATCTT	CTTTACTACT	CACCCCCAGO	GAGATAAGTT	CTCTAGAGAC	240
ACAGCCGTGT	CTGAGATGGA	CATTROTAGE	GAGCGGGAGC	CATATGAATC	CTCTAGAGAC	300
NCHOCCO101	CIGAGAIGGA	CATTGCCAAC	ACAGCTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:112:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TTCGGNCTTC	ATGGCCTACT	CTCATAAAAA	TATTCAAAGA	TCAACCCCAA	ACGTGCCTGC	60
ANTTTGGACA	ATGTNAGCTA	AAGCTATAAA	TGGAACAGCA	GTGGTCATGG	ATGATAAAGA	120
TCAATTATTT	CACCCAATTC	CAGAGTCTGA	TGTGAATGCT	ACACAGGGAG	AABATCACCC	180
AGATCTAGAG	GATCTGAAGA	TCAAAATAAT	GCTGGGAATG	TCCTTCAVCA	AAAAICAGCC	
CTTTGTGGTC	CNTCTTGGCA	TTCTGTAGTG	CTRCACRORA	1CG11GANGA	cccrccrccr	240
ATAAAACTTC	TCACACTCAC	TICIGIAGIG	CIACACIGIA	CAAACTGAGG	CATCTGAGTT	300
ATCCAMCACA	I GAGAGICAG	TACTCTGTCA	ACCCAGAGCT	GGCCACGATG	TCTTACTTTC	360
ATCCATCAGA	AGGIGITICA	GATACATCCT	TTTCCAAGAG	TGCAGAGAGC	AGCACATTTT	420
TGGGTACCAC	TTCTTCAGAT	ATGAGAAGAT	CAGGCACAAG	AACATCAGAA	TCTAAGATAA	480
TGACGGATAT	CATTTCCATA	GGCTCAGATA	ATGAGATGCA	TGAAACACTC	GAG	533

- (2) INFORMATION FOR SEQ ID NO:113:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAATTCGGCC AAAGAC					60
TCAGTCCTCA CCAGAT	TTGT CAAGTGAAGA	AAGTGAAACA	GAAAAGGAAA	TTAAAAGGAA	120
AGCTGAAGTT AAGAAA					180
GAGCACAAGA AACACA					240
AACAGAAAAG GAAATT	AAAA GGAAAGCTGA	AGTTAAGAAA	ACCAAAGCAG	GAAACACCAA	300
AGAAGCAGTG GTTCAC	CTGA GAAAGAGCAC	AAGAAACACC	CTCGAG		346

- (2) INFORMATION FOR SEQ ID NO:114:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAATTCGGCC	AAAGAGGCCT	AGGCAGGTAT	TCTTTGCTTT	GGGAAATTCT	TCTTTCTGTC	60
CTCCCTTCCC	TCACTTTTTC	CAAATTCTGG	GCACAACAGC	AGCTCTCTCT	CTTCTGTGGC	120
AGGTGTGCAT	CCTATTGGCT	GGCTGGTATT	TCTTGTTTTT	TTTCCCCCTT	ATTCTTTTTA	180
AATGGGGGTG	GGGGTATAAA	AATATGTGTA	TGGGGTACAT	GCAATAATGT	TGTAATGTTT	240
CTTGTTGTTT	AATGGATAAT	TAATTGCAAA	ATAATTGTTT	TAA ITATAAC	ATGTTTGAGT	300
AAATGCTAAA	TTAGTATTTT	TTTCTAATAT	AATAATGAAT	TTGAAATCTA	GCATTCCTGT	360
AACAATGTGT	CTATGTTTGT	CTGTCTGTGT	CTGTCTAATA	GTAATTAATA	TCTGTGGTCC	420
GCACCCACTC	GAG					433

- (2) INFORMATION FOR SEQ ID NO:115:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC	AAAGAGGCCT	AAGCAAAGCT	TAGCTTACGG	GGAAAAAAAA	AAAAAAAAA	60
AAGTAGAGCT	TNCCTTGAAT	CTGGAGAAAT	TAAGCACACA	GGTGTCCTGC	AATATTAGTT	120
AAGAGACTAC	TGCACCCATC	ATACTGTAGC	TTAAGACAGT	TTCTTCTTTT	AGTTTTTTCT	180
AAAATGTCTC	CATGTCTGTG	TTATGCCACA	AATAACACAG	CCTTGGTTAA	CTTTTGGACT	240
AAAAAAAATC	AACTTATTGG	CCAAGCATGG	TGGCTTACAC	CTATGATTGT	AGCACTTTGG	300
ATAGGTCTCG	AG					312

- (2) INFORMATION FOR SEQ ID NO:116:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAATTCGGCC AAAGAGGCCT AATTTTCCTA ACTGTGTGCT GCCTTTTGGG TTAATTAGAA	60
TTGTAGCATT TCGTTTTGAT TATTTTTTTG GCTCTTTAGC TGTTCTCTCA CATTTTTTAA	120
AATGGTAACT CTAGGGATTA TAATATGCAT CTTTAATTTA TCAAAGTCTG TTTTTACTAC	180
TTCGTGTAAA ATAAACGAAC CTTGCATTTA TAGTTACATT TATTCCTCTC ATCTCGAG	238
(2) INFORMATION FOR SEQ ID NO:117: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 184 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:	
GAATTCGGCC AAAGAGGCCT ACTCAAAAGT AGATGAGCAA TTGGTCAGAA TTGTTAGAGG	
ATATTATTTG AGCTAAATGT TTCCTCTCTC TGTTTCAGTG GTGTATGTGC AAGTGTGTGT	60
ATATGTTTT TGTTGGGGAC AGTTTCAGGT AGATGGTATG AAGAGGCAGC AGGAGACTCT	120
CGAG	180
	184

- (2) INFORMATION FOR SEQ ID NO:118:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCCGCC	TTCATGGCCT	AATTTTCTAA	AACCTGGAGA	CAAACCACAT	AAATACAAAA	60
CAAGTCTGCT	TCTTCAAAAT	TCTGCTGGTG	AGAACTCAGA	TATCAGTGAT	CTTATTAGCT	120
TTTTCACAAG	CCAGAACATA	ATGGTGACGA	TGATTAATGA	CAGTGACTAT	GTATCCGTGG	180
CTCCCCATAG	TGCGGCTTTA	AATGTGATGC	ATTCAGAAAA	GGACTATGTT	TTTGCAGCTG	240
TTTTCAACAG					AGTAACTACT	300
ATCTTTATCA	TTTAAATGTG	ACTGAAACCA	TCCAGCTCGA	G		341

- (2) INFORMATION FOR SEQ ID NO:119:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

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GAATTATGCT	GTGCTGTTTT	CCTGGACACT	CAGAATCAAA	CAGGCCTTCC	ACCCCATCCC	60
ATCATGTTGA	ATTACAAAGT	ATTTTGAGCA	TCGTTTGGTT	TGTTTCTTTC	CACCCATACC	120
TGTGTAGGGC	AGCGGTAGCA	GTCTTCAACA	ATGCATCCTC	TTGGACAATG	CATTGTAATA	180

AAATTCATTC CACACTGTCA TCCCTTTGTC CTAACCAGAA TCTCGAG

TCTCTCTTTC AAATTCTGTT TCACATAGTC ATTTCTCATG TTCTGTTGGA GACCCCCAAA

240

287

(2) INFORMATION FOR SEQ ID NO:120:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 196 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	,
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:	
GAATTCGGCC TTCATGGCCT AATGTATGGT AGACAATTTT TTTTTAAGAC ACAGAGATAA ACGTTTTCCT GCTTTGGTTA CCTTTCCTTT	60 120 180 196
(2) INFORMATION FOR SEQ ID NO:121:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 117 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:	
GAATTCGGCC TTCATGGCCT AGTGATTGGG TGCAGAGGAA ACAGGAACCA GAGAAGGGTC ATCTCAGCTG CCTGTCCCAC TCCCTATGCT TGGTGTTACC TGCGCCATAG TCTCGAG	60 117
(2) INFORMATION FOR SEQ ID NO:122:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 234 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:	
GAATTCGGCC TTCATGGCCT AGTAAGTGCT CTGAGTATAT TAGGAAAAGG AAATCTTATA CATAAAAATC AAAGCTGTTG CTAATTTTTC CACTAGTGAG TCAGTCTATT AACATTACTC ATGGTAGGTT TTGCCATACA GAATTTTAAT TTTTTTATAT TATTTTTGGC TTTGTTATTA TGCTTAGAAG TCCATGGGGA CCCAAAGATC AGAAAAGATT CATCTGTACT CGAG (2) INFORMATION FOR SEQ ID NO:123:	60 120 180 234
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

					TGCTAATTCC	60
CACTGTCATG	TTCACAGTGA	TGGCCGTCTT	TTCCTTCATC	GCCCTCAGCA	TGGTTCATAA	120
ATTTTACCGG	GGAAGTGGGG	GGAGTTTCAG	CAAAGCTCAG	GAGGAGTGGA	CCACAGGGGC	180
CTGGAAGAAT	CCACATGTGC	AGCAGGCAGC	CCAGAACGCA	GCCATGGGGG	CAGCCCAGGG	240
	CAGCCAAGAC					265

- (2) INFORMATION FOR SEQ ID NO:124:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTTGCCA CACCATG					60
CCATCCTGCT CCCGTTC	GTC TACCTCACGG	CGCAAGTGTG	GATTCTGTGT	GCAGCCATCG	120
CTGCTGCCGC CTCAGCC	GGG CCCCAGAACT	GCCCCTCCGT	CTGCTCGTGC	AGTAACCAGT	180
TCAGCAAGGT GGTGTGC	ACG CGCCGGGGCC	TCTCCGAGGT	CCCGCAGGGT	ATTCCCTCGA	240
ACACCCGGTT CCTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:125:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

TGTCGTTTTT CACTGCCTAT AGGACCACT CATTTTATAA CAACAACAAC TGCTACTAC	I CGTGTTTTAC TTTAATAAAC CTGAAAGAAC A CAAAGCCGCA AAGAAAAATT AGACTTGTTT I GCTACTAGTT AGATACCGTT TGCTCATTTA A AACACTTGGC ATTCATCGTC TTTTTCAGTC	60 120 180 240 248
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- (2) INFORMATION FOR SEQ ID NO:126:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

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5		PCT/US98/06955	
GAATTCGGCC TTCATGGCCT ACTGTCTTTT CATGCAGATT TCATTGCTTC TTGACCTTCC TGGCAGGTGT CGCTCAGTTT CCTCTCCACA CCTGCTATCC CGTCCCACTC CCATCTACCT TGCTGAGTTT GTGACCTGCT TCATTCCCAT TTCATTTCTA GAACCGTTCC CTTTCCCTCT CCTACCCCCT CCTCTGCAAC AGACAGAAAG CAGCCAGCCA CGGCGGGAAG TCTCGAG	CTTCCTGTTT CCCGGGAAGC GAGGGTTTAG	CCCTTCCTGT CAGCCCTGCA AGGTGACCTG	60 120 180 240 300 337
(2) INFORMATION FOR SEQ ID NO:127:			
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear			
(ii) MOLECULE TYPE: cDNA			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	127:		
GAATTCGGCC TTCATGGCCT AACTTATTTC TTTTGTTGAT TCCTTCCCTC CCTCCCTCCT TCCCTTCCTT CCTTCCTTCT TGTGGCCAGG TTGGTCCTGA GCTTAAGTGG TCCTCGCACC GATTACAGGT GTGGGCCATC ACGCCTGGCC TTACAGTAAA AACACACCTC GAG	GTAGAGATGA TCAGCCTGGC	GGTTTCACCA AAACTGCTGG	60 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:128:			
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 319 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear			
(ii) MOLECULE TYPE: cDNA		•	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	128:		
GAATTCGGCC TTCATGGCCT AGGACGGGG ACTCAGGTTC TGTATCATGT ACCAGGTGG GAGAAGTGTA GCAAATCTCA CAGTCATTCC AGGAGAAGAG CTGAGGGGAA AGAGCTGTTG ATTATCCAGT CACCCTCCTG CCACATGGCA GAAGCCAGGT AAACAAAACA CACAGTCTCT GGCAAGCCCC ACCGGGAAAG GGGTCCGGAT ATCCTCGAG	GTGCCAATTT ACTTTCATAA GGCAGTGATG	GAGGGGAAGC TGCAGTCTTA GTGGTGGGGG	60 120 180 240 300 319
(2) INFORMATION FOR SEQ ID NO:129:			
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 348 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear			
(ii) MOLECULE TYPE: cDNA			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	129:		

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GAATTCGGCC TTCATGGCCT ACAATAAAAG CCCATAGGGA AGAGAGAGAG GATATAGGGA

AACAGAATCA GATGTGTAAT ATACTTGGCA CAGCGAAAAA ATGGATTTAA AAGACAAAAA

TGGAGGTCCA GGTAGATGTA ATTCACACAG ACTGAAAGTG AGTTCGGGCT TGTGTAAAAC

WO 98/45436

i		PCT/US98/06955	
TTGGTGGCCA	GGATTTGACC CCTTGGCTCT CAAGTGTCCC CTTAGATCTA TTAGATCGAG TCAGTTTTGA TCTGCATCAC TTAGTTATTG AGGAAAATTT TTTTAGATTA TTTGGCGTAC GGCTCGAG	GAACTGCTCC GGAATTTCTT	240 300 348
(2) INFORM	ATION FOR SEQ ID NO:130:		
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 420 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:130:		
CAGTGGGTCC ATTTTATAGA TGCTGCCTCC GAAGTTCTTC CTCAGTCTGG	TTCATGGCCT AGGCACAGTG AAACCCGTGG AAATTCAAAG TGTATCTTGA TCTTTACGGA TCTTTCTCTT CTTGAATCCT CAGGAAGACT GAGGCCCGAA AGTTCTGTCT GACTCTGAGC CGTTGTCCTG TGAGGCTGTG TGGTCACAGC ACCCAGGACT CTCACCCCGC AAAGGCTTCA TGAGCCCTAC TGTGTGCCAG GGCGATAAAC ACAGGGCAGA TTCTGAAAGC CTGTGTGAGG GCTGAGAGGA GACCCTGGAG AGGAAGGGAG TCAGGGCCAG	CACAGCACCC CTGGCCTCTT TGAGAGGAGT GCCAGCCCTG GAAGTTCTAG	60 120 180 240 300 360 420
(2) INFORMA	TION FOR SEQ ID NO:131:		
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 433 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:131:		
GAGCAAAGAT TGATGATAAA TGATGATGAA ATTTCTGAGA CCTAATCTAT	TTCATGCCTA AGCTGATGGA GACTGTAAAT GAACCAGAAA GCAGTCATTG TAAAGCAGGA GAAAAATAAT GAATATTGCC TTGTCAGAAT CAGCAGAGGA TGATGGTGAA GATGATACCA GATAGTAACC CTAAAAAGAA TACTCAGGCC CCACTAGAGT GCAGAAATGG CCCGAGAGTA CCAGCTGGCA AAAAAATTAT GAACCAGAAA ATCCTGAGGC CAAGGAGTTT TTCACACTTA GAGAAAACTC AGAATCATGA GCAAGACGGT GAAAACAGTG GAG	TTCAGGATAT ATGATGAAGA TAATGGCAGA GTCAGATGAT TTGAAGAAAT	60 120 180 240 300 360 420 433
(2) INFORMA	TION FOR SEQ ID NO:132:		
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 280 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:132:		

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GAATTCGGCC TTCATGGTCT ACAAAATCAA CTGCAAGCAG CCATCATCAG TTTGGAAGAA

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		PCT/US98/06955	
CATTCCTTTT	CCCCCTGAAG AGTACTCCTA TAAGAAATCA ATAAGAAAC GTCCTTCTGT TGATCACTTA TGGTATCATG ACTGGTGCC TTAAATCAAA TGATATTGAC ACAACTCGAG	T TTTATTCAGT	180 240 280
(2) INFORMA	TION FOR SEQ ID NO:133:		
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 398 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:133:		
NCTCTGAACT CTGAAGAAGT TGGTAACATC TATCTGTTGT TCAATGATGT	TTCATGGCCT ACGCGAGCGG CAGGTGTGCA CAGGAGGTT CGCGGTCAGG ATGGTTTCT CTGTCAGGCA GTGTGGCCA TTTACTGACG TTCAAGATAT TCCTTGTCAT CATTTGTCT CCTGGAAGAA GATACTGATA ATTCCAGTTT GTCACCACC CAGTTTTGCC CCCTCCTCA ATGGTACTCC AGAGGTTGA TACTTTAAGC TTACTCCCTT CAAACGAAAC AGAAAAAAAC CTTCAATGCA TCAGGCGTCA ATCTCGAG	T GTTGGCAGAA T CATGTCGTTC A CCTGCTAAAT A ACAACAAGCC T AAAATCACTA	60 120 180 240 300 360 398
(2) INFORMA	TION FOR SEQ ID NO:134:		
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 403 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:134:		
CTCCACCAGA TGGAGTTTTG ACAGCTGTAT CAGTGGTCTG CTATGTGGTT	TTCATGGCCT AGGGCGATGG TGGGCAGAGG ATCCTTAGT ACCACGGACT TGAAGGAGAA GAGACTCTCG GTTCCAGGT GACACAGATC CTCCTGGCCA GAGAAGGATG CTTGAGAAT TAGGTTGTCC ACGATGACCG GGCAGTAGGT CTCTCTCTT CCAGAGACGG GCGTGAGAGA TCACATTCAG AACGCACTC CCTTGGATCA TCAACAAGGC TAAGCACTTT CTCGGGAAG GGTGAGCCAG AGGGCCTGCT TTACACCCTC GAG	A GCAGAAAACG C TGAGATTTAC G GGGATTTCCT G TCTTGGTTCT	60 120 180 240 300 360 403
(2) INFORMA	TION FOR SEQ ID NO:135:		
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:135:		

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GAATTCGGCC TTCATGGCCT ACTCCATTTT TCGAATGGCT TATTTAGGCC CAGCTCTTGC

GTTTGCATTG TCCCTTCAGG CCCAGAACTT TCTCACGTCA TCGTCACCAG GCCTAGCTTC

TGCATCTGGT CAGCCTTTTA AGGCCCAGCT TTTGCCTCAT AAACTCAGCT CCTGTTTAAT

205

GGCGGCCTCC CGGGTCCCAC TCGAG

(2) INFORMATION FOR SEQ ID NO:136:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 112 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:	
GAATTCGGCC AAAGAGGCCT AGTTTTATTA CTTTGGTTAA GACATCAGTT ATTTTAGTCT TTGATAATTC ATTATCTAGA TAATGGTTAC TTTGTATTGT CTGTTTCTCG AG	66 11:
(2) INFORMATION FOR SEQ ID NO:137:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:	
GAATTCGGCC AAAGAGGCCT ACACAGAGCC CTTCAGTACT TTTAATTCTT CTTAAATTGG TGGTTCATGT TAATTAAATT ATTATTATTT TTTTTTGAGA CGGAACTCGA G (2) INFORMATION FOR SEQ ID NO:138:	60 11]
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 324 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:	
GAATTCGGCC AAAGAGGCCT AAAGATGTTT TCCATGAGGA TCGTCTGCCT GGTCCTAAGT GTGGTGGGCA CAGCATGGAC TGCAGATAGT GGTGAAGGTG ACTTTCTAGC TGAAGGAGGA GGCGTGCGTG GCCCAAGGGT TGTGGAAAGA CATCAATCTG CCTGCAAAGA TTCAGACTGG CCCTTCTGCT CTGATGAAGA CTGGAACTAC AAATGCCCTT CTGGCTGCAG GATGAAAGGG TTGATTGATG AAGTCAATCA AGATTTTACA AACAGAATAA ATAAGCTCAA AAATTCACTA TTTGAATATC AGAAGAATCT CGAG	60 120 180 240 300 324
(2) INFORMATION FOR SEQ ID NO:139:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GAATTCGGCC AAAGAGGCCT AGGTCCAGAA ACATTTAAAA AAAAAAAAA GGGGGCTTGA 60 GAAAAGGGCT TCCAGTGCCA GGCAGAAATA TGTTTTTCTT AATAGGGC 108

- (2) INFORMATION FOR SEQ ID NO:140:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCGGCC	AAAGAGGCCT	ATGAAAACGT	GGATTTGCTT	TGTAAACTTG	AGAATACATT	60
TTGTTGCCAA	CAAAAAGAGA	GAAGAGAAGA	GGAAGATATT	GAAGAGAAGA	AATCGATTAA	120
GAAAAAAATT	AAAGAACTTA	AGTTTTTAGA	TTCTAAAATT	GCCCAGAACC	TTTGTAAGTA	180
TCATATTCCA	ATACCATTCA	AAGACAGTGG	AAATATTTCT	TTAAATGATT	TCATTTTCTT	240
TAAGACCGAT	TATTCATTAT	TTGCTATTTT	CATTTTGTTA	TTATATGCAT	GATAAATTCA	300
CAGATACTCT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:141:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAATTCGGCC	AAAGAGGCCT	AGGGTAAGAC	TAGAGTGTTT	TAAATCATCA	ATAAAAAGTG	60
GAGAAAACAA	AGGTTATTCA	GCGATTGAAT	TCTAGACCTG	CCTCGAGCCC	TGCCTTTCCT	120
TTACTTTTAC	TTTTTTTTT	TTTTTCTTTG	GAAGAGAGAA	GAACAGAGTG	TTCGATTNTG	180
CCCTATTTAT	GTTTNTANTC	GGGAACAAAC	GTTGGTTGTG	TGTGTGTGTG	TTTTCTTGTG	240
TTGGTTTTTT	AAAGAAATGG	GNAGAAGAAA	AAAAAAATTC	TCCGCCCCTT	TCCTCGATCT	300
CGCTCCCCCC	TTCGGTTCTT	TCGACCGGTC	CCCCCTCAAC	CTGCCTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:142:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GAATTCGGCC AAAGAGGCCT AGAGAGTCTG GATGACAAGC AAAGCTCAAT CTCAAAACAA

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TATTCATGGG AGTGTCTGGA AAAGGGACAA AGAGCGGCTA TCTCGAG

TAATTTTTAA AGTAATGATT ATCTTAACCA TTCTTAAATC CTTCTGTCTA GTAGGAATCT

120

(2) INFORMATION FOR SEQ ID NO:143:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 216 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:	
GAATTCGGCC AAAGAGGCCT AGTGTTTCAC AAAAGAATTG GAAACCATAG TCCTGAACTC TCCCTAAGTA GTATAAGCTT TAAATAGCAC TCAATCCATA TTAAGTCTTC TTAGTGTAGC ATGGTTGCTC TCATGCGTCT TTCTTATGTT TTAAATGGTG TAAATTTTAG TCGTTTGTCA TTCAGAAGTG GCTTTGCAAA TACAAAATAT CTCGAG	60 120 180 216
(2) INFORMATION FOR SEQ ID NO:144:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 301 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:	
TAATCTTTAC TGGTGAAAAG GATGGAAAAA TAAATCAACA AATGCAACCA GTTTGTGAGA AAAAAAAAAA	60 120 180 240 300 301
(2) INFORMATION FOR SEQ ID NO:145:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 177 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:	
GAATTCGGCC AAAGAGGCCT AGTCTCTGTT AATCCTACTC TGCTTTAGCC AGAATAGCCT AGTATTTAT TTCTATTTTA TATATTGAGA TTTCTTCTAA CATTTCCTTT GATAAAAATC TTCTGCTTTT TGAAAAGTGG TATGTATCAT ATTTTTATGT TTCTGGTGTG TCTCGAG	60 120 177
(2) INFORMATION FOR SEQ ID NO:146:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 310 base pairs	

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAATTCGGCC AAAGAGNCGT AGGGAAAGA	T TTCAGCTATT	AATCAACTGG	AGGAAATTCA	60
AAGCCAGCTG GCTTCTCGGG AAATGGATG	T CACAAAGGTG	TGTGGAGAAA	TGCGCTATCA	120
GCTGAATAAA ACCAACATGG AGAAGGATG	A GGCAGAAAAG	GAGCACAGAG	AGTTCAGAGC	180
AAAAACTAAC AGGGATNTTG AAATTAAAG	A TCAGGAAATA	GAGAAATTGA	GAATAGAACT	240
GGATGAAAGC AAACAACACT TGGAACAGG	A GCAGCAGAAG	GCANCCCTGG	CCAGAGAGGA	300
GATTCTCGAG				310

- (2) INFORMATION FOR SEQ ID NO:147:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGTGGCCTTG	GGTCAAGATT	CGCACCATGG	TGGGCACAAA	CCCAGGAGAA	CACTTTCCTG	60
TAAACGTGTT	TTCATGCTGG	AGCCAAGGTT	TTGACTTGGG	TTTGGATTTT	TATTTATTTA	120
TTTATTATTA	TTATTACCAG	GTTGCATCTA	AAGGATGTTT	TGGAGGAGCA	CAGAGTTTGT	180
CTGGTGAGGG	TAGGCTCTGG	GCAGATTTTT	CTGTGAGTCT	CCCCTGCCTG	CGGCATCAGG	240
ATCATCCCTG	GTGCCCTGTG	GTGGCACCAG	GTGGCTGCCC	ACCCACAGGC	GTGGCCTTCA	300
CAGTGGGGGC	CATCTCAGCC	TGGGGTAGCG	ATCTGCCTCC	GACCTGCCTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:148:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGCCTGCATC	GCAACAGCCA	GGAGGGCCAG	GCCACCCCAG	GCAGGAGGCA	GTGGGCTGGC	60
AGCCACCCTG	GGCACAGAAG	AGCAGACGCA	GACAGTGCTG	GGCAACGAGG	GGCTTTCTTC	120
ATGGGCCCGC	CTGCCCTGTC	CCTCCCCCA	GGTCCCCACC	TTCTAGGGTT	AAAGTGCAGC	180
TGGGAGGGAG	GAGGCAGGCA	GAATTGGGGA	GCTAGAGAGA	GCCCAAGTGA	ACCCTGACTG	240
TCCACGCAAG	TCCCATGTCC	TCCTCGTCCT	GGAGTTCCTC	GAG		283

- (2) INFORMATION FOR SEQ ID NO:149:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GAATTCGGCC TTCATGGCCT	AGACCTGCCT	CGAGTTCCTT	TTGTTATTTC	CCTGCATCTT	60
ACAACGTTAA GGCCTTGGTC	CCTGCTAATA	ATAAAATAAT	AATCAACTTT	ATAAAGAGCT	120
TACAATATGC CAGATACTGT	ACTAAGTGCT	TTATATTTTT	TTTTTGGGTG	GGGGGTGGCT	180
GTTGGGCAGT GTCTCGCTCT	GTCACCCAGG	CTGGAGGGCA	GTGGCACAGT	CATGGCTCAC	240
TGCGGCCTTG ACCTCCTGGG	CTCAGGCCTC	CCGCCTCAGC	CTCCCAGGTG	GCTGGGGCTA	300
CGGGCGTGCA ACATTCTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:150:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAATTCGGCC TTCATGGCCT	ACGTAATTCT	GGAAAAGTGA	ATACTTGTGA	AGAGTCGTCT	60
TGAATGATTT GTAAAAAATC	CTGTTCTTAT	ATTCAACGAG	TTTCGAATCT	TTGTCAGAGG	120
AGTATTACCA TTAGATTGAA	AAAAAGGAAA	ATAAATAATA	AACACTTTTA	AAAAAACTCC	180
CCATTCTCTT ATTCTCACTT	TTAGGAAAAG	AGACTGACTA	ATATCTTCTG	CCACAAATAC	240
CGATGTTCTT AAAAATATTT	ATGGGACTGC	TTTTGGCAAC	CAGCCCTATT	TTGTTTTCAT	300
ATCCCTTTTT GCTCCCATCT	TTCCAAACTC	ATAAACTCGA	G		341

- (2) INFORMATION FOR SEQ ID NO:151:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAATTCGGCC TTCAT	GGCCT ACTCGCCTCT	АСТАЛАЛАТА	CAAAAATTAG	CCAGGCACGC	60
GCCAGGTGGT GCGCA	CCTGT AATCCCAGCT	ACTAGGGAGA	CTGAGGCGGG	AGAATTGCTT	120
GAACCTGAGA GGTAG					180
GAGACTCTGT CTCAA	ААААА ТАТАТАААТА	AATAAATGAA	AAAAAATAAT	TGTATAACAT	240
CTATACTATA GCCTC	GTAAG CATTAGCTAC	TTAATATTT	TGGTATATTT	AATAATTTTA	300
ATACAGCATT TTTGA	TTACT AGTGAACATG	AATATTTTCC	CATATTTGTT	AATTATACTT	360
TCCTCTTACA GAAAT					405

- (2) INFORMATION FOR SEQ ID NO:152:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCGGCC TTCAGGGCTC CTTCTTCCTA GGCTAGTATT TATCCCACTA CATCTGACTC ATTCTCTACT ATCGCTGTTG ATTTCCTCTT GGCTACTAAA TCTGTTGAAC ATGTTGCCAG GCTTACTGCT GGTATTATGG GATAGCATTT GGCTAGTGGC AGCTTCTAAA GGAGACTCCG	60 120 180
ATGGCACTAA GCAGTTTCCA AAAGTTTATC TTGCAAGTTC AACCCAATTC GAG (2) INFORMATION FOR SEO ID NO:153:	233
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:	
GAATTCTAGA CCTGCCTCGA GATGTTTTTT TCGTTATTTG AAATCTTTGC TCTTTTATTT	60
TTCAGCTCCC AGATCCTCTC CCTCTCTTTA GCTTTCACTG TGTTTGATAT CAAGAATATG AAATGTGAAT TCCACGGACT CGAG	
(2) INFORMATION FOR SEQ ID NO:154:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:	
GAATTCGGCC TTCATGGCCT AGGCAGGAAG GAGGCTGGAA TAAATAAAAA TAAAAATAGA	60
CAAGTAAGAC AGCATAAATA ATACATTTTT AAACATGTCA ACATTGATAA TACAATGAAG ATTTACCATA AAAAGTATCA TATCTAACCA AGATATGCAA AAGATGCATT CAGTAAGCTG	120 180
TAACGTTGAG AAATGTAACT GTGAAATCAG CTCACCAGTT CAAGTCACTA GGTTTGCCAC	240
TTGGACCGTC TTGGTTTCAG CGAGCATAGC GAGTGGCTGT AAGAAATTGT CCATGCCACC	300
AATTCCACTG CTACTTGCCC AGGTGGTCTC GAG	333
(2) INFORMATION FOR SEQ ID NO:155:	•
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 275 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:	
GAATTCGGCC TTCATGGCCT AGGAAGTGGA GGGAAGCTGG GTCGCTGCTG GAAGGGAGGG	60
AGGCTGACTC TCTACCCCTC ACCTCTGCAA GGAACTGAGG CCTGTAGGGT TGCGGCTGTC ACTGGCTACA GGCGGCATCT TTCTGTAAAA AGCTTTTCAG GCATGAAACC CATTTCTGTA	120 180

TGGACTGGGC TGTGTTGACG GTGGTGCTTG GGCCTTGTGT GCCAGGCCTC TCTGGGTCCC

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275

CTCCCTGGCC TTTGCCTTCC TCTCACCTTC TCGAG

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 244 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:	
GAATTCGGCC TTCATGGCCT AGAGTCATAG GTCAGACCAC TTTCTAGGAG CTGTTCAGTG ATAAAATTAA TAACAGTGAC TTTTGAGTCA AAATAGATTT TTAAAGTACT TGATTTTCTC TTTGATTTGG AAACATCTTT GTTTAGCTTA ATTGAAAATGA TCTAAAATAT TTGAAGGATT TTATACTTTA CACAGAGGCA TGTATTTGGA TAATTAGCTT TTATTAAACC CAGGCTTCCT CGAG	60 120 180 240 244
(2) INFORMATION FOR SEQ ID NO:157:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 249 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:	
GCGATTGAAT TCTAGACCTG CCTGAACCCC ACCCTTCACG TCCTACTTGG GCTGCCAAAG TCATCTTCCC AAAACATGAC TTTTCCTCAG TCACTTTTCT TATTAGATTT TATCATATTC CACATCCCTT CCCTGGCCCT CAAGGGTGCC TGTAACCTAG AACCATCTTA CCTTTCCACC CTTGTTTCCA AACCTTCCGC TTTACTTAGA CATGCCTTCC CATTTCCCTC CCGACCCACC CCCCTCGAG	60 120 180 240 249
(2) INFORMATION FOR SEQ ID NO:158:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 274 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:	
GAATTCGGCC TTCATGGCCT AGAAAAAAC AAGTAGTTTG GCAAGGAGG CAGAAAAATA AAATTCCACT GTGTAGGCAT TTGGAGATTT AGCAAGAGCA ACCTAGAGTC TGCCCCCAGA GACACTGCAC GTTGTTTCTG ACACAGAGGA TGCACTAATT CTATTTCCTG TGCCACCTGA AAAAATCATA ATTTGAGAAG AGAAACTGTT AGGCCATTTC TAGTGAACTA TTTTTCCAAA CCCTCACGGA ACCCTGAACA GGGCGTGTCT CGAG	60 120 180 240 274
(2) INFORMATION FOR SEQ ID NO:159:	-
(i) SEQUENCE CHARACTERISTICS:	
141	

- (A) LENGTH: 298 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GAATTCGGCC	TTCATGGCCT	AAGCTTGCTC	ACTCTTCTGT	GTGTTTGAAA	TAATGGTAAA	60
ATACAATAAT	ATTGTCAAGC	ACAGTGGATC	GGAGATTTTT	CTTCTCAGGA	CTATTCTGCT	120
TATAGGTCTA	CTTCCTATAG	CTATTTGTCA	TTGTCCTCCT	GGTCCTTCTC	TTTTCTTCTC	180
TCCTGTGCTA	GATGCTCTCT	CTTCCTATCC	CTCCCTCTCT	TCCCACCCC	ACCTCCCACT	240
TCTCTGTTTA	TATCCTGATT	TTGGTGGAAC	ACATCCTCCA	GGCTCCCTGG	CACTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:160:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATGGCCTAAG	GTGCCCNAGC	TTGCCAATTA	ATTCCCAGTA	GAAATTTTTA	AATGTTAAAG	60
ACAGTAATTA	ААААААААА	AAAACCACAC	TGTTTTGACA	TTTTACCTCG	TGCTTTGTGT	120
GTGACTAGAT	TATGCACTAG	AATTTCATTC	AGTATTCTTC	CAAATAAGTT	ATTTCCCAGG	180
TGTTCGCTGG	TATCTAACCA	ANTANTCAAT	AAAGTATTCT	TGCTAAGTNG	GCCATGAAG	239

- (2) INFORMATION FOR SEQ ID NO:161:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GAATTCGGCC	TTCATGGCCT	AATATCATGA	TCACTGAAAT	TACATCTAGT	GAAACACACA	60
CGTGCTTATC	TGCACGTGTG	TGTAAGTTAG	AAAGAAAAA	CAAAGGCCTA	ACAGTGATTG	120
TCTTAGGTTG	ATAGGATAGT	GGGTGGGATT	TGCAGAATTT	TTGTATCTGC	AGAATTTTTG	180
CAAAGTGCCC	ATTAGTTTTG	TAAAGAAAAA	AACCTAAATG	TATAACTTCT	AAAGAGATAA	240
TTTTTTCTTT	CATGTTTTTG	CTACCTATAT	CTAGGAAAAT	AACTTAGAAT	TGTAATTATT	300
TTGAAGCTCT	GGAATTATTA	TGTTCAAAAA	TTACAGAACC	AAAAAGTCTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:162:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 469 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GAATTCGGCC TTCATGGC	CT ACTTGCTGTG	GCTGACTCGG	TTATTGACTT	TACTTCTTTT	60
CTTTTCAGGT TTTTATGG	GA CTGTTTCTAG	CCCTGATTCA	GGTGTGTATG	AAATGAAGAT	120
TGGCTCCATC ATCTTCCA	GG TGGCTTCTGG	AGATATCACG	AAAGAAGAGG	CAGATGTGAT	180
TGTAAATTCA ACATCAAA	CT CATTCAATCT	CAAAGCAGGG	GTCTCCAAAG	CAATTTTAGA	240
ATGTGCTGGA CAAAATGT	AG AAAGGGAATG	TTCTCAGCAA	GCTCAGCAGC	GCAAAAATGA	300
TTATATAATC ACCGGAGG	IG GATTTTTGAG	GTGCAAGAAT	ATCATTCATG	TAATTGGTGG	360
AAATGATGTC AAGAGTTC	AG TTTCCTCTGT	TTTGCAGGAG	TGTGAAAAA	AAAATTACTC	420
ATCCATTTGC CTCCCAGC	CA TTGGGACAGG	AAATGCCAAA	CAACTCGAG		469

- (2) INFORMATION FOR SEQ ID NO:163:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GATTTATTCA 1	ITCTTGATTA	AATGCACTGA	AAAGTAAAGG	GTCTGTTTGT	GTCATGTTCA	60
TGAAAATGCG (GTTAGAGAGG	TGCTATTCAA	GTGATTCTGA	AGGCACCCCA	AGGTATATCT	.120
GTAATTTAAA (GATTACTGCA	AATATCTTTA	CTTTACTGTG	GGTTTTTAGT	ACATCTGTTA	180
ATTTAGTGTT 1	TCTTTGTGTG	TTTTGTAGAC	TAGTGTTCTT	CCATCCTTCA	ACTGAGCTCG	240
AG						242

- (2) INFORMATION FOR SEQ ID NO:164:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GAATTCGGCC	TTCATGGCCT	AGCATTTTTT	TTCTTTAAAT	TATTGTATCC	ACTAGTTCTT	60
GCCAGTATAA	AGGAATACAA	TTGACTTTTG	TGTGTTTCAT	ACGCTACAAC	CTTTCTAAAT	120
TCACTTATCA	GGTCCAGAAC	TCTTCTACTA	ACAATGCACT	TTTATAAAGC	CCTAACACCT	180
CTCCTGATCT	CTGTCTCACC	CTCCCACCTA	TCTCACTGTG	GGATGGGAAG	GAAGTCAATG	240
GAAAACACAG	GAGCGCATTC	TAATAATACC	CCACATGGTA	TACTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:165:
 - (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAATTCGGCC	TTCATGGCCT	AGCTCGATCC	AAGAAGAAAA	ATTAAAATGA	CAGCTTTTCC	60
CATTGATATA	ATCATCTTAC	TTTGCTCTCT	ACAAGAAATA	TGCATTAGGA	ACCTTCATTA	120
TAGGTCCACA	GAAATAGCAG	AACACAAAAG	CGCCCCCTA	CCCCCCCCCC	CCGGTAACCA	180
GAAATACACA	GAGGCAGAG					199

- (2) INFORMATION FOR SEQ ID NO:166:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE LESCRIPTION: SEQ ID NO:166:

GAATTCGGCC TCATGGCCTA	GAATTAACCA	ATTAAGAATT	AATAAATTAC	TTATAAAATT	60
AAAAATCAGG AATACCAGGC	TTAATGCATT	CATTTATTCT	ATTTAGCAAA	CTTTTTTTT	120
TTTTTTGAAT GCCCACAATG	TCCTAGGTTC	TGGAAATACA	AAATTACTTG	GTACCAGTAA	180
CTCGACTGTC ACCTTTCCAG	CCATGGACTT	GGTTCAGACA	AACCCCCAGT	CCACGGTTGT	240
CGTCCACTTG CAGTGCCCGC	CGACTGTGGA	TATATGCTGG	GGATCCCAAC	ACAACGCAGC	300
TACTCTCGAG					310

- (2) INFORMATION FOR SEQ ID NO:167:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAATTCGGCC	TTCATGGCCT	AGTAAATATT	TTCTTCTACT	TTGTGTTTTG	CCTTTTTGTT	60
TTCTCAGCAT	TATTTTTTGA	AGACAAAAAG	ATTGATTTTG	AAGAAGTCTA	ATTTATCAGG	120
TTTTTTCTAG	TAGTTTGTAG	CGGATTTNTG	CATGCTGCTT	TAAAAAAAT	CTTTGCTAAC	180
CCTCGAG						187

- (2) INFORMATION FOR SEQ ID NO:168:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

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GAATTCTAGA	CCTGCCTCGA	GCCTTGCCCA	GAATCAGCAA	GTAAACTGCA	CTAATTTGTC	60
TTATATTTGA	CTTTCTAACA	CTGATTTTTC	TGATTTTTCC	CTGTTCGACC	CTCCAATTTA	120
TAAAAATGTG	TATAATTGTT	CTGCTGCTTC	TGCTTTTGCC	TGCTTTGGCT	GCTGCATATA	180

CAGGTGAAGA TCTGGAAAGA AATGATGGAT CTACAGAAAA ACCCTACTTC GTAACCCCTA ACCTGCATGG AATTCTGATC AAGAAGCAAC TCGAG	240 275
(2) INFORMATION FOR SEQ ID NO:169:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 287 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:169:	
GAATTCGGCC TTCATGGCCT AGTTTCACAT TGTCTGTACT GTGTTGTGCA GTACCAGAAG TTGCTGGTAG CTACTTGGTC TTCTGGGACC TGCCATTGCA GACGTGGTGA TTGTAATCTT AATCTTGTTG AAACAGGATG GATTTATGAC TGGGATGGCC GGAAGCCACA CCAGACACCC AGTCACCTGG TCATGGGAGA GGTACTTTGT TGGCTTTTCA TAGTACTTAA CACTGTGAGC TGCTTCCTGA AGTGGCACTC TTAAGGCCAG GTGCCCCCAC CCTCGAG	60 120 180 240 287
(2) INFORMATION FOR SEQ ID NO:170:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 314 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:	
GAATTCGGCC TTCATGGCCT AAGACAGACA TTTTTGGCAG AGCATAGATG AAAATGGCAA GTTCCCTGGC TTTCCTTCTG CTCAACTTTC ATGTCTCCT CCTCTTGGTC CAGCTGCTCA CTCCTTGCTC AGCTCAGTTT TCTGTGCTTG GACCCTCTGG GCCATCCTG GCCATGGTGG GTGAAGACGC TGATCTGCCC TGTCACCTGT TCCCGACCAT GAGTGCAGAG ACCATGGAGC TGAAGTGGGT AAGTTCCAGC CTAAGGCAGG TGGTGAATGT GTATGCAGAT GGAAAGGAAG TGGAAGACCT CGAG	60 120 180 240 300 314
(2) INFORMATION FOR SEQ ID NO:171:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 195 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:	
GAATTCGCCT TCATGGCCTA CACCAAGTTG AATCCCTATG CAGGAGGAGA CGGCCTTCAG AACAACCTGT CCCCCAAGAC AAAGGGCACT CCTGTGCACC TGGGCACCAT CGTGGGCATC GTGCTGGCAG TCCTCCTCGT GGCGGCCATC ATCCTGGCTG GAATTTACAT CAATGGCCAC CCCACATCCC TCGAG	60 120 180 195

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GAATTCGGCC	TTCATGGCCT	ACACTCCTGG	TCATTTTGCA	TTTTATCCAG	CTTTTTTCA	60
TCAACCATGT	TATCCTGACA	GACACATTTA	TTGGATATTT	AGTTGGAAAT	ACCTTATGGT	120
TGGTTGCAGT	TGGCTATTAT	ATCTATGTAA	CTTTCCTGGG	ATACAGTGCA	TTGCCATTTT	180
TGAAAAATAC	AGTAATTCTT	CTGTATCCAT	TTGCACCTCT	GATTCTGCTC	AACTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:173:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GAATTCGGCC	TTCATGGCCT	AGGCTAACGT	AATTGAGAAA	ACCAAATGAA	ATATATCTTG	60
ACCAATAATT	TAAAACCATA	TCAGAGATTC	AGTTTGGTTC	TGTCTTCTGC	TTTACTGATT	120
TTAGGATCAG	CCTCATACAA	AAGGGTAATG	GTGGCAGCAG	CTCCAGAACT	CATATCATAT	180
CCTCCCATGT	TABAGTCAAA	TGAGAAAAGT	CTGTCTTCGC	CCCAGGATCT	CGAG	234

- (2) INFORMATION FOR SEQ ID NO:174:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GAATTCGGCC	TTCATGGCCT	ACTCAGTTCC	ATTGTTAAGC	AAGGAAAAAC	AAACAATACA	60
TTGAATTTGA	CAACCCACTG	AAGTTGCAGA	TAATGAGGAC	TTACCATTGT	ATACCATTAT	120
TCATCTGGAC	CTATATGTTC	CATACAGTTG	ACACCATCCT	ATTACAAGAA	AAACCTAACA	180
GTTATTTATC	AAGCAAAAAG	ATAGTGGGTC	TGACAAAAGA	TGACGGTAAA	ATGCTACGTC	240
ACACCCTCGA	G					251

- (2) INFORMATION FOR SEQ ID NO:175:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

${\tt GAATTCGGCC}$	TTCATGGCCT	AAACCACTGC	GCACCATATT	TCTTAAGGAT	GTTCTGAAGA	60
CCCATGAATG	TCTGGTCAAG	TCTGCTGATC	TCTTAATGAG	GGACAACCTG	TTTGAAATAA	120
TAACAAGCTC	CAGGACATTC	TACGTACAGG	CAGACAGTCC	AGAAGACATG	CACAGCTGGA	180
TTAAGGAGAT	TGGCGCAGCT	GTCCAGGCCC	TCAAGTGCCA	CTAGGCCATG	AAGGCCGAA	239

- (2) INFORMATION FOR SEQ ID NO:176:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 254 tase pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GAAAACCCCA	GATATTCCTT	ATTATGGAAG	AAGAAGCAGG	AAATATGTTT	TTGAATAATG	60
TGGGTCAGAG	AATTGTGCAT	TTATTATTGC	TAGGATGCAT	ATACACATTG	AACTCAGTCA	120
ACTTACTCTC	TCTAAATTAT	CTCACCGGTG	GAGACATTGC	CTCAGGAGTC	GAGCCCTGTG	180
GTGTGCCTCC	TGCTGTCACC	ACATTTGACC	ACCTAACTGA	CCCCACTGTG	GTCACCTTTG	240
CCACCAATCT	CGAG					254

- (2) INFORMATION FOR SEQ ID NO:177:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAATTCGGCC	TTGCCAGTAT	TCATGCTGTT	GCTTCAGTCA	AGAATGAATT	CCTCAGCGCT	60
ACCTCTCTTG	ACCTTCACAT	CTTACTTAGT	GCAAATGCTG	TCTCCTCCTG	AGACTTGCCT	120
GACTTCGGAT	ACTCTCCCTG	TGACATCTTA	TCTAAAATGT	CAAGTGAGAC	TCGAG	175

- (2) INFORMATION FOR SEQ ID NO:178:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GAATTCGGCC	TTCATGGCCT	AAGTGGCTGT	GTGGTATTTC	CTAAGTATTT	TTAAAATTTT	60
		AAAATGCAAC				120
		ACTAATTTAT				180
TGAGCACTAA	CTATGTTCAG	GCACTGGGCA	GGGATATCGG	GATACCAAGA	AAGCTCGAG	239

- (2) INFORMATION FOR SEQ ID NO:179:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAATTCGGCC	TTCATGGCCT	AGAAAATAAT	TTAGAGAAAG	AATAGAAAGT	CATGGAAAAT	60
CTCATAGGTA	GGAGACAGAA	GAGAGAACAT	TGTAAATAAG	TTTAAAAAAG	ATAAGAAAAT	120
CAGGATAAAG	TAGTATGGAC	TCTGAGGTGG	GAGAGAATTT	TAAGATTAGC	AGGAAAGTAG	180
TGTAGTTGGT	ACTTTTTAGT	TATTAACAAA	GCACTCACTT	CTTACAGAGT	CTCGAG	236

- (2) INFORMATION FOR SEQ ID NO:180:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GAATTCGGCC	TTCATGGCCT	ACGAAGATTA	TAATGTATTT	TTATTCTGTT	TTCAGCTTCA	60
TGTTTCCTGT	TGCAGGTGGG	ATAAGACCCC	CTCAAGGCCT	GATGCCGATG	CAGCAACAAG	120
GATTTCCTAT	GGTCTCTGTC	ATGCAGCCTA	ATATGCAAGG	CATTATGGGA	ATGAATTACA	180
GCTCTCAGAT	GTCCCAAGGA	CCTATTGCTA	TGCAGGCAGG	AATACCAATG	GGACCAATGC	240
CAGCAGCGGG	AATGCCTTAC	CTAGGACAAG	CACCCTTCCT	GGGCATGCGT	CCTCCAGGCC	300
CACAGTACAC	TCCAGACATG	CAGAAGCAGT	TTGCCGAAGA	GCAGCAGAAA	CGATTTGAAC	360
AGCAGCAAAA	ACTCTTAGAA	GAAGAAAGAA	AAAGACGCCA	GTATCTCGAG		410

- (2) INFORMATION FOR SEQ ID NO:181:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GAATTCGGCC	TTCATGGCCT	ACACATTTGC	ATTGTCTGCC	CATGGACTGG	TTGGAGCAGA	60
AACCTCCATA	CCTCAGTCTC	TTGGTATTTG	TCTGCCCCAA	CTGCTGCTTT	TTGTTGGGAT	120
GTTTGTGTGT	GCTGGGGTCT	CGGCAGCATC	GGCTGCTTCC	CGGTGCGCAC	TGACATGCAC	180
TTGTTCTCCA	CGATGGCTTT	CTCTACCTTC	TGAGATGCTC	CATTATCAGT	CCTGCCTTTG	240
TTCCGGAGAG	TTGAGATGGT	ATCACTTCTC	ATCCATCCTT	AGAAATACCC	CTCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:182:
 - (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 272 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GAATTCGGCC TTCATGGCCT AGGGGGCTGG	TAGTGAAATA	TTTGGTACTG	AAAGTGTGAA	60
GACCTCTGCT GGGGACTGAA CAGAGGGAGT	GTCTTCTGCT	GGTGGTGTGA	AATCTATCTC	120
ATCATCAAAA TTATCTTCAA ATTCCTTAAA	GTCTATTTCT	GGGTCCTTAC	AGCAGGATAC	180
ACAGTTTGCA ATTAACACTA TTAATATTAT	TAAACTGCAC	ACACACAGGA	TCACAAAAGA	240
TGAGGAAACT TCTGCAGCAG GTGGCGCTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:183:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCGGCC TTCATGGCCT ACTACTTATC	ATCCCTGCTC	ACACACCCTT	GTCCAAGGCT	60
TTATGCATCG GATTTATTTT TCCAAATCAA	GAGGACAGTG	ATAGATGCAT	TTTCCCCAGG	120
CTGTCTCAGA AAGGTCGCTA AATGTATACT	GTTGTCAGAA	TTGCTGAGAT	CTCCCCCCAC	180
TTTTGGTTTT TGCAGCAGTA AAAACTCTTT	CCACTGTGAC	TTATTTTCTC	TCTCAGGCAG	240
CAGACTCGAG				250

- (2) INFORMATION FOR SEQ ID NO:184:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC	TTCATGGCCT	AGATCTTCTC	CCCATTCAGC	AAAACTTTCC	CATTCCGGTT	60
AATGGTTTTG	ACAAGCAGGG	CACCACGGGG	CATAAAATTG	TATCATCCAG	CCTCCTTCCA	120
GCAGCTCTCT	CCAGTTCTTG	TCTGTGATGA	TGCGTACGTT	GCTCTGCCGC	CTGTGGGTCC	180
AGGGAGCACC	CCCAAGCAAC	AGTACCAGGA	CTGCCAGCGG	AACTGCAAGA	CTCCTGGAGG	240
GTGCCATGTC	TGCCACTTGC	CCACCTCACA	GCAAGCGTGG	CGGCCCAACA	CTAGGTTTTT	300
TAAAAACTGT	GACTATCAGT	GTTTTAAAAA	TTGCCCGGTA	ACTCTAGACT	TCAAAAGTGG	360
GATAAGTAAT	GATAAACCAA	TAATAAACCC	TGCCTCGAG			399

- (2) INFORMATION FOR SEQ ID NO:185:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 base pairs
 - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

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GAATTCGGCC	AAAGAGGCCT	AAAAATTAAT	ATTACCTTAT	GACTGCCTTT	ATCATGACTC	60
TCTTAGTGGG	GATTTCTGTC	CTCCACATGC	CCTGGGGGAT	GTGCAGCCCC	CGTGCACTCC	120
CCGCCTTGGC	CGGCCCCTTC	CCCCATGCCC	AGGTAGACTC	TGAGCTCTTA	GCCCAGCAAC	180
TCGAG						185

- (2) INFORMATION FOR SEQ ID NO:186:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC	AAAGAGGCCT	AGGGAACTAA	TCTTAAACAC	TGAACCTCTT	TTCAGCAAAT	60
TGGCTTTCTA	GTTTCTCAGC	TCTCTCTTTA	CACCTCTAAA	TCTCTTTCCT	GGCAAGATCA	120
TTTATTTGCC	TTGGTTTATG	GTGATACTCT	TCATTGTTAT	ACTGGTGGGT	GATTGTTTTA	180
ATTCATAGCT	GTTTTTTTCT	ACTTCAGGAA	GATGACACTG	CTGGCTCTGC	TGGCTCTGAT	240
GTTTACCTTG	TGGCTAATGC	CTGTGTTTGC	CTGTGTTCAC	ATTTATTCCA	CGATTCATTT	300
GTTAACATTT	ACTAAGCTCG	AG				322

- (2) INFORMATION FOR SEQ ID NO:187:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCGGCC	AAAGAGGCCT	ACTCATAACA	GCGTCAGAGA	GAAAGAACTG	ACTGAAACGT	60
TTGAGATGAA	GAAAGTTCTC	CTCCTGATCA	CAGCCATCTT	GGCAGTGGCT	GTTGGTTTCC	120
CAGTCTCTCA	AGACCAGGAA	CGAGAAAAA	GAAGTATCAG	TGACAGCGAT	GAATTAGCTT	180
CAGGGTTTTT	TGTGTTCCCT	TACCCATATC	CATTTCGCCC	ACTTCCACCA	ATTCCATTTC	240
CAAGATTTCC	ATGGTTTAGA	CGTAATTTTC	CTATTCCAAT	ACCTGAATCT	GCCCCTACAA	300
CTCCCCACCT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:188:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs.
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

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		ATTATGCTGG				60
AGTCTGGCTA	GACTCTGCTA	CCGCCTAGCA	CTGAGGTGTG	GTCCTTTATC	TGTTATTACA	120
TTCTTCGTGA	TAATGAAATT	CTGAAACACA	TGCTCCAGGC	ACCTTTGTAA	ATGTGAAGGT	180
GAATAAAGTA	TTTGTTTGTT	GTCTGAAAAG	AGATCTTTGA	AATGTTAAGT	TGCCACAGAC	240
		AGAGTTTTAA				300
		ATATTCAAGA				360
					AAGTTATGGC	420
TACCTCTTGG	AGTAGAGAAA	ATCTCAAAGG	CCGCTACTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:189:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAATTCGGCC	AAAGAGGCCT	AGTGGGCAAC	TTGGAGAAGA	GTGAAAAACA	CTAAAGAATC	60
ATCTCTTTTC	CGAGTCACAA	AGTCCCATGA	ACTTTGTGAC	TCAGAGACAC	TTTTCGTGAA	120
AATTACCTTT	CGGCGGGACA	CCGTCTCAGG	GCAGCTTTTT	CAAGGCTTCG	CTTGACATGA	180
TTTCCTTCCC	TTCATCAGTC	ACTTTGGATC	CAGCTGAATA	TCTCTCTCGG	GTGAGAGCGG	240
ATGTGGACTG	GCCTCCCACA	GAAGAAGAGT	AGGTGGCTTT	GGTGGGGGTT	GGGGTGCGGG	300
CTGGCTTCCT	GGTCTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:190:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GAATTCGGCC	AAAGAGGCCT	AGTGAAAAGA	AAGAGACTGT	NAAATAATTC	TGCATATCCT	60
CAGTGGATAA	TTCTGTNACC	TATCTGTCAG	CTATTCCATA	TCAATAAAGG	ACACAGCTGG	120
TAATCCAAAA	GGAAAGGATC	TCTTGATGAA	AGTGTTCTGC	CATTCTTATT	AAAGTCAACA	180
TACAAGATAC	ACTCTTAGTG	ATTTTTGAAC	CCATAATTAT	ATTTGTCTGA	TAATAATTGG	240
CACTTAACGG	TTACAGAACA	CTTTCACTGA	TATTTTCCTT	AGTGAATCTT	AACAACAATT	300
CTACCAGTAA	TTTCTAATAT	TTGCCATGAT	TAGACTTTCA	AAATTAGTCC	ACGCACTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:191:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

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GAATTCGGCC AAAGAGGCCT AAGAAACATG GCGGCCGCGA CGTTGACTTC GAAATTGTAC 60
TCCCTGCTGT TCCGCAGGAC CTCCACCTTC GCCCTCACCA TCATCGTGGG CGTCATGTTC 120
TTCGAGCGCG CCTTCGATCA AGGCGCGGAC GCTATCTACG ACCACATCAA CGAGGGGAAG 180
CTGTGGAAAC ACATCAAGCA CAAGTATGAG AACAAGTAGT TCCTTGGAGG CCCCCATCCA 240
GGCCAGAAGG ACCAGGTCCA CCCAGCAGCT GTTTGCCCAG AGCTGGAGCC TCAGCTTGAA 300
GATGATGCTC AAGGTACTCT TCATGGACCA CCATTCGCTG TTGGCAAGAA ACGGCTTTAC 360
TTACAAAACA GTCTCGAG

- (2) INFORMATION FOR SEQ ID NO:192:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAATTCGGCC	AAAGAGGCCT	ACTCTGAATT	AATGCAAATT	CCCGTTGTAC	TGTATTTAAT	60
TATGCACAAA	ATGGTGCCCT	TGACTCAGAT	TTCAGTGAAG	AACTTCATTT	TTTTACTTTT	120
AAGTCTCCAA	GTAGGAAATT	CAATTAGCGT	TATGAAAGAA	ACACTAAAAC	TCGAG	175

- (2) INFORMATION FOR SEQ ID NO:193:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 700 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GAATTCGGCC	AAAGAGGCCT	AGGCAGCAAT	GTTATCTGTC	CTTCATTCTT	GCATGTTTTT	60
GGAAATTGCT	TTTGCTTTTA	CTTTTGGTCG	TCATGGCAAT	CACGTGCCTT	CTCTGGTTCA	120
TTTTGCACAG	ACCTGCCTAG	AGCTGGAACG	TTACCTCCAG	AGCGAGCCCT	GCTATGTTTC	180
AGCCTCAGAA	ATCAAATTTG	ACAGCCAGGA	AGATCTGTGG	ACCAAAATCA	TTCTGGCTCG	240
GGAGAAAAAG	GAGGAATCCG	AACTGAAGAT	ATCTTCCAGT	CCTCCAGAGG	ACACTCTCAT	300
CAGCCCGAGC	TTTTGTTACA	ACTTAGAGAC	CAACAGCCTG	AACTCAGATG	TCAGCAGCGA	360
ATCCTCTGAC	AGCTCCGAGG	AACTTTCTCC	CACGGCCAAG	TTTACCTCCG	ACCCCATTGG	420
CGAAGTTTTG	GTCAGCTCGG	GAAAATTGAG	CTCCTCTGTC	ACCTCCACGC	CTCCATCTTC	480
TCCGGAACTG	AGCAGGGAAC	CTTCTCAACT	GTGGGGTTGC	GTGCCCGGGG	AGCTGCCCTC	540
GCCAGGGAAG	GTGCGCAGCG	GGACTTCGGG	GAAGCCAGGT	GACAAGGGAA	ATGGCGATGC	600
CTCCCCGAC	GGCAGGAGGA	GGGTGCACCG	GTGCCACTTT	AACGGCTGCA	GGAAAGTTTA	660
CACCAAAAGC	TCCCACTTGA	AAGCACACCA	ACGGCTCGAG			700

- (2) INFORMATION FOR SEQ ID NO:194:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAATTCGGCC	AAAGAGGCCT	AGAAAAATAC	TTCCCCCAGAA	AGAAAATATC	ΔΤΓΔΔΔΤΔΔΓ	60
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ACCIAITICI	TTTCAGCTAT	AGAGATGGCT	GGATATCAAA	AGCACCACGG	GAGCTTTGCA	120
ATTTGCTGCC	TCTTTTCAGC	CCTCAGCTTG	ACTCTCAGTT	TTCAAGAGGG	AGAAAATGAA	180
TGTTTCCCAG	CATTCTCTGT	CCTTTGCTCC	AAAGAAGAGA	GCAGGTGTTG	GCTTCCAAAC	240
CTTCCGTATT	TTCTTATTGC	TGTTAGGGGG	ATCAACTGCA	TGTTTCCTGA	GGGAAAAGGG	300
TGGCTCACTG	ACCTACTTGA	AGGCATTCTC	TCAGTGGAAG	CTGGGCAAGA	GAATCCAGGG	360
ATTTCTTTTG	CAGGTTTCTG	CGCAGTGCCC	CTGCCATCAA	GCTGCCTAAA	ATGTGAATAT	420
TGCTTCCCTG	CGTTTCAGAG	GTGGCCGCTC	GAG			453

- (2) INFORMATION FOR SEQ ID NO:195:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GAATTCGGCC	AAAGAGGCCT	ACAAAATGTG	AATGGAACAA	ACCTGCACGT	GTACCCTTGG	60
ATGTGTGGAT	GTTCTTTGTT	TTTATTTGTT	AAACCTGATG	TCTTGTCTGT	ATGACACATT	120
TATTGGAAAC						180
GAGCAGATAT						240
CTTTTTGTAT	CCTATTTCAG	AAAACTTTGG	CTACTTCAAG	GTCACAAAGA	TTTTGGATTT	300
GTTTTAATCT	ACAAGTTTTA	TAGCTTTGAC	TTTTATATAT	AAGTCTGATT	CATTTGGAGT	360
TAATTTTTGT	GTACAGTGTC	AATTAAGGGT	CTAGGTTCAT	TTATTTTCTT	ATGAATATCC	420
AATGGTTCCT	CGAG					434

- (2) INFORMATION FOR SEQ ID NO:196:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GAATTCGGCC	AAAGAGGCCT	ACAAACACAG	AACATTTCCA	TCGTTGCAGA	GAGTACTATT	60
AGAGAGCAGT	ATTCCAGAGC	CTGTGATCTT	AATCACTACA	CCTAAAGCCT	CCCAGTTGAC	120
AAAGTTACCA	CCTTTTTTTG	GTGTGTGTGC	ACGTGCGTGT	GTGTGTGTGT	AAGTATATAT	180
AATTTAAATC	ATTCCATTAA	ATTTACCTCT	GAAATTCAAA	AGACTGAAAC	AGATCTTCTT	240
TTTATCAAAT	AAGTTGATTG	CAGAGATTAT	ATTGGTGTTT	ACATTTCAGG	CAACCTGCTC	300
ATGAAATTAT	CCATTGCTCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:197:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTCGGCC AAAGAGGCCT	ACTCCTCCGC	CTGCAACCAT	TGTTTCCTAC	CACTGGATTA	60
TTCTGAAGCA AATTTTAGAC	ATCATATATA	TTTATCTCTG	AAAGAGGACT	CTTAAAAAACA	120
TGCACTTATA CCTCTATTAC	ACTGACAAAA	TTGGTAACAA	TTCCTTTATA	TTATCAAATT	180
TCCTTATTGA GTTCCTGATG	TTCAAATTTC	TGATTCTCCA	GATGCTCCAA	ACTTCCAGAA	240
ACACAGATTC CCAGATGGAA	TCCTGGGGAA	GGCTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:198:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 448 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GAATTCGGCC	AAAGAGGCCT	ATTTTCTAAT	AAAAACTATT	TTATGGTAGG	TTTTGTGGAT	60
TATTGAATAC	AATCTGGCAT	TCTGTTTAAT	ATGTATGTTT	TCCTGAATGA	GGGGGTACAT	120
TGTAATTTTA	ATTATTAAAC	TCACAATGTT	TTTGGTTTTA	AAAATAAAA	TTTTAGGAGC	180
AAGCAGTGTT	CCTGCCTTCT	TTTCTGAAGA	TGATTCTCAA	TCGAATGACT	CAAGTGATTC	240
TGATAGCAGT	AGTAGTCAGA	GTGACGACAT	AGAACAGGAG	ACCTTTATGC	TTGATGAGCC	300
ATTAGAAAGA	ACCACAAATA	GCTCCCATGC	CAATGGTGCT	GCCCAAGCTC	CCCGTTCAAT	360
GCAGTGGGCT	GTCCGCAACA	CCCAGCATCA	GCGAGCAGCC	AGTACAGCCC	CTTCCAGTAC	420
ATCTACACCA	GCAGCACTCC	ACCTCGAG				448

- (2) INFORMATION FOR SEQ ID NO:199:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAATTCGGCC AAAGAGGCCT AACTTTIGTA ATTTGAATTG GGTCCCGCTT AGTTCTTGAA	, 60
TTGTTATGAA AATCCTATAT CTGTTTGTAT ATTTGCAAAC CCTTTGTATT ATAATTGTTG	120
ATATTTCCC TTTTTAAAAA ATACCATTGA AATCAGCATG ACAAAAATAA CACTGTGGGC	180
ACTCGAG	187

- (2) INFORMATION FOR SEQ ID NO: 200:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double :
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

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GAATTCGGCC	AAAGÄGGCCT	AGACCAGAAT	AAGCCTTTTA	AGGTAAACCT	CAAAATTATC	60
ATTTTATGGT	AATACTGACC	ATTTTAGTCC	CCTAGGTTTG	ACATGGGAGA	TAGTGACTAC	120
ACTGGTGTCT	GACTTTTTTC	CTAGAGATTT	CTCCCTGAAA	AATACAAGGG	CTGTTGGTGA	180
GAGCAGACTT	GAGGTGATGA	TAGTTGGCCT	CTGGTCTACA	AAGATTTCAT	AACTCCTTGG	240
AAAGCTTCTT	ATAATCATTC	TTAACTTCTT	GGTAGCTAGA	AATTTAGAGT	AGTTGAAATC	300
TTTAGGAATG	AACTTCTGAG	GGCCAAAAAA	TGTGACTGAC	ACACTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:201:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GAATTCGGCC TTCATGGCCT	ACATCACCAA	TTCGGCTGGG	TAAGGGTCCC	CATGAAGGCG	60
CAGCCGGGTA TAGAGGTGCA	GGGGAGAGCA	GCCTGGGGAG	TCCCTATCTG	GATAGGCTCC	120
AGCCTGGGTC GGGGCGGTCC	TGGTGCCCGG	TGAAGCGTCA	AAAGAGGGAG	CCTGAGCGGG	180
GCAACGCAGA AGGGTGGAGA	GGAGGGGGTG	GCGAGGGCGG	GCAGCGAGGC	CTGGAGCCGC	240
CAGGAGAGGG GCGGGGGGCG	GCCCTTCTCC	AGGAATTTCC	GGGGATCGTG	TTACAGCGTT	300
GGCGGAGCCC GAGCGGAGTG	GGACTCGAG				329

- (2) INFORMATION FOR SEQ ID NO:202:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GAATTCGGCC	TTCATGGCCT	AGAAAGGGGA	GGGAACGTGA	CAGGCAGGTG	TGGGATAGGG	60
ACTTCTCTTC	CGGTCAGAGC	AAGGGTCGTC	CGAAACCAAA	ACAACCCTCT	TCCCTTCATC	120
TCGCCCCGGA	TCCAAAGTCT	TGGGGCTAGG	CTGGGGCGGG	AGTGGCACGG	AGATGTAGGA	180
ACACTGCCTT	TCGTTACTTC	TCCTGCCATG	GCTGACCTTT	TTGTCTCTTG	TTTCATGGTT	240
TTACACGTAT	GAATGGCTTG	AGACTGAGGA	TTTAGGGAAG	AAGCGAAGGC	ATCATCTAGG	300
GCTGTGCTGT	GCCAAGTTGA	GCAGTTGTTT	AAACTGTTAG	AATTTTTGAC	TGGTGTAAAA	360
ACCCTCTATG	CTCGAG					376

- (2) INFORMATION FOR SEQ ID NO:203:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GAATTCGGCC TTCAAGGCCT ACGTGAAACC CCATCGGCTT CATTGGCTCC TTGATTTAAA

60

CCACGCCCGG	CTNTCTGCCC	TCTTTGATGC	TGCTGGGCCA	GGTTGCCCAG	CCATATCCCA	120
GCCCCGTCTG	CAGGGAGCCG	GAGGCNGCTG	CTGCTGCTAT	TGTGTGGATG	CCGCGCGTGT	180
CTTCTCTTCT	TTCCAGAGAT	GGCTAACAGG	GGCCCGAGCT	ATGGCTTAAG	CCGAGAGGTG	240
CAGGAGAAGA	TCGAGCAGAA	GATCTCGAG				269

- (2) INFORMATION FOR SEQ ID NO: 204:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GAATTCGGCC	TTCATGGCCT	AGATGTGTTG	AACCTTATTC	TTGTACATTC	ATTCAATCAA	- 60
GGCAAACTTT	TATAATTTTT	CTTTTGTTTC	CAATGACCTT	GAAATGTTAT	AGCATGGTAA	120
TATTCTATGC	AACTATAGTT	ATACTTTTTG	GTTTGACACT	GTATTTTTTC	ACATTGATTT	180
ACTGGTTGAG	GCTCGAG					197

- (2) INFORMATION FOR SEQ ID NO:205:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GAATTCGGCC	TTCATGGCCT	AGCAAGACCT	TTTAAGTATA	TACTCTGAAA	GTGTGGCTAA	60
TATGATCATG	ATGCTGTAGG	AAAAAAGGT	TATATGTCCA	AGTGTATGTA	CTTGTAAATG	120
TGCCTAAAGA	AACCTGGAAG	GATACACAGG	TCTTCCCTGG	GGTACAAGAC	GGAGAACTGG	180
GATCATCATC	TTAACTCTAC	TCTTCCTTTT	TACTCTTCTG	TCCTCTTAGA	GACTTTTGCC	240
TGTATACATG	GATTACTGTT	ACTTAGCAGG	GGCGACCGGT	TGGCCAAAGC	CTTGGTGTGC	300
CCTTGGCACA	ATTCTGCCAA	GACCCTTACC	CTCTCCTCTC	CTCANGGCTC	CCTTAACCCC	360
TCTCCCCACA	TCTGGAAAAC	CCTGGATACA	TTTTCT			396

- (2) INFORMATION FOR SEQ ID NO:206:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GAATTCGGCC	TTCATGGCCT	AGGAAGAGGT	TGAGAAGACT	CCTGGGCTTC	AGCCTCTCCC	60
ACCCAGCCCT	GCCCCTCACC	TGCCTGCCCT	CCCCTCCCCC	ACTCTATACT	AGGGACTGGA	120
TCTCAGCCTC	TGATCAGTTT	CACAAAGTTT	GTTCCCTAAG	GAAATCAAAT	CCCATTGTCA	180
CCTAACTCTG	AAGATCTAAA	TAGCCCTTGG	ATCAGTACGG	GAACCCCAAA	TCCCACAGGG	240
CCAGATGTGG	AGTCTGTGTC	TGCCCCCGTC	TTCTCTCCAT	CCTCAAAGCC	CCCACTTCTC	300

TCCAGGCTGC	TTCTCGAG		318

- (2) INFORMATION FOR SEQ ID NO:207:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GAATTCTAGA	TCCTGCCCTC	GGAACAATGG	GACTCGGCGC	GCGAGGTGCT	TGGGCCGCGC	60
TGCTCCTGGG	GACGCTGCAG	GTGCTAGCGC	TGCTGGGGGC	CGCCCATGAA	AGCGCAGCCA	120
TGGCGGCATC	TGCAAACATA	GAGAATTCTG	GGCTTCCACA	CAACTCCAGT	GCTAACTCAA	180
CAGAGACTCT	CCAACATGTG	CCTTCTGACC	ATACAAATGA	AACTTCCAAC	AGTACTGTGA	240
AACCACCAAC	TTCAGTTGCC	TCAGACTCCA	GTAATACAAC	GGTCACCACC	CTCGAG	296

- (2) INFORMATION FOR SEQ ID NO:208:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GAATTCGGCC	TTCATGGCCT	AGTCTCTTGA	AAAGCCGCAT	TTCCAGGCGC	TTGGCCAGTG	60
GCCTGGGAAG	TAGCCTGTGC	TTGTATTGAG	ACAGTCCCCC	AGCAGCAAAC	CATGTTCCAG	120
TCATTCCCTT	TCCTACTTTG	GGGATTGTTG	CCTTTTCTGC	TTGTTTAAAG	TAAAACAAGC	180
ATGTACTTGT	TTGTATGTAT	GTATGTATGT	AGTTGTACGG	TGGGCACAAA	TAAAAAGAGG	240
GCTGTATCCA	AATAAATCAT	TTCTGGCTGC	TCACTGGCAC	AGTCCCTTTG	CTCCGTCCCC	300
TCCTGGCTCG	AG					312

- (2) INFORMATION FOR SEQ ID NO:209:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

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GAATTCGGCC						60
TGGATTGCTA	CAAGAACTTT	GTGGCCAAGA	AGTGTGCTGG	ATGCAAGAAC	CCCATCACTG	120
GGAAAAGGAC	TGTGTCAAGA	GTGAGCCACC	CAGTCTCTAA	AGCTAGGAAG	CCCCCAGTGT	180
GCCACGGGAA	ACGCTTGCCT	CTCACCCTGT	TTCCCAGCGC	CAACCTCCGG	GGCAGGCATC	240
CGGGTGGAGA	GAGGACTTGT	CCCTCGTGGG	TGGTGGTTCT	TTATAGAAAA	AATCGAAGCT	300
TAGCAGCTCC	TCGAG .					315

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GAATTCGGCC	AAAGAGGCCT	AGGAAGATGG	CGAAGGTCTC	AGAGCTTTAC	GATGTCACTT	60
GGGAAGAAAT	GAGAGATAAA	ATGAGAAAAT	GGAGAGAAGA	AAACTCAAGA	AATAGTGAGC	120
AAATTGTGGA	AGTTGGAGAA	GAATTAATTA	ATGAATATGC	TTCTAAGCTG	GGAGATGATA	180
TTTGGATCAT	ATATGAACAG	GTGATGATTG	CAGCACTAGA	CTATGGTCGG	GATGACTTGG	240
CATTGTTTTG	TCTTCAAGAG	CTGAGAAGAC	AGTTCCCTGG	CAGTCACAGA	GTCAAGCGAT	300
TAACAGGCAT	GAGATTTGAA	GCCATGGAAA	GATATGATGA	TGCTATACAG	CTATATGATA	360
GGATTTTACA	AGAAGATCCA	ACTAACACTG	CTGCAAGAAA	GCGTAAGATT	GCCATTCGAA	420
AAGCCCAGGG	GAAAAATGTG	GAGGCCATTC	GGGAGCTGAA	TGAGTATCTG	GAACAATTTG	480
TTGGAGACCA	AGAAGCCTGG	CATGAACTTG	CACTCGAG			518

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GAATTCGGCC	AAAGAGGCCT	AATTGAATTT	CATTTCCTTT	GTAGACTAAT	GTTACAATAA	60
ATAAATGGGA	ATTTTAAATA	CCTGCATGTT	CTGTTTTTCT	CTTTTTTCTT	TTTTCAGCCA	120
TAATGAAAGG	AAAGTGACCT	GCAAACATCC	AGTCACAGGA	CAACCATCAC	AGGACAATTG	180
TATTTTTGTA	GTGAATGAAC	AGACTGTTGC	AACCATGACA	TCTGAAGAAA	AGAAGGAACG	240
GCCAATAAGT	ATGATAAATG	AAGCTTCTAA	CTATAACGTG	ACTTCAGATT	ATGCAGTGCA	300
TCCAATGAGC	CCTGTAGGCA	GAACTTCACG	AGCTTCAAAA	AAAGTTCATA	ATTTTGGAAA	360
GAGGTCAAAT	TCAATTAAAA	GGAATCCTAA	TGCACCGGGC	GATCTCGAG		409

- (2) INFORMATION FOR SEQ ID NO:212:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

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GAATTCGGCC	AAAGAGGCCT	AGTACAGTCC	CAATCAAGAA	GCCTTATTAA	CCTTCTGTGT	60
GAGGGACTAG	ACTCAGTGTT	GGGTTTGGAG	GATCCACTGG	TGAGGAGCAT	TCAGTCTAGC	120
AGGAGAAATG	TCAGCATTAT	TTATTACACA	ACAAGATCTG	ATGCATTCAG	ATGTACTTAC	180
AGGTCTAGGA	ACTGTTCAGA	GGAGCACAAA	TGAATGAGAG	AGAGAGGGAG	AGAGGGAGAT	240
TGAGTGAGTT	AGAGAGTTGT	TGGTGCTCCA	CAAGGAGCAG	TAAAGTATTT	TAAAAATAAA	300
AAATAATAAG	GCTGACTCTG	TGTCCTGCCT	AGGGGTTGGC	CATGCTCCAC	AAAAAGCAGT	360
AAAGTGTTTT	TTGTTTTGTT	TCGTTTTTTT	TTTAAAGACA	GACGTCTCGA	G	411

- (2) INFORMATION FOR SEQ ID NO:213:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GAATTCNGCC	AAAGAGGCCT	AGTTTNATCT	TCTTACCTAT	TTACTGAATG	CNACATTACT	60
GCACACCAAG	ACAAAAGAGC	TCTCCAGGAA	AACATTGGAT	ATATTGAGAG	CATTAAAAGA	120
TACTGCAAAA	GCTCTAATAA	ATTCAGTCTG	CTTATTTTCC	AAATTTCATA	AACTACATAC	180
TTAGGAAACT	GTGCTTTCAG	TGAGCTAAAC	TTCTTTTTTT	AAGTAACTAT	CATAGTTTTA	240
AGAAAAACAT	TTTAAGAAGA	CAAAAAGTAT	TTATTAAGCC	CATCTAAAAG	GCTAATGCAA	300
ATTCCCAAAA	AAGGAGCACA	TAGAGATAGG	CATCTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:214:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GAATTCGGCC	AAAGAGGCCT	ATTGAATTCT	AGACCTGCCT	CGAGACACTA	GCCCTTTTTT	60
CTGTTGGTTT	AGCACAAATA	CTTCCCTCCT	CCGGCACCTC	CAAACCTACC	CCACAGTCAG	120
TGTACTTGTT	TTATATATAT	TTAATCTTAT	TCAATGGAAA	CCATGCTTTT	GTCGTTTTAT	180
ACTTTGCTAG	GTAGACTTCT	CGAG				204

- (2) INFORMATION FOR SEQ ID NO:215:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CTCGAGAGGC	GCATCTTCAC	TGGCATATGA	CAGGCTGTCA	CTGCAGCTAA	TGTTGGTACA	60
GTTTTTCCAA	AGACCTACTG	ATGCATCTAC	CGTATTGGAA	ACCAACCAGA	CATTGGCAAT	120
GGTGCTAACA	AATAGCATAA	TAACAGTAGC	GATGTGGACC	ACAAAGATAC	CAGCCAGCAA	180
TACCAACATG	TTGGCTCTTT	TTTTTTTGGT	AACTTGTGAG	CAAAGAGAGT	TCTGAAGGGT	240
CCCAGCGACA	GAGGCACTCG	AGGCAGGTCT	AGAATTCAAT	TAGGCCTCTT	TGGCCGAATT	300
C						301

- (2) INFORMATION FOR SEQ ID NO:216:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs

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- (8) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC	AAAGAGGCCT	AAAATATTTG	AGTCTAAACT	TATAAATTTT	GCATTCTCCC	60
TAACGAAAAA	ATTTCTATTA	CTGTGGTGGA	TTTCTTTAAA	TTTTGAATAT	AGTTACTGAA	120
ATATTAATTC	TTTCAATTAA	ATTTATATTT	ACTCACTGGT	TCCTTCCCCT	TCTTTAAGGA	180
GACAGAAAAC	ATTAACACTT	TTTAACCTCT	CATTTGTTTA	AAAATTTATT	GACCTCTCCT	240
CTGAGACAGT	TTGTATTCCT	AGATCTCTTT	AAACATAAAT	ATGCTTATTT	TCAAGTTTTT	300
GTCACAGTAT	TCACTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:217:
 - (i) SEQUENCE JHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GAATTCGGCC AANGAGGCC	T ATTTAGATTT	AACCCAGTTT	GTAGACATTT	GCATAGATCA	60
AGCAAAACTA GAAGAGTTT	G AAGAGAAAGC	ATCAGAACTT	TACAAGAAAT	TTGAAAAAGA	120
GTTTACCGAC CACCAAGAA	A CTCAGGCTGA	ATTGCAGAAA	AAAGAGGCAA	AGATTAATGA	180
GCTTCAAGCA GAGCTACAA	G CTTTTAAGTC	TCAGTTTGGT	GCCTTGCCAG	CTGATTGTAA	240
TATTCCTTTG CCTCCCTCT	A AAGAAGGTGG	AACTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:218:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC AAAGAG	GCCT ACCTGGCTCA	TTTATAACCT	CCTCGATCCT	ATTACTGATT	60
TGCATTCTTA ACTACA	GGTA AGAGAAAACC	AGTGCAACCT	AGCTTTCAAT	AGACAGGAAT	120
TTGCTGGCTC ATATAA	ATGA GACATCCAAT	AAAGAAGAAA	AGTTGGAAAA	AATGTGTCAA	180
ATGTAGCATC CTCTCT	CTCT CTTTCTCTCT	CTCTCTGTTT	TTTCACCTAG	GCTTGTGCCA	240
TAAACCTGCT TCTACA	TCAG TTACTGTGGT	TATGGGCGTC	TTGTTGGCTG	AGCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:219:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GAATTCGGCC	AAAGAGGCCT	ACTTAGCAGA	ATATATTCTT	TAATAGCTCC	CATAAAGCAA	60
ACAAACCCAA	AATATATTCT	CCTGACCCTA	CATTCACTTC	CAACTATCAC	CCTACATCTA	120
CATTCTCCTT	TTCATACCAA	ACTTTTTCCA	AGCAGTTGTC	TATATTTATG	TCTCCACTTC	180
TTTACCTCCT	ATTCTTGCTT	CAGTATGCTT	CAGTTGAGCT	TCGTCCCCCT	GTAGTCCACC	240
ACCAACTCGA	G					251

- (2) INFORMATION FOR SEQ ID NO:220:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GAATTCGGCC	AAAGAGGCCT	AGATTGATTC	TGTGTTGTGG	TATTGGCCCT	TACATACAAC	60
TGGAGGAAGT	GTGAATTTCA	TCATGTTGAT	AAATTGGACT	GTCATGATTC	TTTATAATTA	120
CTTCAATGCC	ATGTTTGTCG	GTCCGGGCTT	TGTCCCTCTG	GGGTGGAAAC	CGATGTGTGA	180
TGAAGATGGA	CCATCACTGT	CCTTGGATCA	ACAACTGTTG	TGGTTACCAA	AATCATGCTT	240
CGTTCACACT	GTTTCTCCTT	TTAGCACCAC	TGGGTTGTAT	CCATGCTGCT	TTCATTTTTG	300
TGATGACTAT	GTACACACAG	CTTTATCATC	GGCTCTCCTT	TGGGTGGAAC	ACAGTGAAGA	360
TCGACATGAG	TGCAGCACCC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:221:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GAATTCGGCC	AAAGAGGCNT	ACCCNGATTA	TAGTTTTTGT	ATTGTTTTTA	CAATTTTTGT	60
GAATTAGGAT	CCAAATAAGG	TCTGTAAATA	TTACATTGGG	TTTAGGTAAT	CGATACTTTT	120
TTTCTTTTAA	TCTATAAGTT	TTCCTCTATC	TTTTTATTGT	GGTTATTCCC	ATACAATTGG	180
TTTGTTGAAG	AAGCCAGGTC	TTTGCCCTAT	AATACTTCTC	AGAATCTAGA	TTGTGTTGAT	240
GAGATCCCAG	TGGTTTCATG	TAATATGTTC	TTTTGTCCCT	TGTATTTTCT	GTAAATTTTG	300
TTTATTTTAT	TTTTTTTATT	TCTATTATTT	GAGATGGAGT	CTTGCACTGT	CACCCAGGCT	360
AGAGTACAGT	GGCATGATCT	CAACTCACCG	CAACCTCGAG			400

- (2) INFORMATION FOR SEQ ID NO:222:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GAATTCGGCC	AAAGAGGCCT	AAGAGCCTAT	AAGGTTTACA	TATTTCACTG	GAGAGAGAAA	60
TAGGGACATA	CAATAAATGA	TTTTATAATA	AATTTCCATG	AAAAGTGAAT	CTGAAAACCC	120
CACCGGAAGG	CAGAGTAGTG	CAGCCAAAGG	AGCATGAATT	GTGGAATCAT	ACAGCTCTAG	180
GTTCAGATCC	TACCTTTACC	ACTTGATAGC	TAGGCAGACT	TCAACAAGTT	AGTCTAATTT	240
GAGCTTCAGT	TCTCTCATCT	GTGAAAAAGA	GAAAATACAG	CCACTTTATA	ACATTATTTT	300
AGATGCCATA	AGGTAGGTAA	AGTGCCAGAC	ACATAGATTC	AAAAATCTCA	ATAAAATAGG	360
AAGGCTGGAA	TTTCCAAAAT	TTTTTCTTGC	TTTCACAATC	TGGGTTCTAA	ATTTATTATT	420
ACTCTACCCA	TCACTTCCTC	CTTCTCCCTC	CACAACCTCA	CTATAAGCCC	AACATCTCGA	480
G						481

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GAATTCGGCC	AAAGAGGCCT	AGTGTCATGT	AGAGGTCTCA	GCATTTCTCT	TAGTATTTGA	60
CTGTATTAGT	TTTACATATT	TCTTCTTTTG	TTTAGAGTAT	AACCGCTTCT	TACATTTCCT	120
TCAGTCGTTT	TCTAAAGAAG	AAATTAATCT	TTTTAGAAAT	CCTGGCAGTT	ACCCCGCAAT	180
TGATGTTTTG	GTGGAAAATT	AGAGCACACC	AGTTTGTCAT	AACTTTAAGA	AACATTTTCA	240
CTTTATTGAT	ATTCTGAGGA	TTTTAGTGAT	TTGGGTAATT	TGGGTCTAAT	AAAGAGTAAA	300
TTGTTGAATA	CTCATTTGTT	TTGAGTCATC	TATATTTTA	AACCCTTTCT	TTAGTTGTTT	360
TTTCATCCCT	AATACAAATG	CAACTTTCCC	ACTTGCTCGA	G		401

- (2) INFORMATION FOR SEQ ID NO:224:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GAATTCGGCC AA	AGAGGCCT AAA	CTGATGT CT	CCATTTG C	CTGGATAGGA	CATGCTGACT	60
GATGACCTCA CA	GACTGTTC TTA	TGCCCTC ACT	TACTCACC T	TCACCACCTA	CAGTCATAGG	120
CTGACTAGGA GT	TGGTTGTG TAC	ATTCCTA AAG	CCTTTTTG (CCCTCTTTAT	TTGTCTTTCT	180
AAGTGTGTAT TC	AGTACTAT GTA	AATTGAT AA	AACATGAG 1	TGTGAAAATA	TTTTTTTTG	240
CTATAAAAAT GT	AAATTGAA TTO	TTTGGGG AAG	GAGCTGAT A	AAAATATGTC	ACTTAAAGAT	300
CTTGTTAAAT TA	GATGAGGG AGA	ATATAGAT GA	CAGAAACT (CTTTCAACAA	ATATCTAAAA	360
AGATGTGCCA CT	CCAATTAT TTT	GTGAGTG TC	TTCAAGTT 7	TITGTCCCAC	TTTAAAGAAA	420
ACCAAACTGG CC	ATCATAGC CA	ATGAATTA TG	CAGGAGTC 1	TCGAG		465

- (2) INFORMATION FOR SEQ ID NO:225:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GAATTCGGCC	AAAGAGGCCT	ACACATTATA	TTAGATTTCA	TAGAAACTGT	TGGAAATATC	60
TAGCACATGT	GCTTTATCCC	ACAATAATTA	CATAGAAAAT	TAAAAAGAAT	TAATTCTAAT	120
GTAACCATCT	TTTTACTTGA	CTTTTTTTTT	TTTTGCTCTG	CTCACAGGTC	TAATTGTTGT	180
TATTCTCACT	TTATTTTTCT	ATAAGGTAGG	AATAATATCC	ACTTCATTAG	CTCATCATGA	240
GGGATAAGTA	GGATTGGAAA	AGATACTTTC	AAAGGGCACC	TAACTGTGAA	GAAGATGCCT	300
TCATTTGCAT	TTCTTTCTTG	GCACATTTCT	TGTTATCCAG	TCATTCATTA	GGACTCCATG	360
TTTATTGAAC	ACCTACTCTG	TGCCAGGCAC	TTTTCTCTGT	TCTGGAAATA	TCACCATGTA	420
AAAACAAATA	GCTGAAGAAT	GCCCTGCCCT	CATAGAGCTT	ACAGACATAG	AGCTCGAG	478

- (2) INFORMATION FOR SEQ ID NO:226:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GAATTCGGCC	AAAGAGGCCT	AGCGTTTCTG	ACTTTATTAC	TGGTAATTTA	TTGCACAGGT	60
TTTTCTGCAT	CAAAAAAGTA	TCTGCTAAAA	TAGAGAAAGT	TGTGTCTGAA	TTCACATTTC	120
CCCCCAACTT	CTAAAAATAT	TTCCCCTAAA	AAAGAATCCA	CTCATCTAAT	TTTAAAGAAA	180
ATATACTTCT	TACACAAGAC	AATCCAAACT	GATGCAAAAT	ATTTATTCCA	AGTTAGTTAT	240
TTTATGCAGT	AGTTTCCCCC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:227:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GAATTCGGCC	AAAGAGAGAA	ATTTTAATCT	TGAAAGACTT	TTCAGGGTAT	CTCATTTTTT	60
AGGTGGGGGT	GGCAGGTGTA	TTTCTTTTTT	AACAAATAAA	AGGCATTTAA	GTAAAACTAA	120
AATGAAAAA	GTAGGCCTTC	TGACATTGTG	TACTTGGTGG	TTCTGTCCCT	CTGCCTGTAA	180
CAAATCTCAT	TTTTGTTACC	AAGAACTGTA	TGAAAGAAGT	AAATCCACCC	CTCTCGAG	238

- (2) INFORMATION FOR SEQ ID NO:228:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GAATTCGGCC	AAAGAGGCCT	ATGCCTGTGT	TGGGTTGACA	GTGAGGGTAA	TAATGACTTG	60
TTGGTTGATT	GTAGATATTG	GGCTGTTAAT	TGGTGTTGTA	GAATATTTGA	GCACAGGTGG	120
AGTAGAAACA	AATCACAAAG	ACTTTAAGGA	GTTGAGGTAT	AATGAAAGTC	TCACAAACTT	180
CAGCTGTCAT	GGGAAGAATG	GAACCACCAA	TGGAAGGATC	ACTCATGGTT	TCAAGTTACA	240
GAGTGCCTAT	GAGAGTGGCC	TGATGCCTTA	CACGAATTAC	ACATTTGATT	TCAAGGGTAT	300
AATAGACTAC	ATTTTCTATT	CTAAACCTCA	GCTGAACACC	TTAGGCATCC	TGGGCCCTCT	360
GGACCACCAC	TGGCTGGTTG	AGAATAACAT	CAGTGGCTGC	CCGCACCCCC	TCATCCCCTC	420
TGACCACTTC	TCACTTTTTG	CACAACTGGA	GCTCTTACTG	CCTTTCCTGC	CCCAAGTCAA	480
CGGCATTCTC	GAG					493

- (2) INFORMATION FOR SEQ ID NO:229:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 572 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GAATTCGGCC	AAAGAGGCCT	AAGAAATCAA	AATTAAAGCA	ATCAAATAAT	ACTCACATTT	60
ATATAAGAAA	TACTTCAATT	TACTTTCCAA	TGAGTAAAGT	TTTATATTTA	ATGTTTTAAT	120
ATTTCATATT	TTAGTTTCTT	GCAATTATTT	ACTTTTTCTA	AAACCTACTT	AAATTAGGTT	180
TAAAAGTCTA	CTATATATAA	TTTGAAATTT	TATTCAGTTT	GCCTACAGGT	GTGTTTTAAC	240
CACTGTGTAC	ATAGTATTTA	ACGGTCTGCT	TTTTTTTTT	TAATIJATGGT	TCATGTNTGA	300
ACATCTGTAT	GTTCATACTT	TTCTTGACAA	AGTTCTAAAG	GTTACTGTGT	TGAAGCATAC	360
TGAACGATTA	CTGATAATTT	CTATTTTGAG	GAACAGGTAT	GTCAGTTCTT	TCTCTCTGTT	420
TGATAATTCT	CTCTTTTCCC	CTTAGGAATC	CAAAAATCCT	TGTGGAGTGT	CTTACTCCTG	480
ATTTTCGAGG	TGATCTCAAA	GCAATAGAAA	AAGTTGCTCT	GTCAGGATTA	GATGTGTATG	540
CACATAATGT	AGAAACAGTC	CCATTGCTCG	AG			572

- (2) INFORMATION FOR SEQ ID NO:230:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAATTCGGCC	TTCATGGCCT	ATCGAGATAC	GCTTTCGCGC	ACCAGGTACG	CCTGGTGTTT	60
CTTTGTGGTT	TTTCGGATTC	TTTTTGGGGA	GTGCGGGGAG	TCACAGTTAG	AAGGCGGCCG	120
GGTGTTGCTG	GAGGAAAGTG	CTGAGGTCCA	GAGCGTAGTC	CGAGGGCTCC	GAAGTCAGAT	180
TAAAGGGCTC	GAG					193

- (2) INFORMATION FOR SEQ ID NO:231:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 608 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GAATTCGGCC	TTCATGGCCT	ACATAATGAT	GCTGCCTCAA	AACTCGTGGC	ATATTGATTT	60
TGGAAGATGC	TGCTGTCATC	AGAACCTTTT	CTCTGCTGTG	GTAACTTGCA	TCCTGCTCCT	120
GAATTCCTGC	TTTCTCATCA	GCAGTTTTAA	TGGAACAGAT	TTGGAGTTGA	GGCTGGTCAA	180
TGGAGACGGT	CCCTGCTCTG	GGACAGTGGA	GGTGAAATTC	CAGGGACAGT	GGGGGACTGT	240
GTGTGATGAT	GGGTGGAACA	CTACTGCCTC	AACTGTCGTG	TGCAAACAGC	TTGGATGTCC	300
ATTTTTCTTT	CGCCATGTTT	CGTTTTGGAC	AAGCCGTGAC	TAGACATGGA	AAAATTTGGC	360
TTGATGATGT	TTCCTGTTAT	GGAAATGAGT	CAGCTCTCTG	GGAATGTCAA	CACCGGGAAT	420
GGGGAAGCCA	TAACTGTTAT	CATGGAGAAG	ATGTTGGTGT	GAACTGTTAT	GGTGAAGCCA	480
ATCTGGGTTT	GAGGCTAGTG	GATGGAAACA	ACTCCTGTTC	AGGGAGAGTG	GAGGTGAAAT	540
TCCAAGAAAG	GTGGGGGACT	ATATGTGATG	ATGGGTGGAA	CTTGAATACT	GCTGCCGTTA	600
TACTCGAG						608

- (2) INFORMATION FOR SEQ ID NO:232:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 518 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GAATTCGGCC	TTCATCGCCT	ACAGCGCTGC	CTTTCCTTAT	GAAGAAGACA	CAAACTTGGA	60
TTCTCACTTG	CATTTATCTT	CAGCTGCTCC	TATTTAATCC	TTTCGTCAAA	ACTGAAGGGA	120
TCTGCAGGAA	TCGTGTGACT	AATAATGTAA	AAGACGTCAC	TAAATTGGTG	GCAAATCTTC	180
CAAAAGACTA	CATGATAACC	CTCAAATATG	TCCCCGGGAT	GGATGTTTTG	CCAAGTCATT	240
GTTGGATAAG	CGAGATGGTA	GTACAATTGT	CAGACAGCTT	GACTGATCTT	CTGGACAAGT	300
TTTCAAATAT	TTCTGAAGGC	TTGAGTAATT	ATTCCATCAT	AGACAAACTT	GTGAATATAG	360
TGGATGACCT	TGTGGAGTGC	GTGAAAGAAA	ACTCATCTAA	GGATCTAAAA	AAATCATTCA	420
AGAGCCCAGA	ACCCAGGCTC	TTTACTCCTG	AAGAATTCTT	TAGAATTTTT	AATAGATCCA	480
TTGATGCCTT	CAAGGACTTT	GTAGTGGCAA	ATCTCGAG			518

- (2) INFORMATION FOR SEQ ID NO:233:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GAATTCGGCC	TTCATGGCCT	ACCTTGATAC	ATCAGCTGAC	CTCATTTCCG	GATACCTTTT	60
CCCCCCGAA	AAGTACAACA	TCTGGGCCGC	CCCAGCCCGA	AGACAGATCG	TCGCTCCCTG	120
GACAATCAGA	CGAATTCTCC	CCCCCCCCC	AAAAAAAAAG	CCATCCCCCC	GCTCTGCCCC	180
GTCGCACATT	CGGCCCCCGC	GACTCGGCCA	GAGCGGCGCT	GGCAGAGGAG	TGTCCGGCAG	240
GAGGGCCAAC	GCCCGCTGTT	CGGTTTGCGA	CACGCAGCAG	GGAGGTGGGC	GGCAGCGTCG	300
CCGGCTTCCA	GACACCAATG	GGAATCCCAA	TGGGGAAGTC	GATGCTGGTG	CTTCTCACCT	360
TCTTGGCCTT	CGCCTCGTGC	TGCATTGCTG	CTTACCGCCC	CAGTGAGACC	CTGTGTCTCG	420
AG						422

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAATTCGGCC	TTCATGGCCT	AAGAGATTAA	GTGATTTACT	CAAGGTCATA	TTCCTTGGAA	60
GTAGCAAAAC	TTCTGGACCA	GATTTCTGAT	TCCAAAGGCG	GTACTGCTTG	TACAACACTC	120
TGAGAAGTAA	TTACTGTGGA	GCAAAGCAAA	AAGAAGTCTA	AAAGCAGGTG	ATAGGTGTAG	180
ATTTAGATAG	TGTAAGGGTA	GGCTAAAGTG	TTGTAACAAA	TGCACCCTCA	AGTAGGTAAT	240
GGCTCAAACA	CAATAGATGT	TCACTTCCCA	CATCTCAGAG	CAAATTGGGT	TCTCCTCATC	300
AGCTAAAGCT	TTCCTACATG	GGATGATTTG	GGGAGCAAGA	CACTCCATCT	ATGGCTCCCT	360
TACCCTCCAA	GGCCTTCTTA	TTGTCTTTAT	GTAACCAGTG	GAAGAGCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:235:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GAATTCGCCT TCATGGCCT	A GGCTTCTTCG	GAGCTGTGTA	NTCTTAATTT	GCTTTGCTGC	60
TGGCTGGCTG ACAGCTGAT	G GGGGACTCCT	CANGACGGAC	TCCCTTCCAG	ATGCACCCAT	120
CTCCATCCTT CTCAACTCC	C CAACCTTTGT	CCTCCCCACT	CTTCGCTCGC	GCGGCGGTCT	180
GAGACCACCA GGACCAGTT	r caggggtttc	CTTCTCCAGC	GAGACTTGGC	AGAACAGGCT	240
TTAAAAGCAA AGGAGGCAG	C GGAAGACTGT	GAATTCCTTT	GGACAATTGA	TGATATTTAT	300
CATTGTGCCC AGTTTCTAC	A AATAAAAGAT	GGGTGGATTA	TTTTCTCGAT	GGAGGACAAA	360
ACCTTCAACT GTAGAAGTT	C TAGAAAGTAT	AGATAAGGAA	ATTCAAGCAT	TGGAAGAATT	420
TAGGGAAAAA AATCAGAGA	T TACAAAAATT	ATGGGTTGGA	AGATTAATTC	TGTATTCCTC	480
AGTTCTCTAT CTGTTAACA	T GCTTAATTGT	ATATTTGTGG	TATCTTCCTG	ATGAATTTAC	540
AGCAAGACTT GCCATGACA	C TCCCACATCT	CGAG			574

- (2) INFORMATION FOR SEQ ID NO:236:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GAATTCGGCC	TTCATGGCCT	AGGCGCGGCC	CGGGTTCCCG	TTCCCCGCGG	AGCCATGCGG	60
TACAACGAGA	AGGAGCTGCA	GGCTCTGTCC	CGGCAGCCGG	CCGAGATGGC	GGCCGAGCTG	120
GGCATGAGGG	GCCCCAAGAA	GGGCAGCGTG	CTGAAGCGGC	GGCTGGTGAA	GCTGGTGGTG	180
AATTTCCTCT	TCTACTTTCG	GACAGACGAG	GCCGAGCCCG	TCGGAGCCCT	GCTGCTGGAG	240

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CGCTGCAGAG TCGTCCGGGA AGAGCCCGGC ACCTTCTCCA TCAGCTTCAT TGAGGACCCT GAGAGGAAGT ATCACTTCGA GTTCAGCTCG AG	300 332
(2) INFORMATION FOR SEQ ID NO:237:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:	
GAATTCGGCC TTCATGGCCT AATTGCAAGA TCACGGAATC TCCTGAATCA TTAAGAAAAG ATAAAATATC ACAAGCATCT TTAGTGTTAT GTGTATTCAG TAATTCTTTG GAGTTGTATT TATTAAGCTT ACCAGATTTT AAAGGCATAT AAAATGTGGT AAGATATGAG ACACATACTG AAATATCAGT GCAAAGGGAG AATGGTAGTT GAATGGTCAG AAACGAAAAA GCCTCGAG	60 120 180 238
(2) INFORMATION FOR SEQ ID NO:238:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 180 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:	
GAATTCGGCC TTCATGGCCT AGAAGCATTT TTTGTTATTG TGAAACATTT TTATACTTTC ATTATAATTT GTTGAGCCTA GAGTTGGGCT ATTTGAATAT TTATTATGAT AATCTTTTGG CTAATGGTAA CAGCATATCT TGTTCTAACA AAATTACTGT TAACAGCAAT CGAACTCGAG	60 120 180
(2) INFORMATION FOR SEQ ID NO:239:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 578 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:	
GAATTCGGCC TTCATGGCCT ACTGAGATCC AGACCAGCTC CTCCCAGACC TCTCCAGAAG AAGCCATGGG AACCCCTCGT ATCCAGCATT TGCTGATCCT CCTGGTCCTA GGAGCCTCCC	60 120
TCCTGACCTC GGGCCTAGAG CTGTTTTGTC AAAAGGGTCT GTCCATGACT GTGGAAGCAG	180
ATCCAGCCAA TATGTTTAAC TGGACCACAG AGGAAGTGGA GACTTGTGAC AAAGGGGCAC	240
TTTGCCAGGA AACCATACTA ATAATTAAAG CAGGGACTGA GACAGCCATT TTGGCCACGA	300
AGGGCTGCAT CCCGGAAGGG GAGGAGGCCA TAACAATTGT CCAGCACTCT TCACCTCCCG	360
GCCTGATCGT GACCTCCTAC AGTAACTACT GTGAGGATTC CTTCTGTAAT GACAAAGACA	420
GCCTGTCTCA GTTTTGGGAG TTCAGTGAGA CCACAGCTTC CACTGTGTCA ACAACCCTCC ATTGTCCAAC CTGTGTGGCT TTGGGGACCT GTTTCAGTGC TCCTTCTCTT CCCTGTCCCA	480 540

ATGGTACAAC TCGATGCTAT CAAGGAAAAC CTCTCGAG

540

578

- (2) INFORMATION FOR SEQ ID NO:240:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GAATTCGGCC	TTCATGGCCT	ACATGAATCC	ACTCCTGATC	CTTACCTTTG	TGGCAGCTGC	60
TCTTGCTGCC	CCCTTTGATG	ATGATGACAA	GATCGTTGGG	GGCTACAACT	GTGAGGAGAA	120
TTCTGTCCCC	TACCAGGTGT	CCCTGAATTC	TGGCTACCAC	TTCTGTGGTG	GCTCCCTCAT	180
CAACGAACAG	TGGGTGGTAT	CAGCAGGCCA	CTGCTACAAG	TCCCGCATCC	AGGTGAGACT	240
GGGAGAGCAC	AACATCGAAG	TCCTGGAGGG	GAATGAGCAG	TTCATCAATG	CAGCCAAGAT	300
CATCCGCCAC	CCCCAATACG	ACAGGAGACT	CGAG			334

- (2) INFORMATION FOR SEQ ID NO:241:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GAATTCGGCC	TTCATGGCCT	AGGGCACCAC	TGAGTTCAGT	ACTTCAAAAT	TGCCGTGCTC	60
TACCTCTCCC	CAGTGCACAA	AAACACTCTC	CACACCAAGC	TGCTGCTGCT	GGGGGATGGA	120
GGGATGGCGT	CAGCGATTCA	AGACTGTTTT	TCCTACCTGT	TCAGCACTTC	TTTCAGCGAT	180
ATGAAGTTAA	ATCCAGTCTT	TCCCTGTCTC	CAGGCATCAT	CGCCATCAAC	ATACAGCCAT	240
ACTCCAGGAT	TGCCCATCTT	CAACATAAAC	GGACTCTCCT	GGACTCCACT	TCCCACATCA	300
GTCACAGCCA	CACTTCCTGA	GAAAGAAGTC	TACACTCTTC	ATTCACTTTC	ATTCACCCAC	360
TGCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:242:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GAATTCGGCC	TTCATGGCCT	AGAGAAAATA	AAGAGTTATA	TCAGAAATTT	ACAAACATAA	60
CTTTTTAAAT	TTTAAATTGC	AAAATATATA	TCATACGAAA	ATGAAAATTA	TAATTCTTCT	120
TGGATTCCTG	GGAGCCACAT	TGTCAGCCCC	ACTTATCCCA	CAGCGTCTCA	TGTCTGCCAG	180
CAATAGCAAT	GAGTTACTTC	TTAATCTTAA	TAATGGTCAA	CTTTTGCCAC	TACAACTTCA	240
GGGCCCACTT	AATTCATGGA	TTCCACCTTT	CTCTGGAATT	TTACAACAGC	AGCAGCAGGC	300
TCAAATTCCA	GGACTCTCCC	AGTTCTCTTT	ATCAGCTCTA	GACCAGTTTG	CTGGACTGCT	360
CCCAAATCAG	ATACCCTTAA	CAGGAGAGGC	CAGTTTTGCC	CAAGGAGCCC	AGGCAGGCCA	420
AGTTGATCCC	TTACAGCTTC	AAACACCGCC	TCAGACACAA	CCAGGCCCAC	GTCTCGAG	478

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(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GAATTCGGCC TTCATGGCC	T ACTTACAGAA	CCTATTCACT	GGGAAGGAAG	CCCTCATTAT	60
AATGATTTTC ATTCTTATG	T GTGTTTCAGG	ACGACTGGGT	TTGGATTCAG	AAGAGGATTA	120
TTATACACCA CAAAAGGTG	G ATGTTCCCAA	GGCCTTGATT	ATTGTTGCAG	TTCAATGTGG	180
CTGTGATGGG ACATTTCTG	T TGACCCAGTC	AGGCAAAGTG	CTGGCCTGTG	GACTCAATGA	240
ATTCAATAAG CTGGGTCTG	A ATCAGTGCAT	GTCGGGAATT	ATCAACCATG	AAGCATACCA	300
TGAAGTTCCC TACACAACG	T CCTTTACCTT	GGCCAAACAG	TTGTCCTTTT	ATAAGATCCG	360
TACCATTGCC CCAGGCAAG	A CTCACACAGC	TGCTATTGAT	GAGCGAGGCC	GGCTGCTGAC	420
CTTTGGCTGC AACAAGTGT	G GGCAGCTGGG	CGTTGGGAAC	TACAAGAAGC	GTCTGGGAAT	480
CAACCTCGAG					490

- (2) INFORMATION FOR SEQ ID NO:244:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GAATTCGGCC	TTCATGGCCT	AGAAAAAAGA	AACTGTCGTG	GATACTGTCA	GTGTATATAT	60
TTATGTGGTA	CCTGAGAGCC	ACCCCAAATT	AGATTGACTT	TAGATCGTTT	ATACAAAAAT	120
AGCTTGAAGA	ACTGTTTTTT	CCATGGTAAA	TGCTTTTGAA	TATTAACTTA	GTTATGTTAG	180
ATTCCTACCT	CAGTGGTACT	GTCACAGCCA	TTGGTTACAT	TTCTGAAACC	CTTCAGAGTA	240
AGAGTTTTGG	TTTTTTGTTT	TGTTTTGTTT	TGTTTTTTGA	GATGGAGTCT	TGCTCTGTCG	300
CCCAGGCTGG	AGTGCAGTGC	AGCAACCCAG	GTGGAGTGCA	GTGCAACCTC	CACCTCCCAG	360
GTTTAAGCGA	TCCTCCTAAC	CTCGAG				386

- (2) INFORMATION FOR SEQ ID NO:245:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GAATTCGGCC	TTCATGGCCT	AGCTTCAGTA	GCAAATAAGG	ACATCATCTG	CTATAACCTA	60
CAAGCAGTTG	GACAGATATT	CTACATTTCC	TCATTTCTCT	ACACCGTCAA	TTACATCTGG	120
TATTTGTACA	CAGAGCTGAG	GATGAAACAC	ACCCAGAGTG	GACAGAGCAC	ATCTCCACTG	180
GTGATAGATT	ATACTTGTCG	AGTTGGTCAA	ATGGCCTTTG	TTTTCTCAAG	CCTGATACCT	240
CTGCTATTGA	TGACACCTGT	ATTCTGTCTG	GGAAATACTA	GTGAATGTTT	CCAAAACTTC	300

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	AGTCAGAGCC ACAAGTGTAT CTTGATGCAC TCACCACCAT CAGCCATGGC CCTTCTGCCA ACACATCTGT CTGTAGCACA CTCGAG	TGAACTTCCA	360 396
	(2) INFORMATION FOR SEQ ID NO:246:		
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 514 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	•	
	(ii) MOLECULE TYPE: cDNA		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:		
	GAATTCGGCC TTCATGGCCT ACACCTTCA CTTATCTTAT	AATAGATTTT TCTCAACAAT ATGCACACTG TCTTCCGCCA CTTGGTATGT TACTANTACT	60 120 180 240 300 360 420 480 514
	(ii) MOLECULE TYPE: cDNA		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:		
	GAATTCGGCT TCATGGCCTA GGTTTTCTGT ACATGGAGAT TAAACTGTCT AGAGTTTATT GTTCTAGATC TTGAGCACAA AGGTTGGTAT ACGTTAATAA AAGGGAAGAA AATCATTTCC TTCATACCAA GTAAGAGAGC ACTTATCATG GCTTTGCAAT TATGAGACCA GTAGTAGAAA TAGCTTTAGT TTCCTCAATT ATTCTTCAGA CTTTCTTTAC ACTGCTCAAG GTGGGGCGAG TGGCAGGGCG ACCTGACGCT GCGGAGGCTC GAG	AAAAAATAGC GTAGGCACTG TTCCTGGAGT	60 120 180 240 300 323
	(2) INFORMATION FOR SEQ ID NO:248:		
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 423 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: cDNA		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:		

GAATTCGGCC TTCATGGCCT AGGAACAGTG TGTGTTTTTG TGTGTGGCTT GCATTCTCTC 60 CTCCGTTTTT GGAGCAGCGT GAGATTATTG CAATGCTACA TTTCCTCCCT CTGCGCCCTC 120 CTACCCCATC AATGTCTCAT GGGTGGTGTG ATAGAGGCTA TGGGAGTGAA GACCACTGGT 180

GTTAGTCTGT GTATAGTTCC TGGGGTGTGG CGAGTACCAG CTCTGACAGC GGAAGAGAAC TATACTGTTG ATTCCCATTA TTCTCAGTAG GTGTGTTCTA TAAAATTGCT GCGAACACCA AATTAGCGAA TCCTGAACCA TCGTTCCCAG AGGAATAGGG GGTTAGGGTC CTGTGATCCT CAAGTTGCAA CATTGTCTTC GACTGATTAA TATGTAACCT TGTTTTATAT GTGCAATCTC GAG	240 300 360 420 423
(2) INFORMATION FOR SEQ ID NO: 249:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 124 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:	
GAATTCGGCC TTCATGGCCT ACCGAAACCA AATAATTCAA GCACTGCTTA TTACAATTTT ACTGGGTCTC TATTTTACCC TCCTACAAGC CTCAGAGTAC TTCGAGTCTC CCTTCACCCT CGAG	60 120 124
(2) INFORMATION FOR SEQ ID NO:250:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 289 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:	
GAATTCGGCC TTCATGGCCT ACATCTATGA CTTTTTAAAC ATGCGGCGTT TTGTGAATAT CATGATAATA ACAAGAGTCA ACAGGCTAAG TGAGAGGAGA GGGATGCTAC GCCTACGCTG CCCCCACCAC GGCCAGCCGG CTTCTGCGCC TTTGGTGTTG GATTTTCTTT GTGATTTTAC GGGGTTTTGT GTTTTTTTT TCTTGTTTTT TGTTTTGTTA TTTTTTCTTG TCCACTTGAT TTGCATGCAA CACCCACAAA AAGGAAACAC AAAACCCCGT CTGCTCGAG	60 120 180 240 289
(2) INFORMATION FOR SEQ ID NO:251:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 302 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:	
GAATTCGGCC TTCATGGCCT ACACTATGAG AGGACCGATT GTATTGCACA TTTGTCTGGC TTTCTGTAGC CTTCTGCTTT TTCAGCGTTG CCACACAATG TCTGGCCTTC CCCAAAATAG AAAGGAGGAG GGAGATAGCA CATGTTCATG CGGAAAAAAGG GCAGTCCGAT AAGATGAACA CCGATGACCT AGAAAATAGC TCTGTTACCT CAAAGCAGAC TCCCCAACTG GTGGTCTCTG AAGATCCAAT GATGATGTCA GCAGTACCAT CGGCAACATC ATTAAATAAA GCAAAACTCG AG	60 120 180 240 300 302

302

(2)	INFORMATION	FOR	SEQ	ID	NO:252:
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GAATTCGGCC	AAAGAGGCCT	ATTTTTTTTT	CTGCAAACAC	TGTGTATAGT	GAGACTTGTT	60
CTACTTTGGA	GAACAGGTTA	CCTTTTGAAA	ATGAGGTTGA	GTTTCTTCCT	TTCTGATGCA	120
TTGATTTTTG	AAGATTTTTT	TTTCCCCCTT	CCCCTCTCCC	TCGAG		165

- (2) INFORMATION FOR SEQ ID NO:253:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GAATTCGGCC	AAAGAGGCCT	AGCTTCTTTG	TATAATTAAA	TCTGAGTTTT	GTTTGAGCAT	60
CTTTCAACAT	GTACCATATT	TATGACAATT	CTCTTCCATA	GGATCTATCT	GTTCTGCAAC	120
AAGTATTGAT	CTTACAGTAA	AATTTTTCAC	AAATTCATTA	GATTCTATGT	CTCTTTTTCT	180
GGTAGGAATT	TTTGTGCAGG	TAGCTATCTC	TTGCCCTAGA	TTATTCTCCT	TGTTTAGCTG	240
CTGATTCTTA	AACTGGCCTC	TAGATTTCCA	GATTTCTTCC	GGTACAGACT	TTCTCTTTGC	300
AAGTTCTTCC	ATCTCTAATC	TTTGAGATTA	ATCTTCTTTT	GAAATGTCCT	GCTGCTCTAC	360
TCTTGATGTT	CTCGAG					376

- (2) INFORMATION FOR SEQ ID NO:254:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TCTCCAAGGG	AAAATAAATG	CTTTTACTAT	CTAGTTTGTC	TCTTTGAGAA	TTAAAACTCT	60
TTTTTTTTT	TTTCATTCCA	GTAGCTTTTG	GGGTAGAGTT	TGGCTCTTTG	AGAATTGCAT	120
ACTAATTAAT	TTTAGGGGTG	ATTTGTACAT	CATCTCTATA	TTCCTGAAAC	ACAGTAGAAA	180
CAGCCAGCAG	TCAGGCAACC	ATCTACCATG	ACCATTAAAA	CATCCCCAAA	GTGAAACACC	240
AGATGTGATC	TGCTAGATTT	AGTGGAGGCG	GCTGGCTCGA	G		281

- (2) INFORMATION FOR SEQ ID NO:255:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 571 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GAATTCGGCC	AAAGAGGCCT	AGCTAGNCTT	GCTCAGCTTT	GTGGATACGC	GGACTTTGTT	60
GCTGCTTGCA	GTAACCTTAT	GCCTAGCAAC	ATGCCAATCT	TTACAAGAGG	AAACTGTAAG	120
AAAGGGCCCA	NCCGGAGATA	GAGGACCACG	TGGAGAAAGG	GGTCCACCAG	GCCCCCAGG	180
CAGAGATGGT	GAAGATGGTC	CCACAGGCCN	TCCTGGTCCA	NNTGGTCNTC	NTGGCCCCCN	240
TGGTCTCGGT	GGGAACTTTG	CTGCTCAGTA	TGACGGAAAA	GGAGTTGGAC	TTGGCCCTGG	300
ACCAATGGGC	TTAATGGGAC	CTAGAGGCCC	ACCTGGTGCA	GCTGGAGCCC	CAGGCCCTCA	360
AGGTTTCCAA	GGACCTGCTG	GTGAGCCTGG	TGAACCTGGT	CAAACTGGTC	CTGCAGGTGC	420
TCGTGGTCCA	GCTGGCCCTC	CTGGCAAGGC	TGGTGAAGAT	GGTCACCCTG	GAAAACCCGG	480
ACGACCTGGT	GAGAGAGGAG	TTGTTGGACC	ACAGGGTGCT	CGTGGTTTCC	CTGGAACTCC	540
TGGACTTCCT	GGCTTCAAAG	GCAACCTCGA	G			571

- (2) INFORMATION FOR SEQ ID NO:256:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GAATTCGGCC	AAAGAGGCCT	ATGCGCAAGG	ATCAAGCCGA	CTACCTGTGC	TGTCTACTGG	60
GACAGCAGTC	TCCGAGCTAC	TCCGTACCTC	CCTCTGCCAG	GTCGTGGAGT	TAGGCCCCAG	120
TCCCTACTTG	TCACTGGTTC	CCACTGTGCT	CCTAACTGTG	CAGCACCTGG	GAGCTCTGGC	180
CTGGGGCTGG	AGGCCCTGGT	AGGAGCTGCA	GTTGGAGGCC	GTTCTGTGCC	CAGCAGCGGT	240
GAGCGGCTCC	CATGGGCCCT	GTGTCTGCAG	GGAGCCAGGG	CTGCGGCACA	TGTGCTGTGA	300
AACTGGCACC	CACCTGGCGT	GCTGCTGCCG	CCACTTGCTT	CCTGCAGCAC	CTCCTACCCT	360
GCTCCGTGTC	CTCCCTCTCC	CCGCGCCTGG	CTCAGGAGTG	CTGGAAAAGC	TCACGCCTCG	420
GCCTGGGAGC	CTGGCCTCTT	GATATACCTC	GAG			453

- (2) INFORMATION FOR SEQ ID NO:257:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GAATTCGGCC	AAAGAGGCCT	ATGTCATGAG	TGAACTTGGC	AATTGCCTTG	TTAAAACCAG	60
TTGGACATTA	TCTTCCACAT	TGCGAAGCTA	TACATGTCTG	ATATGTTCTG	AAAGAATAGA	120
ATTTATAGTT	AGATATACTA	TTTTTGATTA	TTTACTCAGA	AGGAGACATG	TAATTATTCT	180
TATGTTGTCA	TGAAAATCTA	TTAAATGCAT	TTATATTTCA	CATCAATGTT	ACGAAGTTCC	240
ATTATTATTA	TTTTACAGAG	GGGAAGCCAA	GATACAGGAG	TGGAAATTAC	TTGGCCTATC	300
GCTCGAG	•					307

(2) INFORMATION FOR SEQ ID NO:258:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear-
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

GAATTCGGCC	AAAGAGGCCT	AAGAAGATGA	ACAAGCGCCA	GCTCTATTAC	CAGGTTTTAA	60
ACTTTCGCCA	TGATCGTGTC	TTCTGCACTC	ATGATATGGA	AAGGCTTGAT	CGTGCTCACA	120
GGCAGTGAGA	GCCCCATCGT	GGTGGTGCTG	AGTGGCAGTA	TGGAGCCGGC	CTTTCACAGA	180
GGAGACCTCC	TGTTCCTCAC	AAATTTCCGG	GAAGACCCAA	TCAGAGCTGG	TGAAATAGTT	240
GTTTTTAAAG	TTGAAGGACG	AGACATTCCA	ATAGTTCACA	GAGTAATCAA	AGTTCATGAA	300
AAAGATAATG	GAGACATCAA	ATTTCTGACT	AAAGGAGATA	ATAATGAAGT	TGCTCTCGAG	360

- (2) INFORMATION FOR SEQ ID NO:259:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GAATTCGGCC	AAAGGGCCT	ACCTGAAACG	GCAGTCCGGT	CCCTCCGACA	TTGTCCAGCG	60
GAAGGCCTGG	GCTTCACACT	CTGTGCCTCC	CGGCGCTACC	TGGCACGATG	CCGAGCACAC	120
AGCAGATGCT	CAATGAATGC	CCAACCAACC	CTATACCTGG	CTTGGATCTC	AAGCTCCCTG	180
GCCGGGGCCT	GATGGAAGGC	TTTGGGGGCA	CAGGAGGCTG	CCCCCTTGGG	CGCCCCCGGC	240
CACCTCTTCG	CCCTCGAATC	TCAGGCAGCT	TGGTCAGGAA	CTTCTTCTCC	ACGTATTTAG	300
CGTGAATCCA	GGCCTCCTTC	TCCTGCCTGT	GGGAGGGGAG	AAGCACGCAG	TCTTCCCTCT	360
TCTCCTCCAG	GGGTCCCCCA	TTCCCCTCCC	ACCCTABACC	CATAGCTCGA	G	411

- (2) INFORMATION FOR SEQ ID NO:260:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GAATTCGGCC	AAAGAGGCCT	AGGGAGTGTT	TGCGTTTCTT	CTCCGTTTGG	CAGTGAAACA	60
CATCTCAGAA	AGGTGGAGCT	GATCAGAATA	ATGTTCAGCA	TCAACCCCCT	GGAGAACCTG	120
AAGGTGTACA	TCAGCAGTCG	GCCTCCCCTG	GTGGTCTTCA	TGATCAGCGT	AAGCGCCATG	180
GCCATAGCTT	TCCTGACCCT	GGGCTACTTC	TTCAAAATCA	AGGAGATTAA	ATCCCCAGAA	240
ATGGCAGAGG	ATTGGAATAC	TTTTCTGCTA	CGGTTCAATG	ATTTGGACTT	GTGTGTATCA	300
GAGAATGAAA	CCCTCAAGCT	CGAG				324

- (2) INFORMATION FOR SEQ ID NO:261:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GAATTCGGCC	AAAGAGGCCT	AGTGGGGCTG	TATTTTAATA	CAAGAAAGAC	ATTGCTCTAG	60
AACATGGCTC	GCCTTTGCTT	CAGGGCCTAG	CAGTTTATTT	TAGCCATAAG	GGTAAGGGAG	120
CAGGTCAGAA	ATGACTTTTA	GTGTAATCCT	ATCTGTAATT	AAAAATACAA	ATGCTGTCAT	180
AAGATCAAAT	GTTATCAAAA	ATCAGTATTT	AAAATTAAAT	TTACCCCCAA	ATTTCTTTCA	240
AAAAAGTTGT	AATGTTCTTT	TTCAGTGAAG	CCTTTGCACT	GCTAGAGCTG	AAGAATGTGA	300
TCAATCGGCT	TGTTGAATAA	TCCCGCACAG	TAGGTATTCC	GCTGAAGCCA	ACTCTAGCTG	360
GGGGCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:262:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GAATTCGGCC AAAGAGGCCT AAGAA	AATAGG ACTATACAAA	TTTTCAACTT	CTTTTGATAT	60
CAGTTTTGGT AAGATGCATT TTTCT	ITCTGA GAATTTGTTT	CATTTGAATT	TCCAAATTTA	120
TTAGCATGAA GTTGTTAATA AAAAT	CTTAT ATTTTTACTC	AAATTTTGAG	ATAGTTGTAG	180
ATTTACATGA AGTTGTAAAG AATAA	ATAGAA AGATCCTGTG	TACCTTTTCC	CAGTTTTCCC	240
CAAAAGTAAC ATTTTGCATA ACTC	TAGTAC AGTAGCACAA	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:263:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GAATTCGGCC AAAGAGGCC	r aggcaaaccg	TGTACTAAGC	ATCAGTGCAG	AGATAGTGAA	60
TGAGACACAG TATTCCCAC	TTTGAGCAGT	GCCAGTCTAG	TATTAGAATA	TTTTTGGCTA	120
AAAAATTATT TTGAAGCAT	A AAGAAGCTTT	TGTTTGCTCT	GGTGATTTTC	ATAACATATT	180
CACATTCTTA ATGTATTTT	r ggtttttcag	AAAGTTACTT	CTGGCCTGTG	TTCTTTCAGA	240
ATATAGGTTG CAGCTTGTG	TAAGTGCAGG	AACTATTGAT	AGACTGAGTT	TAGAAGAAGG	300
GAAACTCGAG					310

- (2) INFORMATION FOR SEQ ID NO: 264:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GAATTCGGCC	AAAGAGGCCT	AGGACTTTGG	GGCAGGTGAT	TAAATTTATA	TAGGTACCTC	60
AAGAAAAAGA	ACCTGAATAT	GCTGCATTTT	CTTTCTTTAG	CTTTTACATG	TAGCATTTTG	120
TTTTGCTTTT	GTTATTTTTG	TTTTGATATA	TGCTTTTTGG	ACCCCAATAG	ACTGTTGAAA	180
GAAATTTAAA	AATTACTCTT	GTAGGGATAT	AGTATCCTTA	AAAAATAAAA	AAAAAAAA	240
ATTTAAAAAA	ATTGCTGCAA	TATCTGGCTC	GAAGGTTGCC	CTATATTAGA	ATAATACTTT	300
AGCCAAACAC	ATCAGCTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:265:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GAATTCGGCC TTCATGGCCT	TGTGATTCTG	CAAAGGAGGA	ACAATAATTC	ACTGTTTCCC	60
AAACTTATCT GACCATAGAA	CATATNTCTC	AGAGTATTTT	TCAAGAGTAG	TATTTTCTGT	120
AATATATGAT GAAAAATAAT	CGTATCGGCC	ATCTTTGTAC	ATAAGGTCAA	AATGTCAGCC	180
AGCCCTGAAA TAAATGCAAG	CCAAAAGGTA	GAGAGATAAG	TGAATAAAGC	TGGCACACTG	240
TCAGTCCGGA GTACCATGCT	GCATTCTGAG	TCAAGCTCCA	GGAAACTGAG	CTAGGGTTTG	300
TCTCTAAGAA GAAAAACTGG	AGCGTCCAAA	GCTTCTGGAT	TCCATTTAAT	TAAAACCCTT	360
TTAAATTAAA TCCTTGTAAC	TGAAGAGTAT	CGGTGGATGA	AGAAAAAATA	GTCTCACATG	420
TCTTCATTTC CATCCTTGGC	TCAGTACAGC	TCCAGTTCCA	TTATTCTTAA	ACATCTATTA	480
ACATGATTGC TAAATAATTA	CACAGGCTAA	CTGCCAAGCA	TTTTTCACAG	GAAGCAAGGC	540
ACTGCTCGAG					550

- (2) INFORMATION FOR SEQ ID NO:266:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GAATTCGGCC	TTCATGGCCT	AGTTAAGTGG	GAAGTTAAAT	GGCAAGTACT	AGAATGCCAC	60
CTATGGCAAG	CACTAGAATG	GTCTAGGTGT	GAAATGAGGG	AGTAATGTCA	GGGAGTCAAG	120
GTGGCCATCC	ATAGCAGTGA	TTCTTATCTG	GGGTAGGGG	TGAATTTCAC	GTGGAGGGAG	180
GTCTCTGGAC	ATGGACCCCC	AGGCAGGGCT	ATCCAATCAT	CTGAGGGGTG	AGCAGTGTTC	240
AGCTCAGTAA	AAGTAAGGGA	AAAAAAATAG	CAGTCTCTAA	AAGGAACATA	GAGCGCTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:267:
 - (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 353 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GGGGAGAGCA	TCAGGAAGAA	CAGCTAATGG	ATGCTGGGCT	TAATACCTAG	GTGATGGGAT	60
GGTCTGTGCG	GCAAACACCA	TGGCACAAGT	TTACCTATGT	AACCTGCACA	TCCTGACATG	120
TACCCCTGAA	CTTAAAATGA	AAGTTGGAGA	CCAAAAAACA	AAACACCATA	AAACTACAAA	180
ACTTCTTAAA	CAATAAACTA	GTAGAAAATT	TCTAAAATAT	ATAATTCAAG	AATTATAA	240
GAGCTCTTTT	TATATGTAAA	TATAAATTTA	AATACAAGAG	AAACATCTAA	AACAGGTTGC	300
TTCTGAGAAA	CGTGACTGGT	TATTAAGAAG	AGGTATATAG	GGGCTCACTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:268:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CATTATTTAA	CCTTTTAAAC	AATCAAGAGA	TTGCTTTTTA	AATTGTCTCT	AAAAAGGTTT	60
GATTTTTTAC	GAAAGAGAGA	GCACTTGAAT	ATATCTTTAT	GTACCACCGT	GTCTCTTTTT	120
GTTAGATTTT	TCATCTGTGG	GTATAATATA	AAATATTCTT	AAAATGAAAG	CTTTACGCTT	180
GTGTTTGAGA	CTAAGCAACT	TGCATTGTGT	CATGACCCTT	CTAATACCAC	AAACCCTCGA	240
G						241

- (2) INFORMATION FOR SEQ ID NO:269:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GAATTCGGCT	TCATGGCCTA	CACTCAACCA	CTGAAAAAGC	TGAAAATCAA	TGTTTTTAAG	60
GTTCACAAGT	GTGCCGTGTG	TGGCTTCACC	ACCGAAAACC	TGCTGCAATT	CCACGAACAC	120
ATCCCTCAGC	ACAAATCGGA	TGGTTCTTCC	TACCAGTGCC	GGGAGTGTGG	CCTCTGCTAC	180
ACGTCTCACG	TCTCTCTGTC	CAGGCACCTC	TTCATCGTAC	ACAAGTTAAA	GGAACCTCAG	240
CCAGTGTCCA	AGCAAAATGG	GGCTGGGGAA	GATAACCAAC	AGGAGAACAA	ACCCAGCCAC	300
GAGGATGAAT	CCCCTGATGG	CCCCCTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:270:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) -SEQUENCE DESCRIPTION: SEQ ID NO:270:

GCGGGCACCA	TTTCCAGTAT	GTACCAAACC	AAAGCCGTCA	TCATTGCAAT	GATCATCACT	60
GCGGTGGTAT	CCATTTCAGT	CACCATCTTC	TGCTTTCAGA	CCAAGGTGGA	CTTCACCTCG	120
TGCACAGGCC	TCTTCTGTGT	CCTGGGAATT	GTGCTCCTGG	TGACTGGGAT	TGTCACTAGC	180
ATTGTGCTCT	ACTTCCAATA	CGTTTACTGG	CTCCACATGC	TCTATGCTGC	TCTGGGGGCC	240
ATTTGTTTCA	CCCTGTTCCT	GGCTTACGAC	ACACAGCTGG	TCCCGGGGAA	CCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:271:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GCCAGACTAC	CACAAGCCCC	ACCCACACTA	TGCCAAGCCC	TACCCATACC	ACAGCAAGCC	60
CCACTCATAC	TTCCACAAGC	CCCACCCATA	CCCCCACAAG	TCCCACCCAC	AAAACCAGTA	120
TGTCACCTCC	CACCACTACA	AGTCCTACCC	CCAGTGGTAT	GGGCCTAGTC	CAGACTGCCA	180
CAAGTCCCAC	CCATCCTACC	ACAAGCCCCA	CCCATCCCAC	CACAAGCCCC	ATCGTTATAA	240
ATGTAAGCCC	TTCCACTTCT	CTAGAACTTG	CTACCCTCTC	CAGCCCCTCC	AAACACTCAG	300
ACCCCACCCT	CCCAGGCAAT	GACTCCCTTC	CCTGTAGTCC	CCCAGTCTCC	GATTCCTACA	360
CTCAGGCAGA	CCCTATGGCC	CCCAGAACTC	CCCACCCAAG	TCTCGAG		407

- (2) INFORMATION FOR SEQ ID NO:272:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

ACTGAGCTCA	AGGACCCCTC	CAAGAAGAAG	ATGCAGCACA	TCTCCAACCT	GTCCATCGCT	60
GTCATGTACA	TCATGTACTT	CCTGGCTGCC	CTCTTCGGCT	ACCTCACCTT	CTACAACGGG	120
GTGGAGTCGG	AGCTGCTGCA	CACCTACAGC	AAGGTGGACC	CGTTTGACGT	CCTGATCCTG	180
TGTGTGCGCG	TGGCCGTGCT	GACAGCAGTC	ACGCTCACAG	TGCCCATCGT	TCTGTTCCCG	240
GTGCGCCGCG	CCATCCAGCA	GATGCTGTTT	CCAAACCAGG	AGCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:273:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs

ANTENNA DE LA PRESENTACIONA DE LA CONTRETACION DE SELO, ESPACIONES DE LA CONTRETACION DELICION DE LA CONTRETACION DE LA CONTRETACION DELICION DE LA CONTRETACION DE LA CONTRETACION DELICION DE LA CONTRETACION DE LA CONTRETA

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GAATTCGGCC	TTCATGGCCT	AGTCAAGCTA	GGTAAGCTAA	AAAGAAGAAA	ACCTGGTTAC	60
AGCCCGGTGA	ATTGATTTTT	TTCCAGCCGA	GAAATAGATA	TTTCTCTCAC	ATATATTTGG	120
AAAACTTTAG	TCATCTTCAT	AAAACTTAAA	AAGTTACCTA	AGCACACA	GCAAGTTTCT	180
CCTTTCTTCC	TTTTCCACAC	CCTTACCAGT	TCACTATGTT	TCTACCAATC	CAGTGCCCAG	240
TTGCCAATGA	TGTTGCTCTC	ACATGAATTT	ACTGCATTCC	CTTCTGGTTC	CCCAGAAGGT	300
CTTGAAGAAA	GAGGTTCAGA	CTAGTGGACC	CAAACAGAAT	TTCTTGGCTG	GTGATACTCA	360
${\tt GATTGTGTTC}$	AGAGCCTGGT	ATGAAGAAGG	GGCCAGGTGT	AAGAAGTAGT	TAATCAACTG	420
CACGTTGATT	TCAGGCTGAA	TATTCAACCA	TCTGCAGCCA	CCCGTCTCTA	AAAGTCTAGC	480
TGAAGCACAA	TTGATTGTGC	CATAGAATGA	GCAAACGCT'I	GAAAACACAA	GCTCGAG	537

- (2) INFORMATION FOR SEQ ID NO:274:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GCGAGCTCGT	GTTTTAAAGG	ACCAAATAGA	AGTTTACCAG	GAGAGAAGTG	ACAGAAGTGC	60
TGTCTAGATA	GAGGAAGGC	ACACACAGAT	GCAAGCATGT	GCAGAAATGA	GCAAACCACT	120
GAGACGCTGC	CTTGAGCTCT	GTGTCACACT	GCTATGTTGC	AGCCTGGGAG	GCTGTTCCCA	180
GTTGAGCCCT	TCGGAACCAG	CCATGAGATG	GCACGGGTAC	GCGGAAGGGA	GCAGTCTCCA	240
TGGCTGGGTG	GTGATGGGGG	CTTCTCGAG				269

- (2) INFORMATION FOR SEQ ID NO:275:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GATGGCTCCC C	CAGAGCCTGC	CTTCATCTAG	GATGGCTCCT	CTGGGCATGC	TGCTTGGGCT	60
GCTGATGGCC G	GCCTGCTTCA	CCTTCTGCCT	CAGTCATCAG	AACCTGAAGG	AGTTTGCCCT	120
GACCAACCCA C	GAGAAGAGCA	GCACCAAAGA	AACGGAGAGA	AAAGAAACCA	AAGCCGAGGA	180
GGAGCTGGAT C	GCCGAAGTCC	TGGAGGTGTT	CCACCGACG	CATGAGTGGC	AGGCCCTTCA	240
GCCAGGGCAG C	GCTGTCCCTG	CAGGATCCCA	CGTACGGCTG	AATCTTCAGA	CTGGGGAAAG	300
AGAGGCAAAA C	CTCCAATATG	AGGACAAGTT	CCGAAATAAT	TTGAAAGGCA	AAAAGCTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:276:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

•						
GCCACAATAG	CGGGATTGAT	CTCCTTAGGA	CCTATCTTTG	GCGTTGCCAG	TTCCTTTTAC	60
CTTTTGTGAG	TTTAGGTTTG	ATGTGCTTTG	GGGCTTTGAT	CGGACTTTGT	GCTTGCATTT	120
GCCGAAGCTT	ATATCCCACC	ATTGCCACGG	GCATTCTCCA	TCTCCTTGCA	GGTCTGTGTA	180
CACTGGGCTC	AGTAAGTTGT	TATGTTGCTG	GAATTGAACT	ACTCCACCAG	AAACTAGAGC	240
TCCCTGACAA	TGTATCCGGT	GAATTTGGAT	GGTCCTTCTG	CCTGGCAGAA	CTCGAG	296

- (2) INFORMATION FOR SEQ ID NO:277:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

GAATTCGGCC	TTCATGGCCT	AGGATGTAGA	ATCCTGCTTA	TCTGTGAAAT	GCAGTTGACA	60
CATCAGCTGG	ACCTATTTCC	CGAATGCAGG	GTAACCCTTC	TGTTATTTAA	AGATGTAAAA	120
AATGCGGGAG	ACTTGAGAAG	AAAGGCCATG	GAAGGCACCA	TCGATGGATC	ACTGATAAAT	180
CCTACAGTGA	TTGTTGATCC	ATTTCAGATA	CTTGTGGCAG	CAAACAAAGC	AGTTCACCTC	240
TACAAACTGG	GAACAATGAA	GACAATGAAC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:278:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

TCGTTCCCTT	CATCTCTTCC	CTTGCCAGAG	CAGGGACTCT	CTCCATATAA	ACAAAAGGAA	60
AACCACTGGC	CAGGGTATGG	TCAATACCTC	AACATATCCA	GACATCACAG	CACCAGAACA	120
CCAGTATGTA	TATTCCACAA	GTACTCGAG				149

- (2) INFORMATION FOR SEQ ID NO:279:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GCAATCAGAT	AAAGAAAGAC	CTGGCTGACA	AGGAGACACT	GGAGAACATG	ATGCAGAGAC	60
ACGAGGAGGA	GGCCCATGAG	AAGGGCAAAA	TTCTCAGCGA	ACAGAAGGCG	ATGATCAATG	120
CTATGGATTC	CAAGATCAGA	TCCCTGGAAC	AGAGGATTGT	GGAACTGTCT	GAAGCCAATA	180
AACTTGCAGC	AAATAGCAGT	CTTTTTACCC	AAAGGAACAT	GAAGGCCCAA	GAAGAGATGA	240

254

TTTCTGAACT CGAG

(2) INFORMATION FOR SEQ ID NO:280:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:	
GACAGCCTGG AAGTTTGGAG ACCCTGACAC ACCCACCTTC TCACCTGGGC TCTGCGTATC CCCCAGCCTT GAGGGAAGAT GAAGCCTAAA CTGATGTACC AGGAGCTGAA GGTGCCTGCA GAGGAGCCCG CCAATGAGCT GCCCATGAAT GAGATTGAGG CGTGGAAGGC TCCGGAAAAG AAAGCCCGCT GGGCCTCATT CTGGCGGTTG TGGGCTTCGG AGCCCTGATG ACCCAGCTGT TCTATGGGA ATACGGCGAC TTGCATCTCT TTGGGCCCAA CCAGCGCCCA GCCCCCTGCT ATGACCCCTG CCTCGAG	60 120 180 240 300 327
(2) INFORMATION FOR SEQ ID NO:281:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 357 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:	
GCCTGGAACC TGATTCTCCT GACCGTCTTT ACCCTGTCCA TGGCCTACCT CACTGGGATG CTGTCCAGCT ACTACAACAC CACCTCCGTG CTGCTGTGCC TGGGCATCAC GGCCCTTGTC TGCCTCTCAG TCACCGTCTT CAGCTTCCAG ACCAAGTTCG ACTTCACCTC CTGCCAGGGC GTGCTCTTCC TGCTTCCTAT GACTCTTTTC TTCAGCGGAC TCATCCTGGC CATCCTCCTA CCCTTCCAAT ATGTGCCCTG GCTCCATGCA GTTTATGCAG CACTGGGAG GGGTGTATTT ACATTGTTCC TGGCACTTGA CACCCAGTTG CTGATGGGTA ACCGACGCCC GCTCGAG	60 120 180 240 300 357
(2) INFORMATION FOR SEQ ID NO:282:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 306 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:	
GCGGGCTGCA GAATGATAGA CGAGCTCAAC AAAACGCTGG CCATGACCAT GCAGAGGCTG GAAAGCTCTG AGCAGCGGGT CCCCTGTTCC ACTTCTTACC ACAGCTCTGG GTTGCACTCG GGTGATGGGG TCACCAAAGC AGGACCTATG GGCCTTCCAG AAATAAGACA AGTGCCAACT GTTGTGATTG AATGTGATGA CAATAAAGAA AATGTGCCTC ATGAGTCAGA CTACGAAGAC TCTTCTTGCC TGTATACAAG AGAAGAGGAG GAAGAGGAGA AGGACGAAGA CGACGACGAA CTCGAG	60 120 180 240 300 306

- (2) INFORMATION FOR SEQ ID NO:283:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

AATCAATCAA	CTAGGCATAT	GACACAGTAG	TCCATTATAA	AAGAAGACAT	ACATCCAGCA	60
CCATCAACTA	ATTCTTAAGA	TAAGTTATCT	GGGAAAATTG	AAGAACAAAT	AAATTCAACG	120
AAATACTGTA	AAGTGAACGA	AGACATAAAA	CCAAAGAAAA	CTGAGGCCAT	TTCTGCCAAG	180
AAAGGAACAG	CAAAGAGTAA	AGATGAAAA	TATTCTAAGA	TAATACCAGA	AAAAGATAAT	240
TCCTACATGG	ACAAAGATGA	GCATGGTTCA	TCCTCTGAAA	GTGAAGATGA	AGCGCTGGGT	300
AAATATCATG	AGGCCTTATC	CAGAACACAC	AATTCCGGAC	TACCACTCGA	G	351

- (2) INFORMATION FOR SEQ ID NO:284:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

AAGTTAAAGG	TATTAAATAA	ATGAGTTTCT	CCTTAATTTT	GTTAATGCTC	TTTTAGCTAA	60
TAAGACTTTT	TCTAGAGTTA	CATATTTTAA	TCTGTTTCAT	TTTTATTTT	TCCTTTGGTT	120
TTATATTTT	AAAAGCCATT	ATATCCCTCC	CACTGGTAAC	ATACACATAC	ACAGACACAC	180
ATCTATTTCA	AATGAATACT	TACTACTTTA	TCATTTTCAG	TCTTAATTGT	ACT	233

- (2) INFORMATION FOR SEQ ID NO:285:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GCGGCGCCGC	AGCAGTTCCA	GGAAGGATGT	TACCTTTGAC	GATGACAGTG	TTAATCCTGC	60
TGCTGCTCCC	CACGGGTCAG	GCTGCCCCAA	AGGATGGAGT	CACAAGGCCA	GAATCTGAAG	120
TGCAGCATCA	${\tt GCTCCTGCCC}$	AACCCCTTCC	AGCCAGGCCA	GGAGCAGCTC	GGACTTCTGC	180
AGAGCTACCT	AAAGGGACTA	GGAAGGACAG	AAGTGCAACT	GGAGCATCTG	AGCCGGGAGC	240
AGGTTCTCCT	CTACCTCTTT	GCCCTCCATG	ACTATGACCA	GAGTGGACAG	CTGGATGGCC	300
TGGAGCTGCT	GTCCATGTTG	ACAGCTGCTC	TGGCCCCTGG	AGCTGCCAAC	TCTCCTACCA	360
CCAACCCGGT	GATCTTGATA	GTGGACAAAG	TGCTCGAG			398

- (2) INFORMATION FOR SEQ ID NO:286:
 - (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 462 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GAATTCGGCC	${\tt TTCATGGCCT}$	ACACCCAGCC	AATTTTTTTG	TATTTTTAGT	AGAGACGGGG	60
TTTCACCATG	TTAGCCAGGA	TGGTCTCTAT	CTCCTGACCT	CATGATTTGC	CCGCCTCGGC	120
CTCCAAAAAA	AGAACATTTT	ATATTTGAGT	GCTATTTCTT	TTGCGGCACC	AAAACTTTAT	180
AACACACTGC						240
GTTCCCATGT						300
ACTITTAACA						360
TTTTATAAGA	GCCACAAAGG	CCTTCCTCTG	TGTTTTGTTT	${\tt TTGTTTTTGT}$	TTTTGTTTTC	420
ATTTTTGAGA	CAGGCTCTCA	CTGTCCCTCA	${\tt GTGGCTCTCG}$	AG		462

- (2) INFORMATION FOR SEQ ID NO:287:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TGGACAGTCT AGAAGATGCT	GTGGTGCCCC	GGGCTCTGTA	TGAGGAGCTG	CTGCGCAACT	60
ACCAGCAGCA ACAGGAAGAG	ATGCGCCACC	TCCAGCAGGA	GCTGGAGCGG	ACTCGGAGGC	120
AGCTGGTACA ACAGGCCAAG	AAGCTCAAGG	AGTACGGGGC	ACTTGTGTCT	GAAATGAAGG	180
AGCTCCGTGA CCTTAACCGG	AGGCTCCAGG	ACGTGCTGCT	CCTGAGGCTT	GGCAGCGGTC	240
CCGCCATTGA TCTGGAAAAA					281

- (2) INFORMATION FOR SEQ ID NO:288:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

		ACTCGTGTAA				60
CACATTGAAG	GAATGGAGGG	AATCCAATAT	TTCTGCCTCT	GACATAATTT	GGGAGAACCT	120
		CATTGCATGG				180
TCACCCATAT	GTTCCAGATG	TTCTATTTTG	GTCTGTGATC	CTGTTCTTTT	CCACAGTTAC	240
TCTGTCAGCC	ACCCTGAAGC	AGTTCAAGAC	TAGCAGATAT	TTTCCAACCA	AGGTTCGATC	300
CATAGTGAGT	GACTTTGCTG	TCTTTCTTAC	AATTCTGTGT	ATGGTTTTAA	TTGACTATGC	360
CATTGGGATC	CCATCTCCAA	AACTACAAGT	ACCAAGTGTT	TTCAAGCCCA	CTAGGCTCGA	420
G						421

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 417 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289: AAGCCAATGG CTGGTCGTGA TCCTGAATGC CAACGCACAG AAATGATTAA GAAAGAAGAA 60 GAACGTTTGA GGGCTTCCAT ACGTAGGGAA TCTCAGCAGC GCCGAATGAG AGAGAAACAG 120 CACCAGCGGG GGCTGAGCGC CAGTTACCTG GAACCTGATC GATACGATGA GGAGGAGGAA 180 GGCGAGGAGT CCATCAGCTT GGCTGCCATT AAAAACCGAT ATAAAGGGGG CATTCGAGAG 240 GAACGAGCCA GAATCTATTC ATCAGACAGT GATGAGGGAT CAGAAGAAGA TAAAGCTCAA 300 AGATTACTCA AAGCAAAGAA ACTTACCAGT GATGAGGTAA GACCAAATTT ATTCAATTCT 360 AGGGGTTTAT CCTGTACTCA GGAGCCAACT GCTTTGAATG AAAAGCTCAC ACTCGAG 417 (2) INFORMATION FOR SEO ID NO:290: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 314 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290: CAAGCATACA ATCAACTCCA AGCTCGGTAT CACCTGAGCC CAGGAAGTGG AGGCTGCAGT 60 GAGCTATGAT CAGTAAAACA CAAGACAGGT TCACTGGCTC CCATCCCAAC CCGGACCAGC 120 TCCCTAGTAT AACAACTCAC ATGCATGTGG ACTATACCCT TACAGCCTTC TTCTGTGTGT 180 TTATGTGCAT ATATGTAGCC ATAGGAAAAA AAATCAAAAT CCTTTGGTGT TCTTTCTTAT 240 TTTTTCAAAT ATTTCACCTG CCCCATTCTC TTTCCTTTCT CCTTCTAGTA CTCCCATTGC 300 ATGCAGTTCT CGAG 314 (2) INFORMATION FOR SEQ ID NO:291: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 361 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

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GTGTATGTGG	GGGGTAAGTG	TGTGTGTGTG	CGTGTGCGTG	TATGTGCACG	TGTTGTGTGT	60
GTGCGCCTGC	ACACGGAGAG	CCCACTCATA	CGTAGCAGAA	AATCAAATGG	CCCCAAATCA	120
GAAACATGGC	GCATGTGAGC	ATGCCACTTC	TTGTGTGCCT	GTGACTGTTC	AGAATGTACA	180
CGGCCCTGCA	GCTCCCGAAG	GCCAGCTCTG	CTGCAACCCC	TCCTCTGTCC	AACACAGTCC	240
TCACTGGTGT	CTTTTCCTCT	TCAAATCTAC	AGCATTTCTG	ATCTCTGCAA	ACAATTTAAC	300
CCAAAACCAA	GTTCTGGCTG	ACAAGGCTAC	ATCTTGTTTC	TTGTGCGTGA	TTAGCCTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 237 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:
GCGATTGAAT TCTAGACCTG CCTCGAGTCG ATGCACCGAA AAGGGTGAAG TAGAGAAATA AAGTCTCCCC GCTGAACTAC TATGAGGTCA GAAGCCTTGC TGCTATATTT CACACTGCTA CACTTTGCTG GGGCTGGTTT CCCAGAAGAT TCTGAGCCAA TCAGTATTTC GCATGGCAAC TATACAAAAC AGTATCCGGT GTTTGTGGGC CACAAGCCAG GACGGAACAC ACTCGAG 23
(2) INFORMATION FOR SEQ ID NO:293:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 292 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:
GAATTCGGCC TTCATGGCCT ACTTTATTTT TTTAATTATT ATTAGTATTA TTTTGAGACT GAGTCTTGCT CTATCACCCA GGCTGGAGTG CAGTGAGCTG AGACTATGCC ACCGCACTCC AGCCCGGGCG ACAGAACGAG ACTCCATCTC NAAAAAAAAA AAAAAAATCT ATGTTCATGC CTTNACACCT GTTTCTGCAC ATAGCTGTGC AGTATATTCT TCTTCTAAGC AACGACCCAG TGAAGATCCA AACAAAAGTT CACAAATATG TAGTTATCCA AGGCACCTCG AG 20 21 22 23 24 25 26 27 26 27 27 28 28 29 29 20 20 20 20 20 20 20 20 20 20 20 20 20
(2) INFORMATION FOR SEQ ID NO:294:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 136 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:
GAATTCGGCC TTCATGGCCT ACAATCTTTT AACTTTGGGG GTCACAGTTT TAGCCACCTT TCGGGGGGTG ACTGGAGCAG TAGGAGGTGT GGGGTCATTT TATGAATATA ATAAAATGGA GCTGACTGTA CTCGAG 136
(2) INFORMATION FOR SEQ ID NO:295:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 264 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GAATI	CGGCN	TTCATGGCCT	AAAATAACAC	ACAATTAGTA	TAGAAAAATT	GCAAACACAG	60
ATAAA	AGTCC	TTTCCCTGTG	AATTTCTGAA	TGCACCTTTG	AATATTCACA	TCTTACTGCC	120
TAAAA	GAGAT	TGTCTTGTGT	${\tt GCCGTTCTGG}$	AATTTGCTTT	TTTCCAGCTT	ACATGTTCTA	180
GGTCC	TTCCA	GATCAATAGC	TGCACTCCCT	CCTTCCTCTG	CTGGTTTCTC	AGCTCGATGG	240
GCTG1	AAGTG	GCATTACTCT	CGAG				264
(2) I	NFORM	ATION FOR SI	EQ ID NO:296	5:			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GAATTCGGCC	TTCATGGCCT	ACAACCTCAT	AAATCTCATT	CTTAATTTCA	CTCTAGGACA	60
GAATTATTGT	AGCACCTGTG	TTCTGTTATT	TTAGATTCAT	TTTAACTTAC	CTAGACACGG	120
GTACTGTGGT	AGTTGTAGAG	GTACAGATGT	TGAGTTCCCA	TCCTCCTGGC	TTAATGTCAC	180
TGGGGTTATT	AATACACTTC	ATAAGCATTT	TAGGGACACC	TGCTGTCTGC	TCAACCCCCA	240
GCAAACTCGA	G					251

- (2) INFORMATION FOR SEQ ID NO:297:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GAATTCGGCC TTCATGG	SCCT ACATCTGGTA	AATTTTTCTT	TCTGCCTGAG	GAACACCCTT	60
TAGCATTTAT TTAGTCT	GCT GGTGACCAAT	TCTCATATTT	TGTTTGTCTG	AAAAATACCT	120
TTATTTTGTT TTAATTO	TTG AAAGATATTT	GCACTGGTGT	GATTGGATTC	ATGATTGCTT	180
ATTATTTTCT TTTTCTT	TTTT TCTTTTTTGA	GACAGAGTCT	CGCTGTCGCC	CAGGCAGGAG	240
TGCAGTGGCC CGTACTC	CGAG				260

- (2) INFORMATION FOR SEQ ID NO:298:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

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GCTCTGAATC	TATTTTCTAG	GACATTTTTT	TCCCATTTAG	ATTAAGCCAG	AGAGAGCCCT	60
TTCTTGCCTC	CCAAGAGTTT	TTCTTTGTGT	GACTGTTGGT	ATTCTGAACC	TCTTGGATTT	120

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- (2) INFORMATION FOR SEQ ID NO:302:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GAATTCGGCC	TTCATGGCCT	AATCCTCCAG	ATTATTATGG	ATATGAAGAT	TATTATGATT	60
ATTATGGTTA	TGATTACCAT	AACTATCGTG	GTGGATATGA	AGATCCATAC	TATGGTTATG	120
AAGATTTTCA	AGTTGGAGCT	AGAGGAAGGG	GTGGTAGAGG	AGCAAGGGGT	GCTGCTCCAT	180
CCAGAGGTCG	TGGGGCTGCT	CCTCCCCGCG	GTAGAGCCGG	TTATTCACAG	AGAGGAGGTC	240
CTGGATCAGC	AAGAGGCGTT	CGAGGTGCGA	GAGGAGGTGC	CCAACAACAA	TGATCTCGAG	300

- (2) INFORMATION FOR SEQ ID NO:303:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GAATTCGGCC	TTCATGGCCT	AAAAAAAAGA	AGTTTATTTA	AAGAAACTCT	ATAAGAGCAG	60
CTTGGATTTT	ATATCTTTAG	ATCCAGAGTT	TTTACTTTTC	TGGAATTAAA	TATAATTGTT	120
TGGAATTTAC	TCTTTATTGT	TGAATTTTAA	AGCGTGACTA	AAGTAGTGCT	TCTTAAGATA	180
ATTGTCATGT	GTTTTTGTTT	TGTTTTGTTT	TGTTTTTTGG	TGCTGAGTGT	TGCTCTGTCG	240
CTCAGACTGG	AGCTCGAG					258

- (2) INFORMATION FOR SEQ ID NO:304:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAATTCGGCC	TTCATGGCCT	ACAATTCCGA	TAAAGTTTAA	GGTCAGCTGA	TGAAGAACAC	60
TCAAACCAAA	GTCGCCCATT	GGAGGAGCGC	CCTACCTCAC	AGGAATAGGC	CTGCATTATT	120
AGTATACCTT	CTTCATTCAG	TTATTGTTAT	TCTTATGGAA	ACAACCCATG	GGAAATGTAG	180
CCTTGGCATG	ACTGTATCAA	TGGATTCAGA	GAGCAGTAGC	GGGGACCCCC	CCAGTCAATT	240
ACGTTCCACA	GCAAGTCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:305:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs

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(B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:	
GAATTCGGCC TTTCATGGCC TAAATCTCAT AAATAGAAAG NAAAATAATC TAGAAATTTT	60
TCAAAGCTAG TACTCTTTCT CCTTATAAAT GTACACAATT TTAATCTTTT TACAAATTTA	120
TTTAACTGTA CCTACTGTAC TTATTGTAGA TTCAATGACG CAGTTAAGTC ATCACCCAAG	180
GATTTATGAA TTTGAGATTA CTGACCTGTT TTCTTCATAT TGCATTCACA TCAATATTTG	
TGAATTTGTT GTTCAGCTTT TCATTCAAAC AAAAAATATT CCCCCAAGAA AACTCGAG	298
(2) INFORMATION FOR SEQ ID NO:306:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 263 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:	
GCGATTGAGT TCTCCCTGCT GGTTCTTTTG AATCACACCA AATGAATGGC TTGCTACTGT	60
TCCCTCACAC CTTCATATTG TCCATGGTTT TTCCCACCTC CTTAGCTATA CAGCTGCTGT	120
TCCTCCTGCC TAAAATGTCT GAACATTCCC TCAGTGTTCA GCTCAGCCCA CATCTTACAT	180

240

263

(2) INFORMATION FOR SEQ ID NO:307:

ATATTGCGCC ACCAGAACTC GAG

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs

CTTCCCTAAG GATGTTTTTC TGCTGCTATC ATTCATTTTC TTCCTATGAG TTCCTCTGTT

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

TTCATGGCCT	AGCCCCGACT	AGCTTTGCCC	TAACTCCTTC	ATCAAAAGAC	60
CTTCCCACAC	CTCATACGCA	GCCACATCTG	CCCTATTCTC	CATGCTTTCC	120
CCCTTCCTCA	TCTCTCCCTG	CCTGTGCAGA	CCTCCACCCT	TCTTTCCTCC	180
CCCCCAATGC	TTGTAGACCT	TCCATTCATT	CCGTCTCATC	GTGCGTGGTC	240
CATCACCTGA	CCTCGAG				267
	CTTCCCACAC CCCTTCCTCA CCCCCAATGC	CTTCCCACAC CTCATACGCA CCCTTCCTCA TCTCTCCCTG	CTTCCCACAC CTCATACGCA GCCACATCTG CCCTTCCTCA TCTCTCCCTG CCTGTGCAGA CCCCCAATGC TTGTAGACCT TCCATTCATT	CTTCCCACAC CTCATACGCA GCCACATCTG CCCTATTCTC CCCTTCCTCA TCTCTCCCTG CCTGTGCAGA CCTCCACCCT CCCCCAATGC TTGTAGACCT TCCATTCATT CCGTCTCATC	TTCATGGCCT AGCCCCGACT AGCTTTGCCC TAACTCCTTC ATCAAAAGAC CTTCCCACAC CTCATACGCA GCCACATCTG CCCTATTCTC CATGCTTTCC CCCTTCCTCA TCTCTCCCTG CCTGTGCAGA CCTCCACCCT TCTTTCCTCC CCCCCAATGC TTGTAGACCT TCCATTCATT CCGTCTCATC GTGCGTGGTC CATCACCTGA CCTCGAG

- (2) INFORMATION FOR SEQ ID NO:308:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAATTCGGCC	TTCATGGCCT	AGCCAAAATC	ACAAGAAAAA	TAACTTTGAC	TTTGAAAACA	60
AATAAGTTAG	AAATGCAGTG	TTTGCACTTC	GTGGTTTATG	TTTGCTTTGG	TGGCCTCTCA	120
TTCCCACTTA	GCCTCAGTCT	CCAGGGCCTG	GGCTCCACCA	AGGAAGACTC	CATCTGCTCT	180
CTCTATTTGC	ACACTGGGAA	CTTTTTTCCC	CAAGGTACAG	GATATGATTC	AGGGTTTATG	240
GATGACCTCC	CACCCTCGA	G				261

- (2) INFORMATION FOR SEQ ID NO:309:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GAATTCGGCT	TCATGGCCTA	CCTATTCCCA	AACTTTAAAT	GTTGTCTACC	AAATACTGAC	60
AATTATGAAA	ATTCTACCAG	TAGAACACAC	CTCCCCTTTG	AGCTCCAGAG	CACATGCTTG	120
ACATCTCATA	TTAGAAAGAA	TCTTGATTTC	CCCTCCAGTC	TAGTCTTTCA	TGTTTTGTTT	180
TTCTTTGTGA	GAGTCTCCCT	CAGCCTGCAA	TGGCGTGATC	TCGGCTCACT	TCAACCTCCC	240
GTGCTCGAG						249

- (2) INFORMATION FOR SEQ ID NO:310:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAATTTGTTT	NAAAAAAAA	AAAAAAAAA	AGGGCNGGGG	GGAAAAAAAA	AAAAAAGAAC	60
TCCTGGAGAG	GGAAATAGCA	AATGTGTCTT	GCCTTTTGTT	GCTCTCTCTC	TCTTTTTTTT	120
TCTCTCGCTC	TCTTTCTTTC	TCTTCTTCTC	TCTGTTTTTA	AGTCAAGCAT	TGGTCTCGAG	180

- (2) INFORMATION FOR SEQ ID NO:311:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 742 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

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NNNANNNNNN	NNNNNNNNN	NNNNNNNANN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	60
ANNNNNNNN	NNNNNNNNN	NANNNNNNN	ANNNNNNNA	NNNANNNAN	NNNNNNNNN	120
NNNNNNNNN	NNNNNANNNA	NNNNNNNNN	NNNNNNANN	NNNNNNNNA	NNNNNNNNN	180
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NNNNNNNA NNNNNNNN NNNNNNNNN GNANNNNNN NNNNNNNN	300
NNANANANN NNNNNNNN NNNNNNNNN NNNNNNNNN NNNNNN	360
ATNGTTNTCG TTCCCNTTCT TCCTTGTTTC TTTTTCGGCA CAATATTTCA AGNTATACCA	420
AGCATACAAT CAACTCCAAG NTCGGAATTT TAATTACTTC ATGGCCTACT TGATGCAGGC	480
TGGAATGTTA TCCCTGGGGT GTGCTTGGAC CCCACCTGCT TTCTTTCTCT CCTGCCCCTC	540
CCCTACTCTC ACTGTAATTT ATGGACCCTG CCCGCCTGCG TGTTGTGTTG	600
CCTTTTCTCA CTATTGTTTG GGTGTGGGAG GGGGTGGTTT TTCACTGAAA AGGGGGGTAC	660
ACCTATAGCT TTCTTGATGT TCAATCAATC AGTCACTGTG TCCCAGACAT ATTCAATAAA	720
CACAGATTGG TACCATCTCG AG	
CACAGATIGG TACCATCICG AG	742
(2) INFORMATION FOR SEQ ID NO:312:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 270 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(D) Torobodi: Tillear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:	
GCGATTGAAT TCTAGACCCG CCCCAGGAGC CTCCAGCTGC CTAACCAGTG CCATTCTTTC	60
ACAACACGAT TTTCTACAAA TCTACAGCAC AACCGAGTTT GTAACCCGTG GGTTAGTATG	120
AGGACCGGGT TCGTGTACTC TCTGTATCTC CTCTTAAGCT TCGTCCAGGG TTCTTTATTT	180
TTGTCTGCTG CCAATGTCGT CTCGCATGCC TGCACCCTCG CATGCACGCT GCCCGCATGC	240
CACGTGCCAC GCTGTAGCCA CATCCTCGAG	270
and so the strain of the strai	2,0
(2) INFORMATION FOR SEQ ID NO:313:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 262 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) torobodi: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:	
,, ,	
GAATTCGGCC TTCATGGCCT AGTTGATGTC CTCTCATATT TTGTTGTTTA AATACGCAGT	60
GTGGTGGTTG TTATTTAGGA CTGCCTCTGC TCTGACAGAT GTGTCTACTC TACAGAGAGA	120
GAGAGAGACT GTGTCTATTG TCCCACCAGG CTGTCCAGAT CCAAACTCCA ATGACCTTTC	180
TGCACTCTGC CTGGCTATTG GTTACAGTTT ACATTCTACC TTCTCCCAAG GTATTGAGGG	240
AGGCTTGCAT GCAATTCTCG AG	262
(2)	
(2) INFORMATION FOR SEQ ID NO:314:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 311 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOI ECTH E TYDE. ODNA	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:	

60

GAATTCTAGA CCTGCCTCTC CTGACACGGG CCACCAAACC CCTTACCTGG TTCCTTGCTG

TAAAACTTCA CCAAATGAAG CCAGAGTTGA TCATGACCCT CTCGTGCTCG AATCCCTTCT GGGCTCCCCT CTGCCCCCTG CAAAGCCCAC ATGATACCAC AGAGAAGACC TGTCCCCTGC AGGCCAGCTG CTTCAGCCTC TTCCCTCACA CACATCGTCC CGCACACGGC AGCCACCATG GACTCAACAT CCCCGACACA CGGTGCTGCC CTCTGCATGC ACCGACCCCC TGCCCCTCCC ACCAGCTCGA G	120 180 240 300 311
(2) INFORMATION FOR SEQ ID NO:315:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 232 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:	
GAATTCGGCC TTCATGGCCT ACCTAGGTGC TTTTTAAAAT ATTCAGACAA ATATCTATCT TACATTGATT AAACCCGTGT AAATTCATTT GCAGTATCTA CATCGAATGT CAAAAAAGTA TACTTATTTT TGTTCCATAC TTATGTACAA TTTTTTCCCT CTTCAGGCTT TTTCATTTAC CTTTTTGAAA AAGCACTTAC TCTCCCCTTC CCTATCACCC CATCCCCTCG AG	60 120 180 232
(2) INFORMATION FOR SEQ ID NO:316:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:	
GAATTCGGCC TTCATGGCCT ACAGTTGTTC ATACTTCCTT TACAAATATA AAGATAGCTG TTTAGGATAT TTTGTTACAT TTTTGTAAAT TTTTGAAATG CTAGTAATGT GTTTTCACCA GCAAGTATTT GTTGCAAACT TAATGTCATT TTCCTTAAGA TGGTTACAGC TATGTAACCT GTATTATTCT GGACGGACAC TCGAG	60 120 180 205
(2) INFORMATION FOR SEQ ID NO:317:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 299 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:	
GAATTCGGCC TTCATGGCCT AGGGCTTGTC TTTTTCATTG TTGAGTTGCA GGAGTTCTTT ACATATTCTG GATACTAGAC CCTCATCAGA TATGGTTTTA AAATACTTTC TCTCATTCTT TTCACTTTCA AGTATCCCTT TGATGCACAC ACCCAAAAAA GCAAATAGTG TCCAATTGCA	60 120 180

(2) INFORMATION FOR SEQ ID NO:318:

TCTTTCTCTT TCTCTCTC TCTTTCTTTC TTTGAGGCAG GTAGGCCATG AAGGCCGAA

180 240

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:	
GAATTCTAGA CCTGCCTCGA GCTCCAGCTG CCAACACCCT TGGACACAAT ATTCCAGTCT CCACTGCCCA TCTCATGTGG TTCAGGTTCC TCGAG	60 95
(2) INFORMATION FOR SEQ ID NO:319:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 109 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:	
GATGCTTGGC TCACTCCCCG CTACTGGCCC CCAGACTTTT CCACCCCAGG AAATGTCTCC CCTGCCTGCA GCTTCAGCGA AAGCCCAGGA GGCAGGCCAA TCACTTGAG (2) INFORMATION FOR SEQ ID NO:320:	60 109
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:	
GAATTCGGCC TTCATGGCCT ACACATTTCT GTACCTGGAA AAAAAATGTA TCTTATTTTT GATAATGGCT CTTAAATCTT TAAACACACA CACAAAATCG TTCTTTACTT TCATTTTGAT TCTTTTTAAAT CTGTCTAGTT GTAAGTCTAA TATGATGCAT TTTAAGATGG AGTCCCTCCC TCCTACTTCC CTCACTCCC TTCTCCTTTG CTTATTTTTC CTACCTTCCC TTCCTCTTGT CTCCCCACTC GAG	60 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:321:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:	

GAATTCGGCC TTCATGGCCT AGGTTGTAAG TGATTTTATT TTTTCTTTC TATTTTCCAG TGTTTCTGTA ATGCTTTCAT ATTTCTTTTG GTAGTTAGAA AATAAAGGCT AATTTTTAAA AAGAATATCA TAGTCTAAAA AATTAAAGGA TGCATAGAGT TCCCTCTTGA CTATGTGACA TCTAAÂCTGA ATGAACTGTC TGCGTGGCAC AGTGGAACAG CGCAGTCTCA GGATTCTGAC AGATTTTTGG ATCCCAGCTC TACCACTAAC CTTGGGCAGG ATTTTAGTCC CTCTGAGACC TGCTTTCTCG ATTGAATTCT AGACCTGCCT CGAG	60 120 180 240 300 334
(2) INFORMATION FOR SEQ ID NO:322:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 226 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:	
GAATTCGGCC TTCACCTAAA TACTCCTCCT TTTGTATCAT TCAGCCTTTT GTTTTAGTTT GGTAAGTTTT AAGAAATTTC AGCAGCAAAG TTGTTATTCA GTGGGCACGA TGGACTCCAA ATGCCTCAAG TTATGTATAC CTGTGGAGGT CACGTACTTC CAAATTGTTC TCTTCCTCAT CTTCTCCCTT TACCTGCACG CCCAGGTGCG CCAGCCGGGC CTCGAG	60 120 180 226
(2) INFORMATION FOR SEQ ID NO:323:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 164 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:	
GAATTAAAAT AAACAAAAGG CAGCCAAGGA TGAAAGGATT TAGTTCTAAG ATGTTTCACA GTTGTGATTT GTTTATTTTA ATCCTTAGTA GTAAATTAGT ACTAGAAGGA TCAGGTATAT CTTCCTTAAT TCTTCCCAGG GGAGAGAAAG TCCCATTTCT CGAG	60 120 164
(2) INFORMATION FOR SEQ ID NO:324:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 494 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324.	
GAATTCGGCC TTCATGGCCT AAGCCTATGT TGATCTTGAA CTCCTGGGCT CAANCCNTCC TCCTGTCTCG GCCTCCCAAA TTGCTGGAAT TATAAGCACA TTACACAGTG CCCAGTCTAC CTACATTTTG ACAGACATAT AATATTCCAT GGCATGGTTA CATTATTCAG TTAAGAATGT TCCCGGTTTT CTCTAAGATA ATGCTGCCCA TCTGTGTCTC ACTCTGGACA TGTAGAGTAC CTGCAAAGAC TTGGACTGCT TGAGCAGAGG GCCTGCTTTT GTTTTTTGTT CTTCCTGCCT GTTGTAACTT GATGCTGCCA AATGATCCTC TTAAATGATT GTACCACCTT CCCTGCCACC	60 120 180 240 300 360
ACCAGATTTT AAGGATTCTC TGTACCTCCC AACACATGAT GACATCATAC ATGAAAAGTT	420

TTGCCTGCCT GATGGAATAA TTGAGTCAAG AAATAGGATG CTAATGGCAT CTTCGCTTAC CCGGTCTCCT CGAG	480 494
(2) INFORMATION FOR SEQ ID NO:325:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 295 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:	
GAATTCGGCC TTCATGGCCT AGTTGGGTGT TGAGCTTGAA CGCTTTCTTA ATTGGTGGCT GCTTTTAGGC CTACTATGGG TGTTAAATTT TTTACTCTCT CTACAAGGTT TTTTCCTAGT GTCCAAAGAG CTGTTCCTCT TTGGACTAAC AGTTGTCCTG ATGAATAATT TCATTTTCCT CAAGTTTATG ACACTCGGAA CGTCAAGAAC TGGAGGTTTG TGCAATTTGA GACCGGTCGG CACTGTGCAG AGATCAGAGT ACTAAGAGAC AGAGATTAÄA ATGGCTATCC TCGAG	60 120 180 240 295
(2) INFORMATION FOR SEQ ID NO:326:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 418 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:	
GAATTCGGCC TTCATGGCCT ACAAGGATAG AATTCATTCC ACCTATATGT ACTTAGCAGG GAGTATTGGT TTAACAGCTT TGTCTGCAT AGCAATCAGC AGAACGCCTG TTCTCATGAA CTTCATGATG AGAGGCTCTT GGGTGACAAT TGGTGTGACC TTTGCAGCCA TGGTTGGAGC TGGAATGCTG GTACGATCAA TACCATATGA CCAGAGCCCA GGCCCAAAGC ATCTTGCTTG GTTGCTACAT TCTGGTGTGA TGGGTGCAGT GGTGGCTCCT CTGACAATAT TAGGGGGTCC TCTTCTCATC AGAGCTGCAT GGTACACAGC TGGCATTGTG GGAGGCCTCT CCACTGTGGC CATGTGTGCG CCCAGTGAAA AGTTTCTGAA CATGGGTGCA CCCCAGGGAG TGCTCGAG	60 120 180 240 300 360 418
(2) INFORMATION FOR SEQ ID NO:327:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 588 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:	
GAATTCGGCC TTCATGGCCT ACAGACATCT AATCGGAATC TTGCTCTTGT TGCCCAGGCT GGAGTGTAAT GGCACAATCT CGGCTTACTG CAACCTCTGC CTCCTGGATT CAAGTGATTC TCCTGCCTCA GCCTCCCAAG TANCTGGGAT TACAGCCCTG AAAACCACTC GCTTGCAGAG CGCTGGATCA GCAATGCCTA CTAGTTCTTC ATTCAAACAC CGGATTAAAG AGCAGGAAGA CTACATCCGA GATTGGACTG CTCATCGAGA AGAGATAGCC AGGATCAGCC AAGATCTTGC TCTCATTGCT CGGGAGATCA ACGATGTAGC AGGAGAGATA GATTCAGTGA CTTCATCAGG	60 120 180 240 300 360

CACTGCCCCT	AGTACCACAG	TAAGCACTGC	TGCCACCACC	CCTGGCTCTG	CCATAGACAC	420
TAGAGAAGAG	TTGGTTGATC	${\tt GTGTTTTTGA}$	TGAAAGCTCA	ACTTCCAAAA	GATTCCTCCA	480
TTAGTTCATT	CCAAAACACC	AGAAGGAAAC	AACGGTCGAT	CTGGTGATCC	AAGACCTCAA	540
GCAGCAGAGC	CTCCCGATCA	CTTAACAATT	ACAATGCGGG	AACTCGAG		588

- (2) INFORMATION FOR SEQ ID NO:328:
 - (i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA

- (A) LENGTH: 385 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GAATTCGGCC	TTCATGGCCT	ACGACTGGGG	GAAATGTCTA	TTCTCCTGTG	TATCTCTGGG	60
CTTTTCTTGT	TTTTGGCTGC	CTCCTGCTCA	GTTCCTCTCT	TTAGGTATTT	AGTAAAGCGT	120
TCATGTAATG	TCATTCCTGA	GGACCCAAAG	TGATGCTCTT	TAACATGGTG	AACAATGGTC	180
ACTATATGTT	GGGCAAACAG	TTCTGAGGGG	CTACGCTGAG	ACTGAGCTGA	TTGTATGTGC	240
TGGAAAATGG	AACGAAACTC	CTGTTCCTTT	TTGTTGCTAT	GGACTAGATC	TCGGCAAAGC	300
TTGCGTTCCT	GAGCCAATAA	GCCACTGGGT	CGTGCGAGGT	CCTCATCAAA	AGAGTCCATC	360
CGGACATTGA	CCTGTGCCTC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:329:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAATTCGGCC	TTCATGGCCT	AGCAGTTCAC	CACTGCAAAA	CCACGGGGCT	GCGTGGAGGT	60
ATTCATGGGA	CACCGAGTGG	TATCACTAGC	AGCGGACTCT	GCATGCTTAC	TTAGAGCATA	120
AAAGGATAGC	ACCCTTGGCC	ATTGCCTGAC	ATGAACTCAG	TTTGGAAATT	GCAGAGGTGT	180
GGAGAGCCAT	GGATGGGTTT	TATAATTTAT	TCTAATGTAA	TCTCTGTGCT	AAAGGCTGTT	240
TGAAAAAAAT	AATGAAGTTG	ATGTTGCTTA	AGTTATATGC	AAATGTAAAC	TGGTCTTCCT	300
TCAAGATGTT	TGGAATGGAA	TGAATGCCCT	TCCCCTGGGT	ACCTCCCAAT	ACCTACCCTC	360
AAAAGAGCTC	CAGTAAGGCT	TCCTTATCTT	TCCTTGCCCT	GCTTCCTACA	CTGCTGCTGC	420
AGGTGTCTCT	GGGTGATTGT	GGGGGAAACC	ACTGTGGTTA	AGCACCAACA	CCAAGACTCG	480
AG						482

- (2) INFORMATION FOR SEQ ID NO:330:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

GAATTCGGCC	TTCATGGCCT	AAGGCCTTGG	TGCCCTGTGG	GTGGACTCTG	GGGAGGCCAG	60
GGGCCCAAGG	CCACCTTCTA	GGGCCTGAGG	AGCCCTCTGA	GACCTGCACA	CCCACCCCAG	120
GGAGCGCCCC	TCCCTCCACC	TCTGTGCCCC	CCCAGTGACT	CTCGAACCTC	TGTCTGTTTT	180
GCAGATTCAT	CCGGAAGGGC	CGCCAGCCAG	TGGATTTCCC	GGGCCCTCAG	CCCTCTGGAG	240
TGTACGAGTT	TTGGAGAAAC	CTCTTCCTCT	GTATATGCTT	TTGACTTTCC	TGGACTGATG	300
TAAAAATACT	CTTTTCTTTG	ACCTGTTTAT	TTTTAAGACA	CGACGTGATT	GTGTCAGCTT	360
ATATTTTATT	GCTGAAGTAA	ATTTTCAAAT	GTTTTATTAG	TTTTTTTGGA	TCTTTGTCTG	420
CTCATTTTGG	AGTTTTTGTA	ATTTTGATAG	GTGTTCTTTT	ATGCTTTGTA	TTGTTTTCTT	480
AATGACTTTT	ACCTTAGTTT	TTAACAAACC	CATAGTACAG	TGTACCCTCG	AG	532

- (2) INFORMATION FOR SEQ ID NO:331:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GAATTCGGCC	TTCATGGCCT	ACATTTTTGG	ААААААААА	ATCTACTTTG	TGTATGTGTG	60
${\tt GGGTGTGGGG}$	TGTGAGAGAT	ACATTCCTTT	TTNGTGTCTA	AATCTCACAG	TCCACATATG	120
ACTTTCCCCA	CTTGAGAATT	CTCTCTCATC	TGTGTGGCTC	CCTGCATTCT	ATAAAAATAT	180
AAATAAATAA	AATTTTAAAA	AGTATAAAGC	CGGTGCCATG	AGACCCTTGG	GTTGGGCAAA	240
GCCTGTGAAG	TTTGAACCGG	TTAACGCACG	AATACAAGGG	AGTGATTATT	ACAAGGCCAT	300
CCCGCTTAGC	ATCGGGGAAT	CATTTGGGGA	GAGAGATTCA	ATTTCATAAA	GATGATTTTC	360
AAGGGCTGTC	TCGAG					375

- (2) INFORMATION FOR SEQ ID NO:332:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GAATTCGGCC	TTCATGGCCT	ACACGCGGTC	AACTCTGCAG	GGCTGATGAT	AAACATGCCT	60
CTTCTCCTAT	TGTCCTTCTC	CTCTCTAAAG	CAAGGTCATT	TCTGTGCTCG	TCAGGCAGTG	120
GCAGGGGTTG	GGAGGAGGAG	AGAGGGAAAC	ACTGTGGTCA	GGCTCTGGGG	AGAGTTGACT	180
ACAGTGTAGC	TCTTGGATTA	TTTATGAATA	TTGCCCTCAG	ATTTATTTTC	ACTCTGCTCC	240
TTCCATTCAT	ATTCCCAGAG	ACAACCAAGA	GCCGACTGTA	GAAAAAGACT	TCCAGACACC	300
TAGAATATAT	ATCAATAGAC	ACTGTTTAAA	AGGGGAGACT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:333:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

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TGGCCTAAAG	GGGGTGGGTA	CTCCGGTGGG	GTAAGGTCAG	AAGGTCCCTG	TGCAGGGAGG	60
GACTGGTCCC	TTGAGAAGGA	ACAGAGGGCA	AATCCTGAAG	AGTCCTGGAG	GCCCAATGTA	120
GACAGCAGAA	GCTGGGAGCT	GACCTAGGAG	TGATCGGGGG	CCTGATCCAG	ACAGGACAGA	180
CACAGGCTGA	CACCGGAGAG	TCCCAGGTGC	CAACATGAAC	AGT/TAAGGCA	GGGGCTGACC	240
CCAAAGAAAT	CAGGGGCCCG	CAGCTGACCC	CGGAGGGTCC	CAGGTGCCGA	CCTAGACAGC	300
AAAGGCAGGG	CTGACCCCAG	AGGGTCCCGA	GCCGACCCAG	ACGACACAGG	CAGGGCTGAT	360
CCCGGAGGGC	CCCGCCCCGA	CCCGGACAGG	CAGTGAAGGC	ACAGGCAGGG	CTGACACTCG	420
AG						422

- (2) INFORMATION FOR SEQ ID NO:334:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GGGAACGAAA	GATGGCGGCG	GAAACGCTGC	TGTCCAGTTT	GTTAGGACTG	CTGCTTCTGG	60
GACTCCTGTT	ACCCGCAAGT	CTGACCGGCG	GTGTCGGGAG	CCTGAACCTG	GAGGAGCTGA	120
GTGAGATGCG	TTATGGGATC	GAGATCCTGC	CGTTGCCTGT	CATGGGAGGG	CAGAGCCAAT	180
CTTCGGACGT	GGTGATTGTC	TCCTCTAAGT	ACAAACAGCG	CTATGAGTGT	CGCCTGCCAG	240
CTGGAGCTAT	TCACTTCCAG	CGTGAAAGGG	AGGAGGAAAC	ACCTGCTTAC	CAAGGGCCTG	300
GGATCCCTGA	GTTGTTGAGC	CACCTCGAG				329

- (2) INFORMATION FOR SEQ ID NO:335:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCGGCC	TTCATGGCCT	AAAACAGATA	ACGCTATAGA	GAAAACACTG	TTTACTGAAC	60
AGTGCTTTGA	AACCACGAGG	GTGATCAGAG	CCCCATTTCG	CCTTCTAGAG	ATAAACCTGT	120
CTCCCTTCCT	GCAGAGCTAG	CTCCTCCTAT	TGCTTCTGGT	TGTCGTTTGT	CTTCAGTCTG	180
CTTCCTGCCA	GTGCAGCAGC	TCCTGCTAGA	TCTTGACATC	CTAGTGGCCA	GATCCCAGGG	240
GCGGTGCTGG	TCCTATCCGA	GCTCTCTGCC	TCATCTCCCA	TTCCTTTTTT	CCACACTCAG	300
TGTGTATTCT	CTTGGATTTC	CATACCCTGT	TCCTCCTACC	ATCCACCTCT	CTACCTCATC	360
TCCCGACCTG	CCTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:336:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

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AGGGGGCCGG	TTCATGGCCT AGCAGGTCAG GAGCCCGGGG AAGGCCCAGA GGTACTCCAA CTGGTATCTG AAGGCCCCTT GCAGTTAGTG TGTTGTTGAG CTGTGGGCAT	60 120
CATCTCCACT	CAGGCAGACA CTGTTTAGCC AGGGTTTTAA GAAACACGGA GGGTCCTGTG	186
TCACCCCTCC	TCATTTGTCA GGACAGGGAT GGGGACCCCT CTGAAGTATT CACTGTGGGC	240
CTCACTTCAC	TGGCCACACA ACCTCTGTGG GAGGCATCTC TTGCAGTGAA GCTGTTGGTC	300
CICAGIICAG	TGCCCACTGA GGGTAACCAG GCCCCAGCTC TGCACCCCCA CTCGAG	356
(2) INFORMA	ATION FOR SEQ ID NO:337:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 392 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:337:	
GAATTCTAGA	CCTGCCGCAG CACAATCCCG TGGACAGAGC TTACTCCATC TAACTCGTTT	60
TCAAGTGCAT	GATTTTCACT TTCACTTTTC CTTTTTCCTT ATTATGTTGC TTAACTTGTA	120
CAGTGGCAAC	TGAAATGCAT TTCAGAAATA GGAGGTTTCG TCCAGCACCC TCTGCAGCCT	180
TGGTGCCTGT	AGCTCTGGAC TTCCCTGGGC CTTTCCCTGT GGGAGGGCCC TGTAGACCAC	240
ATCAGGGTGG	GGTGGGGGTC ACTTGGCAAA AAGGGCCGAG GTCTGGTGAT GTGGTTCCCA	300
CAAACCCACT	CCTCTCCCAC CCCTCCTGCA GTTGGACTGA ATTCTTCCCT TTCATCCGAA	360
GAAACCCACT	TGCTGTTTCC AGCCAACTCG AG	392
(2) INFORMA	ATION FOR SEQ ID NO:338:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 266 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:338:	
GCAAGATGGC	GACCGAGACG GTGGAGCTCC ATAAGCTAAA GCTTGCCGAA CTAAAGCAAG	60
AATGTCTTGC	TCGTGGTTTG GAGACCAAGG GAATAAAGCA AGATCTTATC CACAGACTCC	120
AGGCATATCT	TGAAGAACAT GCTGAAGAGG AGGCAAATGA AGAAGATGTA CTGGGAGATG	180
AAAAAACTGT	AGAAGAAACA AAGCCCATTG AGCTCCCTGT CAAAGAGGAA GAACCCCCTG TGATGTGGCT CTCGAG	240 266
(2) INFORMA	ATION FOR SEQ ID NO:339:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 288 base pairs	
•	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:339:	

GAATTCGGCC TTCATGGCCT AAACAATGAA TAAAGCCAAG CCAGTTCCTG CCCCCGTGGA

TGCAAGCTGC TAATGTCCAC	AAGACATTGA ACAAGTGATC AGAAAGATGT TGACTGCTGC AGCAGAGGGT TCATGAGTAT ATAACAAGTA GCCCTAACCA AAGCATTCTC TCCCTTGGTT CCATTGAGGT GACTGCTAAA TACTAATCCA TGACTCTATC CCTTGGCATT CATCCACTTA CCTGCCTCTC CAACCTCCCT GCCTCGAG	120 180 240 288
(2) INFORMA	TION FOR SEQ ID NO:340:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 313 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:340:	
TTCACACTTT CCTCTGCCAC CCTCAATTCT	TTCATGGCCT AGTCTCTGCC ATGTTCTAAA CTGAAAACCT CCTAGTCAAC ATTCCCTGAT CCCCATGTC CCGTTAGTGT TTCTTGTAAG CACCGCAGAT CGAACTCTAA TCACATCTCA CCTGAATTAT GGAAAAGTCA CTCACCCATC CCAGCCTCCA CTATGGATTA ATATGCCTAA AGCAGAGCTG TGAGAAAGAT CTGAGAGGGA AGCAGCAGCA AACACAAGAG TCACTGGACA GAG	60 120 180 240 300 313
(2) INFORMA	TION FOR SEQ ID NO:341:	
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 284 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:341:	
AGTAGCTTAA CCAGTTCTCT CTCTGCTTGT	TTCATGGCCT AAGAAAAAAG GATAGACAAA TAGTATTTTT GTGATTTTAC AACTATAGGA TTTTTTTCC CCATTACTTT GCAACAACTG ATACTTTTGA TTCCTAAGCA TTTCTCTCT TGAGCTATTA CCCAAATTGT CCTAGTTCTT CCCTCAGCTA TACACAGTCA CTGAGGCTCT GTGCTTGGCT TCTGTTCCTC GGGATTCCTC ATGTTGGAGT TCATCAAGCT CGAG	60 120 180 240 284
(2) INFORMA	TION FOR SEQ ID NO:342:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:342:	
TGGATGAGGG	TTCATGGCCT ACCACGATAG ACCAGCTGTA GCTCATTCCA GCCTGTACCT GTAGCCTCCC ACTGCATCCC ATCCTGAATA TCCTTTGCAA CTCCCCAAGA AAGTGTTAAT ACTTTTAAGA GAACTGCGAC GATTAATTCT GCATGTCCCC	60 120

240

CTGCCCATTG CCTGCTTGAG GGGCACCACT ACTCCAGCCC AGAAGGAAAG GGGGGCAGCT

CAGTGGCCCC AAGAGGGAGC TGATATCATG AGGATAACAT TGGCGGGAGG GGAGTTAACT

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GGCAGGGCAC TCGAG

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:	
GAATTCGGCC TTCATGGCCT AAAGATGTTA GATATTACAA TTTGACTGAA GAACAGAAGG CGATCAAGGC CAAGTATCCG CCAGTCAATA GGAAGTACGA GTGTGAGAGA TGACTTACAG TCTCTTCTGT TTCACTTTTT GGATGAATGG CTTTATAAGT TCAGTGCTGA TGAATTCTTC ATACCCCGGG TGGGGAGAAG AATTTTCATT GTCCAAGCAC CCTCAGGGAA CAGAAGTCAA AGCAATAACA TATTCAGCAA TGCAGGTCTA TAATGAAGAG AACCCG (2) INFORMATION FOR SEQ ID NO:344:	60 120 180 240 286
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 545 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:	
GAATTCGGCC TTCATGGCCT ACCTCTGTGA AAATTTAATT TTTTATATCC TGATTAATAT ATTGTGACTT TAGGCCCATT TTTCATGTGC TTCACTTTGA TAGAGTTAAT CCATAAAATT GCTCTTTACT TTAGCTTATC AAATGAAGTA TTATTTTGTG GACTGGAGGC CAAAAAGTCA ATGTGAGCTT CTCACAGGTT TTTAAAAGTC CACTAAAAAT AATTATCCAC TTGTCTTTAC TTTTGTTGAC CAGAATAGTT GGTAACTCTG CCAGAGCCTG TACTTACCTG CCCAAAAACAA TTAAATCTGG TTAATGCCTG AAACCAAATC TCCAGGTCTC AAGTGTTATA CTCATGTAT GTGGAGTAAT GAAATTTTGG TTTTACTGTA CCTTTTGCTA TCAAGATAAT ATTCATGTTT GAAATCTTGT CTTTATTTGG AATTTAGTTA CTGTCTGCTT TTAACCTTTG CTTTCCTAAA GAAAGTTTGA GATCCAGAGA GTTCAAGGGA TCGGGGAGTC TCGAG	60 120 180 240 300 360 420 480 540
(2) INFORMATION FOR SEQ ID NO:345:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 301 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:	
GAATTCGGCC TTCATGGCCT ACAATAAGTG TGTTATACTT GCTTTGGTGA TTGCAATCAG CATGGGATTT GGCCATTTCT ATGGCACAAT TCAGATTCAG AAGCGTCAAC AGTTAGTCAG AAAGATACAT GAAGATGAAT TGAATGATAT GAAGGATTAT CTTTCCCAGT GTCAACAGGA ACAAGAATCT TTTATAGATT ATAAGTCATT GAAAGAAAAT CTTGCAAGGT GTTGGACACT	60 120 180 240
201	

TACTGAAGCA GAGAAGATGT CCTTTGAAAC TCAGAAAACG AACCTTGCTA CAGAACTCGA G	300 301
(2) INFORMATION FOR SEQ ID NO:346:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 447 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:	
GAATTCGGCC TTCATGGCCT ACACATTTTG ACAGCTTCCT TTCAGGTTTC TTGAGCTCTC AGAAAAATTA GAAGGAAGTG GGCTGGGGAT ATAGAGAGAG TCCAAACTAC CAACTAATGA ATGAATCTGA AGGAGACACA GAAGGGCAAG TAGAGTTTAG AGTTTGAGAG TGCAGGAAAG TTTTGAAATG GTCAGAACTG CCAGAGTAAT TTCTGAGATC TTACTAAGCA CTCTCCCACC GTTTGCCTTA AAGATACCCC TTCCCCCAAA TTGAAACATC ACAAATCTGC AGAGCTCTTT AATCAGGTGT GTTATACACA ATGAATTTAA TTCTCTTATT GCCCTGGAAG AAAGATAAAC CAGATGTGGC CCTTGCCCCT TTTCAGTAAG TATTTGTTAG ATCTTCATTA CATTTTAGGC CTCCTAGGCC ATGAAGGCCG GCCTTCA	60 120 180 240 300 360 420 447
(2) INFORMATION FOR SEQ ID NO:347: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:	
GAATTCGGCC TTCATGGCCT AAAATTCGGC TGATTTCCCC CTTGGCTAGC CCAGCTGACG GAGTCAAGAG CAAACCAAGA AAAACTACAG AAGTGACAGG AACAGGTCTT GGAAGGAACA GAAAGAAACT GTCTTCCTAT CCAAAGCAAA TTTTACGCAG AAAAATGCTG TAATTTCTTG GGAAGATTTT AATGTACACC TATTTGTAAA GTCATCAGAA TAGTGTGGAT TATTAAAATAT CTAGTTTGGA AGAAAATAAT TTATATAAAT TATTGTAAAT TTTTATGTAA ACTCGAG (2) INFORMATION FOR SEQ ID NO:348:	60 120 180 240 297
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 241 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:	
GAATTCGGCC TTCATGGCCT AGAATAAAAC AAAGCCTTTT CTGCCTTTTA CATTCAGTTC AGTAACCGTC AACACCCCAC CCATATACTC CCATACCATG AGGTGTAATT TTCAAACTCC TCGCATACTT TTAATTACTA GTTTAATTAT TTGCCTTCTC ACTGAGTCTA TAATCTCACT TAGGGTAAGA ACAGAACTCA ATTACAGATG CTCAGTAAAC ACTGGAAGGC CGCGGCTCGA	60 120 180 240 241

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(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:	
GAATTCGGCC TTCATGGCCT AGGGCTGCCC AAGATTGTGA AAGGTAAGTA GTATCTTTAT	60
TTGGGGGTAA CTTAATTATA GATAAAAGAT GGTCCAATAC TGGAAACTGT TCGTTTCTTC CCTTGGATCT AGTCTTCTTC TGCTTTATAT AGAATCCCAC CATCATCTCG AG	120 172
(2) INFORMATION FOR SEQ ID NO:350:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 253 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:	
GAATTCGGCC TTCATGGCCT ACACGTGACA GCCTTTCACT TTTCAGATCA CCTTCCTCAC	60
ACTGATGGTC TCATACAACA TCATTTTGAA TGTCCTCAGC TCTCTGCACC ACCCACCCAA	120
CTCCACTCTG GGCCACCGCT GGTGTATCCA AGATCAGGAC ACCAGTCCCT GGGCACCAGG GAGTATGCTG GCCACTGAAG CAGCTTCGTT TTTCCGGCAC CCATGTTGTA AAATCGACTC	180
CCCCAAACTC GAG CAGCIICGIT TITCCGGCAC CCAIGITGTA AAATCGACTC	240 253
(2) INFORMATION FOR SEQ ID NO:351:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 240 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:	
GAATTCGGCC TTCATGGCCT AGAAAGTTTA AAGATTAGCG TACTGATTAT GATGGGATTT	60
TTACTGAAAA TTAGTTTTGT CAGGCTGCTT GCTTGTCTGT GTATTTTCTA TTCTAATTTA	120
GTTTTTATTT TTATCAAAGC TGTATTTACT TATAATGTAA AAAGTCAATT AGTTTTCCAA	180
GGCTTATTAT GGAAAACAGT AGTTCCCCAG GCTCCCATCC CTATGTCCAA CAAACTCGAG	240
(2) INFORMATION FOR SEQ ID NO:352:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 334 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
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(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:	
GAATTCGGCC TTCATGGCCT AGACCTGCCT CTAAGCCTTT GATTATTCAG CTGCCACTGC CTACAGGCCT TCTCCCATAT TCCTTCCTTC TTGCTAAGTC TGACTTAAAC TAGGCTTAGG CACCAACTCC TATAGGAAGC CTTCCTTGAA CCTGGCCCTC TACTTTTCAC TCACTGACTA CCACTCAATT AACTGAACGG TGAAAAGTAA CCCACAGCTA CGCATTCATG CAGACAACAG AATTTTACTA CTTCTTCTCA CTACTGGTTC ATATTTCTGC AACCAGAAAA TATCATTTCA TCCCTAGTAA CTATGGCTTC CATCTGTTAC TTCC	60 120 180 240 300 334
(2) INFORMATION FOR SEQ ID NO:353:	,
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 92 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:	
GAATTCGGCC TTCATGGCCT AATAATGACT TGTTGGTTGA TTGTAGATAT TGGGCTGTTA ATTGTCAGTT CAGTAGGCCA TGAAGGCCGA AG (2) INFORMATION FOR SEQ ID NO:354:	6) 9:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 280 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:	
GAATTCAGTT CCTTATATAT TCTAGTTATT AATCCCTTAT CAGGTGGATA GTTTGCAGAT ATCTTCTCC ATTCTTTAGG TTGTCTCTC ACTCTGTTGA TCGTTTCCTT TGCTCTGCAA AAGCTTTGTA GCTTGAGATA ATCCCATTG TCTGTTTTTG CTTTTGTTGC CTATGCTTTT GAGGTCTTAC TCAAAAAATT TTTGCCCAGA CCAGTACCCT TGAAGCATTG CCCCAATGGT TTTTTTTTTT	6 12 18 24 28
(2) INFORMATION FOR SEQ ID NO:355:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 398 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:	

60

120

GAATTCGGCC TCCATGGCCT ACATAGATGG GCACACTCAC ACACAGAAGT GTGCTTGTAC

AATCACCACA CACGCACAAA CACACACAC CACTAAAAAT ATAAAACACA TGCGTCACAT

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GGGCATTTCA GATGATCAGC TCTGTATCTG GTTAAGTCGG TTGCTGGGAT GCACCCTGCA CTAGAGCTGA AAGGAAATTG GACCTCATG CAGCCCTGAC AGGTTGTGGG CCCGGGCCCT CCCTTTGTGC TTTGTATCTG CAGCTCTTGC GCCTTTTATA AGTCCATCCT AGTCCCTGCT GGATGGCAGG GGGCTGGATG GGGGCAGGA CTAATACTGA GTGATTGCAG AGTGCTTTAT GAATTCACCT TATTTTATCG AAACCCATTG GACTCGAG	180 240 300 360 398
(2) INFORMATION FOR SEQ ID NO:356:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 331 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:	
GTGTCAGAGC AGGCATTTCC CAACCTAAGG AAATCTTTGT TTTCAAATAT TAGGGTTTTT TTTTAATTGT GGTTAAAGGA TTTTGGACAT GCTTTGTAAA TTGTTAGTAA AAGGACCTAT TTTCCACCTG TATTCTAAGT TATTTTTTC CCTCTTTTTG AATTTTTCAG GTCAGCCCTT CATAAACCCA GATGGGAGTC CAGTGTGTA TAATCCTCCT ATGACTCAAC AACCAGTTAG ATCCCAAGTG CCTGGACCTC CACAGCCACC TCTGCCAGCC CCACCTCAAC AACCAGCAGC TAATCACATT TTCTCACAGG CGCATCTCGA G	60 120 180 240 300 331
(2) INFORMATION FOR SEQ ID NO:357:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:	
GCTGCCTCGA GGTCTCCAAG ACTTTTCAT CTCGTATCGT TTCGGGATCC GTATCCATAC TTTTATTTTC ACTTCTTCC TCTTCCTCCT CGAACTCCTC GTCGCCATCC TGTCTGCCCA GCTTCCCGTA GCCATCCTCG CCTTCTTCT CGTGCTCCTC CCATCCCTCG GCATACTCTC CCTCTTCCTC TCGAG	60 120 180 205
(2) INFORMATION FOR SEQ ID NO:358:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 584 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:	
CAAAAGAGAT GGTACCAGCA AGAGATTAAT ACTAAAGAAA TGCAGTCAGA TTTTAAAGAA ACTGGAAGAA GAGCCATTTC TCCCAGGGAG AAGATTCTAG ATGTGATTGA TGACACCATA GAAATGGAGA CAGGTCTGAA AGCAATGGGA AGAGAGATTT GTCTAAGGGA GAAGACGCCA GAGGTGATTG ATGCCACTGA GGAAATAGAC AAAGATTTGG AAGAAGCTGG AAGAAGAGAA	60 120 180 240

300

ATATCCCCAC AGAAAAATGG CCCAGAGGAG GTTAAGCCTC TAGGTGAAGT GGAGACAGAT

TTGAAAGCAA CTGGATATGA GAGTTCCCCA AGGGAGAAGA CACCAGAGGT GACTGATGCC ACTGAGGAAA TAGACAAAAA TTTGGAAGAA ACTGGAAGAA GAAAAATATC CCCAAGGGAA AATGGCCCAG AGGAGGTCAA GCCTGTAGAT GAAATGGAGA CAGATTTGAA CGCAACTGGA AGAGAGAGTT CTCCAAGGGA GAAGACACCA GAGGTGATTG ATGCTACTGA GGAAATAGAT TTGGAAGAAA CTGAAAGAGA AGTATCCCCA CAGGAAAACT CGAG	360 420 480 540 584
(2) INFORMATION FOR SEQ ID NO:359:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 344 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:	
GAATTCGGCC TTCATGGCCT ATGCTTTCTG AATTGGCAAG ATATTCCAGG CTTATTTGGC ATTCATCTTA CTCTAGACCT ATTATCAACC ATGTCTCCAA GGATAAGTAG ATCCTTTTAA GGGAAAATGG TATTTTGAAA GCATAGTGTG GGATCTGAGG ATACCTATTC CTGTCAGGTT GGTTATTGTT TGTTTTCAGT GAGTAGATCT TGGACTTTAT TAATTTTATT TATTTATTTT AAGAAAAGTA CATCATGAGT TATAAGTAAT AATTCCAACT CAAATTTTAA TATTGCTTAA CTTCTTTGAT TTTATATTTA TCTTTTACAC TGAAAAGTCT CGAG	60 120 180 240 300 344
(2) INFORMATION FOR SEQ ID NO:360:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 362 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:	
GCGGGTGGAC AAAAATGAAG CCAATGAAGA AGGCATGCAC TGGCCTTTCA GGTCCTGGCA GTGGCAGCAA GTCCCCCCA GCCACCAGGG CCAAGGCTCT GAGGCGGCA GGGGCTGGGG AGGGTGACAA GCCAGAGGAG GAGGATGACG AGGCACAGCA GCCGCAACCA CAGTCCGGGC CCGAAGAGGC TGAGGAAGGG GAGGAGGAGG AGGCTGAGGC GGCCCTGGG GCTGAAGGTC CTCCACTGGA GCTGCACCCT GGCGACCCGG CTCCAGGCCC AGCAGAGGAC CCCAAAGGGG ATGGGGAGGC AGGCCGTGG GAGCCCTCAC TCAGCCCCAA GACAGCCCCG TTCAGTCTCG AG	60 120 180 240 300 360 362
(2) INFORMATION FOR SEQ ID NO:361:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 378 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:	
GCACCACCTC TTGCACTGTG AGGAGTTTAT TGATGAATTC AATGGGCTGC ACATGTCCAA GGACAAGAGG ATCAAGTCAG GGAAGCAGTC CAGTACCTCC AAGCTGCTGC GTGACAGTCG	60 120

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CTCCCATAAA CAAGCCCTCT	GTTGAGAAAC TGTCCCACAG ACCTTCAGAT CCTGGAAAGA GCAAGGGGAC CGGAAGCGAA TTAACCCTCC CCTGGCCAAG CCAAAAAAAA GGTATTCAGG TCAGGAGGTG ACAGGGCCAC CAAGACGGTG TCTTACAGGA CTACCCCCAG ATAATGCCCC TGAAAAAAGTC TCAGAACGGG ATGGAAAATG GGGACGCCGG ACCTCGAG	180 240 300 360 378
(2) INFORM	ATION FOR SEQ ID NO:362:	
	SEQUENCE CHARACTERISTICS: (A) LENGTH: 266 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:362:	
ATTTGGGAAT ATGGAGTGAA CCTTGGGAAA	AAAGTCAGAC ATAGGTGTGG AACCAGTTAT GGGAGTGAGG ATAAGTCTAG CAGTCGCAGA GAGGTGGACG ATGAAAGTCT GAGAAGAAAG GATCTTGCTA CTCAGAGCTT GATAAAGGGA GGATGAGTGG AAATGGAGCT CAACGCTGTG TACCTCTGTG GATTGGTGGG AGCACAGTGA GAAATTCAAG AAAGACACAG AACCAGAGAA CTCGAG	60 120 180 240 266
(2) INFORMA	ATION FOR SEQ ID NO:363:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 367 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:363:	
TGGGCTGGAC CCCATCTCCT CCTGTCGTTC TCTGCCTTAG	CCTGCCTCGA GCATTGCCCC CGGCCTAAGA AGCTCTCTTA TCTTGCATCT TCCTACAACA GCCACAACTT CCGTGCTGGT CTCCCAGCTT CTAGCCTTCC GTCGTTTTCG ACACAGCAGC CAGAAGGATC CTTTAAAAAC AGAGGTTGAT CTCAAAATCC TCCAATGCTT TTCCTACTGC ACTCAGAGTA AAAGCCAGTC ATGCTCTGGG ATCCTGTACC CTCTTTGGTC TCATGTCCTA CAATCTGCAT ATGGTCTTCT CTGCTGTTCC TTGAACATTC CAGGAACATT CCCCCCATAC	60 120 180 240 300 360 367
(2) INFORMA	ATION FOR SEQ ID NO:364:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 383 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:364:	
GACAATGAGT	TTCATGGCCT ACTGGGTTCT GAGAAGCAGT GGCCCGAGCT GAAGCATCCA GTTCAGAAGC TGCCAGATTC TCACCTAGCC TTAGAAGTAA CACAGCCACA TACAAACACA TTTCTAAGGC CAGTCCAGAT TCAAACGGAG GGCAATTAGA	60 120 180

TTTGACCCCT TGATGAAGGA GGGCAAGGTT ACACTGAAAA ACAGCATAGG GACTGGGAGA TATTATGATG TCCATTTTTG GAAAATCTGC CACAGACACA GTGAAGACAG AGAGCCCTTC TCTCTGATCG AGGACCTCCA GAATGATCTG CTGAGTCACT CAGGTATGCT GGACCATTCA CACTCACCCC GGAAAAGCTC GAG	240 300 360 383
(2) INFORMATION FOR SEQ ID NO:365:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 356 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:	
GAGGTTCACA GGTTTAAGCA TTTGTTTTTA CAAAAAGGAA TGGGATATGG GGGTGGTCAA GTTTTACGGG TAATAACAAC ATTCTCTCTA GATGCAGGG GGTAAGTCTG CCTGTCCTCC ATTGCTGGTA CCACATAAGG GATACATTAG TAAAGTAGGG AAAGGGTCAT ATGTGTGGTT GACCTGTTCT TCAGAGAGGA ACGTGGGATG GTATCTGCTG TGTACCTGTC TCAGACCAAA CCTGGGGGTG GACCAGTGCC CCTTTCTTCT CAGCCTTCTT CCACAGCCTG ACTGTACTGC CACCCGCACC CATGAGAAGG AGGTNNTGAA GGAAGCTTGA GGACATCCAC CTCGAG (2) INFORMATION FOR SEQ ID NO:366: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 246 base pairs	60 120 180 240 300 356
(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:	
(MI) OBCOLUZ DECENTITION OBC 10 NO.500.	
GAATTCGGCC TTCATGGCCT ACAACCATTG AAAAAATATA GACTTAGAAA ACGAAAGTTC CCCTTAATCA CAAAGAACCA CAGTTGACAG GGTTGATAGA TGTTTTTTCA GATTTTTTT TTCATATGTC TGCTATCTTT CCCCACAGGA ACTGGGTTTT ATTTTAGGTG TTGTTTTTGCA ACCTCTGTTT TTCAGTTGCC AGTTTATCTC AGACATTGTC CTATGTCAGT ACAGGCCCAT CTCGAG	60 120 180 240 246
(2) INFORMATION FOR SEQ ID NO:367:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	• .
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:	
GAATTCGGCC TTCATGGCCT ACAAAAAAAC AACTTTCCAG TGGCTTCTCA CTGCTCTGAG AATAAACTCC AGGCTCTTCC ATTGCAACCA ACAGGATCTG GTGATTCGAC CCCAGCCCCT	60 120

180 238

CTTTCCAGGC CCTCATCACC TTGATCCTCC CTTAACCTAT CCTGCTCCAG CTGCACTGGC TGCCTTCCTA TTCCTCCAGC ATACCAAGAT TGTTTCTGCC ACAGGGCCGC CACTCGAG

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- (2) INFORMATION FOR SEQ ID NO:368:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear .
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GAATTCGGCC	TTCATGGCCT	AGTTTTTTCT	ACTCCTACAA	GTGTAAATTG	AAAAATCTTT	60
ATATTAAAAA	AGTAAACTGT	TATGAAGCTG	CTATGTACTA	ATAATACTTT	GCTTGCCAAA	120
GTGTTTGGGT	TTTGTTGTTG	TTTGTTTGTT	TGTTTGTTTT	TGGTTCATGA	ACAACAGTGT	180
CTAGAAACCC	ATTTTGAAAG	TGGAAAATTA	TTAAGTCACC	TATCACTCGA	G	231.

- (2) INFORMATION FOR SEQ ID NO: 369:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GAATTCGGCC	TTCATGGCCT	ACTTGGTCTT	CTGCACTTTT	GTCTCTGACG	TACTTCCTTT	60
CTTCACAAGT	GCCATTTACA	GAAAGCTGGG	CTTAAACCAT	TCCCAGCTAT	TCCTCCTACA	120
GCTTTCCTGA	ATTATTTCAG	AATACAAAAT	TCTGTATCTC	CAAGAAACTA	TTACAGATTT	180
AGATTTAAAA	ATATGCACTA	TTTTCTACCT	TGTATGTTTT	GCTTACTATT	TTTTTTTTGC	240
AGAGGATATG	TCTTAAAAAT	TGAAATGCAT	CAAAAAT			277

- (2) INFORMATION FOR SEQ ID NO:370:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

GAATTCGGCC	TTCATGGCCT	ACCAAGTCAA	AAAATAGAAC	AGTTCCGGÇA	CCCCAGAAGC	60
CCTTTGCCAC	GTGGTCACAA	CCCTCCCTGT	TTCCACCAAC	AGTAACATTC	TAGTTTTTAC	120
AGTAATTTCT	TCCTTGCTTT	TCTTTGTAAT	TTTACTGCCC	TGTGTTTCTT	AATATGATTT	180
AGTTTTGCCT	${\tt GGTTTTGCCT}$	TCATATAAAT	GAAATCATAC	TGAATATATT	ATTTCATATT	240
TTGCCCAATA	TTTTGTTTGT	AAGATTCATC	CATCTTGTAG	CTCCAATGTA	TTTATTTTCA	300
TTTTTGTATA	ATTATATGAT	TATGCCACAG	TTTGTCAGTT	CACTCGAG		348

- (2) INFORMATION FOR SEQ ID NO:371:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs

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(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GAATTCGGCC	TTCATGGCCT	AGAATTATTA	GGAAACAAAT	GGTTTTGCTG	TCTTTTGGTC	60
ATTAGCTTGG	CCCCATGTTT	AAGCATTCGG	TAACAACTGT	GAAGAGCCTG	CTACAAATAA	120
AGTGGTAGGT	GCTCTGAAGA	AAAATAAAGC	TGTTAAAGGG	AATAGAAAGT	GATGAAGGCA	180
GGGGCTGTTA	GACAGGCTGG	TCAGTGTCTG	AGGAAGTAGC	CCTGCACTGA	GACCTGAAAA	240
GTAAAGAAGC	AAGCCATGGG	GAGTTGGGGA	GGAGCATTCC	AGACAGAGGC	TTGATGTGTT	300
GAACCATCTT	TTCCAAGCTC	TTCCTCTGTT	ACCTTCTCTT	TAGTCACTAT	GTCCCCTTTC	360
TATCCCAGAC	CATAATTCCA	CCATTTATCT	TAAGGCTGAG			400

- (2) INFORMATION FOR SEQ ID NO:372:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GAACGATTGA	ATTCTAGACC	TGCCTCGAGA	TCAGCACTAA	CCCCCCAAC	TCCCAGCCTT	60
TAGTTTGCTG	TAGGCTGTCA	AACCAGATAA	CCAAACTTGT	TAAATTGAGA	ATCAATAGGC	120
TGTACATAGG	GACTACAACA	GAATGACGCT	CATTATTGAC	AGAATCAAGT	TCAAACTCCT	180
TGTCCTGGCG	TCTGTTGGCC	TCTGGCAGCT	GGCTCATCTG	GCATTAGCTG	GTTGCACGAG	240
TTGCTGCAAC	CCTCCCACCC	CGCTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:373:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GTGAGGTTTT	AACTGAGCTC	GAAGAATTGG	AATCAAAAGA	GATAGGTTTG	TCTCAGTCCA	60
GACAGTGGAT	AGCATAAGGA	AAGTACAACT	GCAGAAAAGA	GGGGGACAGC	GAAGAGACTG	120
GATTGATGCG	TTATCTAGGC	GGTACCTGTC	TCCATTCTTT	TCTAGCCAGC	CTTTGAGCAT	180
TTCATCAAGA	ATAGAGGAAT	TCAAAGTACT	GCAGTCTGCT	TGAACCAGTG	CTTGTGAGTG	240
GCTCTAAAAA	AAATACTTGA	ATTTGAACTT	GAAAGAACAC	TCAAATAAGG	TTTGGGGCTT	300
CTCTTTGTTT	AATACTTTAA	GCGTCTTATT	TCTAACATAA	ATATACTGAT	TGCACAGAAT	360
TTGATTGTTC	ATAGCAGCAG	TTGCCTGTAC	TTTAGAATTC	TCAGATATTA	GAGCTGAAAG	420
ATCATCTGAG	TTACTTTATA	AATGGGGAAA	TCTCGATCTC	GAG		463

- (2) INFORMATION FOR SEQ ID NO:374:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GAACGGCAGC	CATTGAAGCA	TATTGGAAAA	GGAACTGGGG	AATTTATTAA	AGCACTCATG	60
AAGGAAATTC	CAGCGCTGCT	TCATCTTCCA	GTGCTGATAA	TTATGGCATT	AGCCATCCTG	120
AGTTTCTGCT	ATGGTGCTGG	AAAATCAGTT	CATGTGCTGA	GACATATAGG	CGGTCCTTGA	180
GAGAGAACCT	CCCCAGGCAC	TTCGGCCACG	GGATAGAAGA	CGGCAGGAGG	AAATTGATTA	240
TAGACCTGAT	GGTGGAGCAG	GTGATGCCGA	TTTCCATTAT	AGGGGCCAAA	TGGGCCCCAC	300
TGAGCAAGGC	CCTTATGCCA	AAACGTATGA	GGGTAGAAGA	GAGATTTTGA	GAGAGAGAGA	360
TGTTGACTTG	AGATTTCAGA	CTGGCAACAA	GAGCCCTGAA	GTGCTCCGGG	CATTTGATGT	420
ACCAGACGCA	GAGGCACGAG	AGCCCCTCGA	G			451

- (2) INFORMATION FOR SEQ ID NO:375:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

GAATTCGGCT	TCATGGCCTA	CTCAGATCTT	AAAATTCACC	CTCTCAAACA	CATTTCCTAT	60
						00
GAGGTTGCTC	TCAATGACTT	CAGGCACAGT	CGGCAGGAGA	TTGAAGCCCT	GGCCATTGTC	120
AANATGAAGG	AGCTTTGTGC	CATGTNTGGC	AAGAAAGACC	CCAATGAGCG	GGACTCCTGG	180
AGGGCAGTGG	CCAGGGACGT	CTGGGATACC	GTCGGTGTTG	GGGATGAGAA	GATCGAAGAC	240
GTCATGGCCA	CTGGGAAAGG	CAGCACTGAT	GTAGATGACC	TCAAGGTTCA	TATAGACAAG	300
CTGGAAGATA	TTTTGCAAGA	AGTCAAAAAG	CAAAATAACA	TGAAAGACGA	GGAGATAAAA	360
GTCTTAAGAA	ATAAAATGCT	CAAAATGGAA	AAAGTCTTGC	CACTGATCGG	ATCTCAGGAA	420
CAGAAAAGCC	CAGGAAGCCA	CAAAGCAAAG	GAGCCTGTTG	GTGCTGGTGT	TAGTAGCACC	480
TCTGAGAATA	ATGTAAGTAA	AGGAGACCTC	GAG			513

- (2) INFORMATION FOR SEQ ID NO:376:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

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CAGAATGGGA TCGAAGCCTG	CCTCCTTAGG	NTCTTTGCCN	TCATCCTCTC	TGGCAAATGC	60
AGTTACAGCC CGGAGCCCGA	CCAGCGGAGG	ACGCTGCCCC	CAGGCTGGGT	GTCCCTGGGC	120
CGTGCGGACC CTGAGGAAGA	GCTGAGTCTC	ACCTTTGCCC	TGAGACAGCA	GAATGTGGAA	180
AGACTCTCGG AGCTGGTGCA	GGCTGTGTCG	GATCCCAGCT	CTCCTCAATA	CGGAAAATAC	240
CTGACCCTAG AGAATGTGGC	TGATCTGGTG	AGGCCATCCC	CACTGACCCT	CCACACGCTC	300
GAG					303

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:	
GAATTCGGCC TTCATGGCCT ACTTCATTGT AAGGTACTTC TTTGCGGCGC TGACAGTGCT	60
CACGCTCCTG GGCCTCCTCC ATGGACTCGT GCTGCTGCCT GTGCTGCTGT CCATCCTGGG	120
CCCGCCGCCA GAGGTGATAC AGATGTACAA GGAAAGCCCA GAGATCCTGA GTCCACCAGC	180
TCCACAGGGA GGCGGGCTTA GGTGGGGGGC ATCCTCCTCC CTGCCCCAGA GCTTTGCCAG	240
AGTGACTACC TCCATGACCG TGGCCATCCA CCCACCCCC CTGCCTGGTG CCTACATCCA	300
TCCAGCCCCT GATGAGCCCC CCAGGTCCCT CGAG	334
(2) INFORMATION FOR SEQ ID NO:378:	
(1) 0000000	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 305 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(5) 10102001. 1111001	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:	
GGATTTTAAG GATCACATTC CAAGGGAAAC TGATATGAAG GTTGCAATGA ATGTGTATGA	60
GTTATCATCA GCTGCCGGAT TACCTTGTGA GATTGATCCT GCATTGGTCG TAGCTCTTTC	120
TTCACAAAAA TCGGAAAACA TTAGTCCAGA AGAAGAGTAT AAAATTGCCT GCCTTCTCAT	180
GGTGTTTGTG GCAGTTTCTT TGCCAACACT GGCCAGTAAT GTGATGTCTC AGTACAGCCC	240
TGCTATAGAA GGGCATTGCA ACAACATACA TTGCTTGGCC AAAGCCATCA ACCAGATTGC	300
TCGAG	305
(2) INFORMATION FOR CEO ID NO 270	
(2) INFORMATION FOR SEQ ID NO:379:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 329 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
ALLA MOLECULE THERE I THE	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:	
GAATTCGGCC TTCATGGCCT ACCCAAACAT TATCCCTCTA CACTGTCCCC ACTATGCTAT	60
ACCCCTGCAC TATACCCCTA TGCTGTCTCC CTTACGCTAT CCCCCTATGC TATGTCCCCT	120
ACACTATCCC CCTTTGTTGT CCCTCCATGC TACTCCCTAC GCTATCCCAC TACTCTATCC	180
CCCTGACGCT GTCCCCCTAC GCTATCCCGC TACACTGTTC CCCCTACACT ATCTCCATAC	240
ACTGTCCCCC TACACTCTCC CCCTACTCAA TTCCCCCTAC ACTCTCCGCG TACACTATCC	300
CCGCTACACT ATCCCCCGAC GCTCTCGAG	329
(2) INFORMATION FOR SEQ ID NO:380:	
// \	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs	
tit manaziri ara mana harra	

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	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:380:	
CATAGCAACA CCTTGGGATG AAGACTCATG	TCTTTACTTC CTTTGTGGAG CCTCCCTGCA CAAGCAGCAC TTTCTTTTGC TGTGCATCAA TAATTCTTTA GTCTGTAATG GTGTCCAAAA TTGTGCATAC AAAATCATTG TAAAGAAAAG AAAAAAGCAG GAGTATTTGA ACAAATCACT GAACAATTAT TGGCATTACT TCAGGGATTG TCTTGGTCCT TCTCATTATT TACAAGTGAA ACAGCATCTC GAG	60 120 180 240 273
(2) INFORMA	ATION FOR SEQ ID NO:381:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 338 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:381:	
CCTCACCCGC CCACCCTAGT CTGGCTCACA CATCCTTTTC	TTCATGGCCT ACATAACTCT CCACAGGCTC CCCTGGGAGG GGTGCCCCCA CACCTCACTT CTCAGCCCCT CTTCCCATCC AAGGGCTCC TGGGCTGCCC CATGATCTCG CTCCTCTACT CTCTCGTAGT ACTTTATTTT TACCTTGCTC TTACATGCTT ATCTTGTATT TATAGATGGT TCTACATATG TCTCCTTTTG TCAAAGCTCC TGTGAGGCCA GGGATGGTTT TATGCCTTTT CTCATCCCCT TATAATGCTT TACACATGTT TACTCGAG	60 120 180 240 300 338
(2) INFORMA	ATION FOR SEQ ID NO:382:	
	SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear MOLECULE TYPE: cDNA	
	SEQUENCE DESCRIPTION: SEQ ID NO:382:	
TTGGTCTTCC	TTCATGGCCT ACTTTCTCTC CTTTTTTCCT GTAACTGTGC TGGTTTTGTT TCTCATACCC GTTTCTGCAT TTCATCTTTT CTTTCTATTG GGACTTCATT	60 120
CCATCGCATG CTCCCAAACT	TTAACCTTAT CTTTTGTTTC TCTTGTTTAT CCCATCCTTT TTGATAAAAT TGTCTTCTTT TTTTCTTTAT TTTCTTTCCT TTCCTTTTTC CTTTTCTTT TTTTCCTTTT CACAGCATTG GAACACGGGA GGTAGTCACC CAGAAGAACT GGTGCCCATC CGAGACCACT CGAG	180 240 300 334
(2) INFORM	ATION FOR SEQ ID NO:383:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 232 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GCAGAAAATA	TGGTATCGGT	TTCATTTAAT	AAAAATGAAA	TTTTAATAAA	CAGTTATCAG	60
TAATTTCTCA	GTTACACAAC	CTCTGCCTTC	ATTTCCGCTT	AGCCATGAAC	TTTTTACTGC	120
ACAAAGGAAT	TTAAAATAGC	CAAATTCTAC	AATTCTGGCT	GGGTGTGGGG	GCTCATGCCT	180
GGGATCTCAG	TAGTATGGGA	CCCCGAGGCA	GGTCTAGAAT	TCAATCCTCG	AG	232

- (2) INFORMATION FOR SEQ ID NO:384:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GCCTCTGCTT	TTAATTCATT	GGCAACTGTT	ACGATGGAAG	ACCTGATTCG	ACCTTGGTTC	60
CCTGAGTTCT	CTGAAGCCCG	GGCCATCATG	CTTTCCAGAG	GCCTTGCCTT	TGGCTATGGG	120
CTGCTTTGTC	TAGGAATGGC	CTATATTTCC	TCCCAGATGG	GACCTGTGCT	GCAGGCAGCA	180
ATCAGCATCT	TTGGCATGGT	TGGGGGACCG	CTGCTGGGAC	TCTTCTGCCT	TGGAATGTTC	240
TTTCCATGTG	CTAACCCTCC	TGGTGCTGTT	GTGGGCCTGT	TGGCTGGGCT	CGTCATGGCC	300
TTCTGGATTG	GCATCGGGAG	CATCGTGACC	AGCATGGGCT	TCAGCATGCC	ACCCTCTCCC	360
TCTAATGGGT	CCAGCTTCTC	CCTGCCCACC	AATCTAACCG	TTGCCACTGT	GACCACACTT	420
CTCGAG						426

- (2) INFORMATION FOR SEQ ID NO:385:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GAATTCGGCC	TTCATGGCCT	AGGCCCTTAA	ACTGGATTCA	AAAAATGCTC	TAAACATAGG	60
AATGGTTGAA	GAGGTCTTGC	AGTCTTCAGA	TGAAACTAAA	TCTCTAGAAG	AGGCACAAGA	120
ATGGCTAAAG	CAATTCATCC	AAGGCCACC	GGAAGTAATT	AGAGCTTTGA	AAAAATCTGT	180
TTGTTCAGGC	AGAGAGCTAT	ATTTGGAGGA	AGCATTACAG	AACGAAAGAG	ATCTTTTAGG	240
AACAGTTTGG	GGTGGGCCTG	CAAATTTAGA	GGCTACCTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:386:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

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GATTGAATTC TAGACCTGCC TCGAAGGCCG AGAGGGAAAG TTGAAAGGTC CCAAATTCAA GATGCCTGAG ATGAACATCA AAGCCCCCAA GATCTCCATG CCTGACATTG ATCTTAACCT GAAAGGACCC AAAGTGAAGG GTGATATGGA TGTGTCTCTG CCAAAAGTGG AAGGTGACAT GCAAGTTCCT GACTTGGATA TTAAAGGCCC CAAAGTGGAT ATTAATGCCC CAGATGTGGA TGGACTCGAG	60 120 180 240 250
(2) INFORMATION FOR SEQ ID NO:387:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 344 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:	
GAATTCTAGA CCCACCTCCA CCTTTAACTC GAAGTAACAC TGCAAATCGT TTAATGAAAA CACTCTCAAA ACTGAATTTA TGTGTTGATA AAACAGAGAA AGGAGAAAGT AGTAGTCCTT CTCCATCAGC TGAAAAAGGA AAGATTCTAA ATGTTTCAGT GATTGAAGAA AGTGGCAATA AAAACGATCA AAAATCTCAA AAAATTATGA AGAAGAAAGA GTCATCTTCT ATGTTGGCTA CAGTTAAAGA AGAAGTCTCT GGTAGTTCAG CAGCTGTTAC GGAGAATGCT GATAGTGATA GAATTTCTGA TGAAGCAAAT AGTAATTTTA ACCAAGGGCT CGAG	60 120 180 240 300 344
(2) INFORMATION FOR SEQ ID NO:388:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 165 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:	
GGAGTAATCA GAGGTGTTCT TGTGTTGTGA TAAGGGTGGC AGGAGTGGAC ATTCTTCACA TACACCCATT ATTGTTTTGA AGTGTTTAAT TACCTTTTTA GCTACATTTT TGCAGCTGAG TTTAGAATGA AAACCACAAG AGTTTTATTG TTGGCTGTAC TCGAG	60 120 165
(2) INFORMATION FOR SEQ ID NO:389:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 252 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:	
GAATTCGGCC TTCATGGCCT AGAACAGAGC TTACTTATTC TTTCTGAAAC CAAGGCTTCT CTAGTGAGCA CCATGAGCCT TTGGAAACAA CAGATGTATA CAATAGCAAA GTTTCATTTC TTTACCTTGA AACGTGAAAG TAAATCAGTG AGATCAGTGT TGCTTCTGCT TTTAATTTTT TTCACAGGTTC AGATTTTAT GTTTTTGGTT CATCACTCTT TTAAAAATGC TGTGGTTCCC	60 120 180 240

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- (2) INFORMATION FOR SEQ ID NO:390:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATTCGGCC	TTCATGGCCT	AGGATGTTCA	CTTGCATGCC	TCTGGATTTT	AAAATTATTG	60
TTCACATGAC	TCCTTTTCTG	TGCGTTGGGA	AGCAGCTACA	GAGCAGTAGA	ATCCACTGAA	120
TTGGTACACT	GAAGCAGGCA	TGCCATTTAA	ATGAAGGCAG	TTAACCTTGA	CTGTTGTATC	180
ACCAGAGTTA	AAGAATTCTG	GTGCCCCTCT	TTAAGTCTTC	AGGAAGTGTT	TAGAGGCTTA	240
TTCACATTAG	TTAAAACAGG	CCCCCCCAC	CTTCCCCAAG	GCAACAGAAA	ACATAACCAT	300
TAGCTCTCTT	CCTGTTTTCC	TTCCTCATTT	CATGCTTGCT	TCGGCTGCTA	AACTGAATTT	360
TTGTTACTTA	GAATATTATA	AAGTGTGGAT	GCTTTCTATA	ATGCTATTGG	TCTAAGTGTG	420
ATTAAATTTC	ATTAAGGTGT	ATAAGCCTCT	AATTATTACA	TAACTGGCAC	TGGCTCGAG	479

- (2) INFORMATION FOR SEQ ID NO:391:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAATTCGGCC	TTCATGGCCT	AGCCTATTAC	ACAGTAAGTT	AATAATTGTG	TCCTTGCAAA	60
TAAGCATTGT	GTTCTGAAAT	GGAATCAGCA	TATTTCCCTA	TAAAGACACT	TCCACTCATT	120
CATTAATTGA	GCAGCCCCAG	TTGATAAAGA	ATCAGTATAT	CATGTTCTGA	TATTTAATCA	180
GCAAACTCAT	TTATTCAGTA	GAAATTTGAA	TTCCTGTGAT	GTGCCAGGCT	TGTGAGGAGG	240
GAGACTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:392:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GAATTCGGCC	TTCATGGCCT	AGTCGACTCC	TGTGAGGTAT	GGTGCTGGGT	GCAGATGCAG	60
TGTGGCTCTG	GATAGCACCT	TATGGACAGT	TGTGTCCCCA	AGGAAGGATG	AGAATAGCTA	120
CTGAAGTCCT	AAAGAGCAAG	CCTAACTCAA	GCCATTGGCA	CACAGGCATT	AGACAGAAAG	180
CTGGAAGTTG	AAATGGTGGA	GTCCAACTTG	CCTGGACCAG	CTTAATGGTT	CTGCTCCTGG	240
TAACGTTTTT	ATCCATGGAT	GACTTGCTTG	GGTATGGAGA	GTCGGCTTGA	CTACACTGTG	300
TGGAGCAAGT	TTTAAAGAAG	CAAAGGAACT	CCTCGAG			337

(2) INFORMATION FOR SEQ ID NO:393:

(A) LENGTH: 216 base pairs(B) TYPE: nucleic acid

(i) SEQUENCE CHARACTERISTICS:

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:393:	
AAAAAAAAAA ACATTCATCT	TCCTGACCTC AAGTGATCTG CCCACTTGTG CCTCCCAGAA CTGGGATAAA ATAGATCCTT GGTATTATTC CATTACATAC GGATTGTAAA ATTCAGTTAA CTTGGTGGGC ATTTATGTAT TTCTTTTGTT TGTTTGTTTG CAGCATTGCT TTTTTATAAG TACATCTCGA CTCGAG	60 120 180 216
(2) INFORMA	ATION FOR SEQ ID NO:394:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 248 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:394:	
GAACTGGGGA TGCTGATAAT	TTCATGGCCT ACCACATTG TAACGGAGCC ATTGAAGCAT ATTGGAAAAG ATTTATTAAA GCACTCATGA AGGAAATTCC AGCGCTGCTT CATCTTCCAG TATGGCATTA GCCATCCTGA GTTTCTGCTA TGGTGCTGGA AAATCAGTTC ACATATAGGC GGTCCTGAGA GCGAACCTCC CCAGGCACTT CGGCCTGGGA	60 120 180 240 248
(2) INFORM	ATION FOR SEQ ID NO:395:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:395:	
TGTGATTTAT TTCCTTACAT	TTCATGGCCT AGCCTTCCTC TACCATTTT AATTTTTTA GACTTCATTT TGCTGCTCTG GGGGCTTCAC ATCCAATCCT TTTATGGTTT CATCTTTCCT TTGTTGCATA TAACAATGGC GTGTTTAGCT ACTGCAGTGA AAAATCAATC CATATTCACA GGCTTGCAAT GGCACCAACG GCTCCTGGAT CTCTCGAG	60 120 180 238
(2) INFORM	ATION FOR SEQ ID NO:396:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 188 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCGGCC	TTCATGGCCT	AAGTTGATCC	GGATACACAC	CTGCTAAAAC	TGCTTAAAAC	60
ATTAGAAGGA	CATGCTTATG	GCGTTTCTTA	TATTGCATGG	AGTCCAGATG	ACAACTATCT	120
TGTTGCTTGT	GGCCCAGATG	ACTGCTCTGA	GCTTTGGCTT	TGGAATGTAC	AAACAGGAGT	180
CTCTCGAG						188

- (2) INFORMATION FOR SEQ ID NO:397:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCGGCC	TTCATGGCCT	ACAGGCATGT	TGAGATTTGG	AAAAGTGGAT	GTAACTGAAA	60
TTCAGATAGC	TTTAGTGATT	GTCTTTGTGT	TGTCTGCATT	TGGAGGAGCA	ACAATGTGGG	120
ACTATACGAT	TCCTATTCTA	GAAATAAAAT	TGAAGATCCT	TCCAGTTCTT	GGATTTCTAG	180
GTGGAGTAAT	ATTTTCCTGT	TCAAATTATT	TCCATGTTAT	CCTCCATGGT	GGTGTTGGCA	240
AGAATGGATC	CACTATAGCA	GGCACCAGTG	TCTTGTCACC	TGGACTCCAC	ATAGGACTAA	300
TTATTATACT	GGCAATAATG	ATCTATAAAA	AGTCAGCAAC	TGATGTGTTT	GAAAAGCATC	360
CTTGTCTTTA	TATCCTAATG	TTTGGATGTG	TCTTTGCTAA	AGTCTCACAA	AAATTAGTGG	420
TAGCTCACAT	GACCAAAAGT	GAACTATATC	TTCAAGACAC	TGTCTTTTTG	GGGCCAGGGC	480
TCGAG						485

- (2) INFORMATION FOR SEQ ID NO:398:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GAATTCGGCC	TTCATGCCTA	GTGGATCCGG	AAACTCTGTG	GCTCTAGACT	TTCAACTATT	60
TTATTTTTC	TTTTGTATTT	TTTGTTTGTT	GCTTGCTTTT	TTACAATGGG	AACTAGAATG	120
TAAGATGCCA	AACTCAGCCT	GTGGGGAACA	TGGATTTTCA	CAACAGCAAC	CACAGAGCGT	180
GGTTTCCATT	TCTATTCCCT	GTTCATGTGG	GAGGCAGAGA	AGGAAATCAG	GTGCTCAGTT	240
CCAGGGACAT	CACAGGACAG	GACTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:399:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

GAATTCGGCC	TTCATGGCCT	ACACCTCTTC	TGCCAACCAG	CTGCTTGGGA	TGACTGCGAT	60
CCCGTGTGCT	TGTCTGGGTA	TCTTCCTGGG	AGGTCTTTTG	GTGAAGAAGC	TCAGCCTGTC	120
TGCCCTGGGG	GCCATTCGGA	TGGCCATGCT	CGTCAACCTG	GTGTCCACTG	CTTGCTACGT	180
CTCCTTCCTC	TTCCTGGGCT	GCGACACTGG	CCCTGTGGCT	${\tt GGGGTTACTG}$	TTCCCTATGG	240
AAACAGCACA	GCACCTGGCT	CAGCCCTGGA	CCCCTACTCG	CCCAAG		286

- (2) INFORMATION FOR SEQ ID NO:400:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GAATTCGGCC TTCATGGCCT	ACCTGCCTCG	AGATGATCAT	TCTTTTCTTG	CTTCTAGGCT	60
CTGTGTCCTC CTGGTTTCCT	CCAACCTCTC	TGGTCCTGTT	TCATTTGCTG	TGGGTTCCTT	120
TTGCCTTTGC CACCCCTCAA	ATGGGGCTTC	TCACTCACAC	TAGTGAGTTT	TCAGTGCTTG	180
CAGACCCAAC ACCCTCTTTT	TATAACAAAT	ATTTTTTAAT	ACGTCCTTTT	CCACAACTCG	240
AG					242

- (2) INFORMATION FOR SEQ ID NO:401:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GAATTCGGCC	TTCATGGCCT	AGTCCCATCA	GAGGGAGCTG	ATGAAGAATG	GTCCCTGTAA	60
GTAAGTCACT	AGGTTCAACA	ACTGCCTGGC	CGAGCACTCA	GCCCGTGGAG	CTCAGGCCAA	120
CACCAGAGCC	CCGGTTTTAG	GGGCCAGGAG	AGCAGGTGAC	CAATTATTTG	GGGAGTCTTG	180
GGTAGAATTT	CCGCCACACA	TTCTCCCCAG	GGCTGCAGGG	GTCTTCCGAG	GCAGGGCGGT	240
GGAGCAGGAT	TCAGGATGTG	GTGGGAATAG	AGTGAGGGGC	AGTGGGTGGT	GCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:402:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

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GAATTCGGCC	TTCATGGCCT	AAAAAACTAG	AATAATGGAA	GAGTAAATAA	ACACAATTCT	60
TAATGTATTA	CAAGAAATAA	AAGGTTTAAA	AGTAGATTTT	TTAATTGAAA	AGAATTAAAT	120
CAGATAAAAA	TATTTGAGAG	GTAATGCAAA	CATTTAAGTT	TGTCAAAGAA	GCTTCAACAT	180
CTGGATAATA	GGAAAGAAAA	AAACCAAAGC	AAAAGAAAAA	TAAGCCACAA	ACTAAAAAAT	240
GTTTAGTTCT	TGAAATTTAA	AAAAGTAAAT	ATTGAAAGAG	CATGCTGTGT	ACCTGAGATT	300

ATTIACCCAA MACTCGAG		310
(2) INFORMATION FOR SEQ ID NO:403:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 355 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4	03:	
GAATTCGGCC TTCATGGCCT AGATTGAATT CTAGACCTGC CGCAGCAGCCT GAGCCGGGCC AAGTCTGAGC CCTTCCGCAT CCCTGCAGCG CGCAGCTAC CCAGGGCTGC TGATCGTGCC CCCTGCAGCG CGTGTCCCGC TGCTATCGCC AGAACCGCTT CGCGGGCGGTC CAAGGCGGTG CTGCTGCGCT CTGGAGGCCT CGCCTCTTCAA GGCCCAGAAC GCACCTTCTC CAGGCCAGTC C	TTCTCCGGTC AACCGCATGT CCAGAGTGTC CAGGACAACG CCCCGTGGTC TGCTGGCGCA GCATGGCAAA GGTGTCGTCG	60 120 180 240 300 355
(2) INFORMATION FOR SEQ ID NO:404:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 346 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA	•	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4	104:	
GAATTCGGCC TTCATGGCT AGTCATGGAA CAAGTCCTTG AGTATTACTG AAACAGATGA ACAAATGCAA GCATATGATC ATTGAAACCC CACAAGATGA GGGTTATGAT GGTCCAGCCT GTCTTATAAA GAAAAAAAAA AAAAGAAGTG GCAGCTCTGT AGGGACAACT GCTGAGGCAG GCACCTGCCC TTGGGCTCCC TGTGGGCTCT GCCTGCCCC CTGTCCAGTC CCCGGGGTGG	ACCTTTCATA TGAAACACCT GGGTGACAGA GCGAGACTCT CTGCTTCTCA CAGAGTTGCT CGGGTGGGCT GCTATTTGCC	60 120 180 240 300 346
(2) INFORMATION FOR SEQ ID NO:405:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 247 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	405:	
GCGATTGAAT TCTAGACCTG CCTCGAGAAC AGGGAACTTT GGAAGTCAGG TGAGAAGCTG TCAACTGGGC AGGCAGTGAT TGTACTTTTT TGTTTTGTTC AAAAAACCTA AAGCATCACG CAGAGAGCCC CCAACAGAGC CAGAACTTGC CAAGAGCGAC GAGGCAG	GAGAATCGTA GTTGTCTTAC CATTTTGAAA GCAGAGTTTG	60 120 180 240 247
(2) INFORMATION FOR SEC ID NO. 406.		

(A) LENGTH: 442 base pairs

(i) SEQUENCE CHARACTERISTICS:

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(*5)	SEQUENCE DESCRIPTION: SEQ ID NO:406:	
(XI)	SEQUENCE DESCRIPTION: SEQ ID NO:406:	
GAATTCGGCC T	TTCATGGCCT ACAACATCAA AACTCCCAAG CAAATGGATG AATTCATTGA	60
GATCCAAAGT 1	TCAACAGGAA CCTGGTACCA GCGCTGGCTG GTCAGATTCA AGACCATTTT	120
CAAGCAGGTC 1	TGGGATAATG CCCTGTACTG TGTGATGGGG CCCTACAGAA TGAATACACT	180
	GTGGTTTGGT TTGCCATGGC ATTCAGTTAC TATGGACTGA CAGTTTGGTT	240
TCCTGATATG A	ATCCGCTATT TTCAAGATGA AGAATACAAG TCTAAAATGA AGGTGTTTTT	300
	GTGTACGGCG CCACAATCAA CTTCACGATG GAAAATCAGA TCCACCAACA	360
	CCTGACTTTG CCCCCTTGCC CATCAGCCAT TTGCCATCAC CCCAAACAAC	420
	GGAAGTCTCG AG	442
(2) INFORMAT	TION FOR SEQ ID NO:407:	
(i) S	SEQUENCE CHARACTERISTICS:	
• •	(A) LENGTH: 154 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:407:	
GCTGCTGGAA	TTCTTGATGC TGGCTGTTTC TCTCACCGTT CCCCTGCTTG GAGCCATGAT TCTCCTATAG ATCCACAGCC TCTCAGCTTC AAAGAACCCC CGCTCTTGCT CATCCAAATG CGAAGCTCCT CGAG	60 120 154
(2) INFORMA	TION FOR SEQ ID NO:408:	
(i) S	SEQUENCE CHARACTERISTICS: (A) LENGTH: 146 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:408:	
TTTTGGATTT	TTCATGGCCT AGTTTACTTC TGCTTGATCT TTATTCTTCC TTGCTACTAA AGTTTGTTCT TTTCTAGACA TTCATTGTTA GATTGTTAT TTACAATTTT TTGATGTAGA CATTTA	60 120 146
(2) INFORMA	TION FOR SEQ ID NO:409:	
143	CECTIENCE CURDACTEDICTICS.	
(1)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 285 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GAATTCGGCC	TTCATGGCCT	AGATGTTGCC	AGTTTTCATG	GAGGAAGTAG	ACATGAAAGC	60
TTGTTTGTAA	TGTGTTTGAC	AGAGTAGAAA	GACATTGAAG	AAGGTGATGG	TATACATCAC	120
TTGAATATTT	TTATTGAAAA	GGGAGGGAGG	AAATGGAGCG	TTAGTTGTAG	GACCAGATGA	180
TGTAAAGAGA	GTTTTTTAAA	GTGTACAAAA	CAATGGCATG	TTGTGATACT	AATGAGAAGG	240
AGCCAATAGA	GAACAAAAAA	TTGATGATGC	AGGAGACGAC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:410:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CTCGAGGGAT	CTGGCTTTCT	CTGTCTTCTC	ATTTACTACA	TNACGCTGGT	GAATTAATAG	60
ATNTCTCAAC	AAAAGGACAT	TTAAATCAAC	ATATGACACC	TGTTTAAATT	CTTAAGAAGC	120
CATTAATTAC	ACATTCTTAA	GAAAATGAGC	TATGACACAA	CTCTTCTCAC	TGTATAACTC	180
CTATCTGTGA	TTCTCAATCA	GGTGACTTTT	CAGCTNCAAG	ACGGATCTTT	TCTATTCATC	240
TCCTCTGGTT	CGGACCAATT	AAATGTNTTC	TTTTGCAATC	ANAACATCTC	ANNTGCCAAA	300
TCTTCAAAAG	CAAAGGAGTT	NGTTAGCAAC	ATATTAGGCC	ATGAAGGCCG	AATTC	355

- (2) INFORMATION FOR SEQ ID NO:411:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GAATTCTAGA	CCTGCCTCTG	TATGTTGCTT	TAGCCAGGAT	TCAGAGCTAA	AGTGTAAGTG	60
TGTGCTTCTG	CTTTCTGGAT	GTATCTCTCA	AAATTGCTCT	GTCTGTTTAT	TCAGCTCCTG	120
GATCTACCTT	CTCTTTTCTT	TGAATTGGAC	ACCATTCATG	TCATTGCTCA	CTCAGAACTT	180
CAGCTGTTCT	CATGATCACA	TGCTTTCTTC	CCTGTTTATG	TCCAAT		226

- (2) INFORMATION FOR SEQ ID NO:412:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

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TTTTTTTTT TGAAACAGAA TCCTGCTCTG TTCTCGAG

GAATTCGGCC TTCATGGCCT AGTCTGCTGC TTAGCTTGTA TTTTCAGTTT AATATATTCG

TGATCATTAA CAAAACAGCG AAGTGAATAA TGGGCATAAA TTTTCCTAAG AAGAATCATT

TTCCATACTT ATTTTCAAT ATTATCAAAA AGTATGTAAT TTTGGGGGGT TTTTTGGTTT

60

120

180 218

(2) INFORMATION FOR SEQ ID NO:413:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:	
GAATTCGGCC TTCATGGCCT ACTTTGAACA ATTCGGCATG AATTGAAACC AGGTTTTCCT GTGGAAAGTT ATAGCTTGAT TGGGAGATAG AAGTTGAATT GAGTTCTTC TTGCAACTCT TAGTGTTTAT TTTTATATCT CAGTAAGACG AGGATACCTT CAGTTTGAAT CTGCATAATG TTCACTGCCA AACTCCTTCT CATTTAATGC TTATGGCCTT CACATTTCTG TATAATAAAG ATCAATTATC AGCACTCGAG	60 120 180 240 260
(2) INFORMATION FOR SEQ ID NO:414:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 258 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:	
GAATTCGGCC TTCATGGCCT AAGCATATGA ATTTTGGAGA GACAGACATA CAGACCATAA CAGTTCTATT TTCTATAACT ATAGTAGAAT ATCGAAATGA GAACATTGAC ATTGGTAAAA GGTGTATGTA TAGTTTATAT GTTATCTTAT CAAAAGGGTA GATTTACAGA ACCAACACAA GTAAGCTATA GAACTAGCCC ATTACCACAA AGATCTCCCA CAAGCTACAG CTTTACAGTC ATACCCACCC GGCTCGAG	60 120 180 240 258
(2) INFORMATION FOR SEQ ID NO:415:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 281 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:	
GAGGACCTTT ATAATCTACT ACTAATTACT GTGAAAGTAA ACATTGTTTA ATATACCAGT TCTTAAAGAA ATATTTTGTC TAGTCATTAA TATTCTAGTT CATCTCAAAG CTTCCATTTG ACAATTTAAA ATTACTTAAA TTTTAATATT AAAGGAAACA GTTTTCCTGA TTCTCATGAA AGTTCCTATT TGCACTGAAG ATGACTAAAC CTTTTAGTCA TAGTTTTAGA AGAATTGGCT TTTTTATAGC CATTTATTT ACATTAGGGT ACGGACTCGA G	60 120 180 240 281

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:	
GAATTCGGCC TTCATGGCCT ACTCAGAAAA GAAAATGAAA ATACCTCTAC ATGTGGTCTT CCTGCTAATC TCTCTGACCT TCCTATTCAC CACCCTCCCC ACTGCCCACT TACTCGAG	60 118
(2) INFORMATION FOR SEQ ID NO:417:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 273 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:	
GCGAGGATGG CATGGACGCT TATCGAGCAG CTTCAGGGTG GCAGCTACAA GAAGATTGGC	60
TACTATGACA GCACCAAGGA TGATCTTTCC TGGTCCAAAA CAGATAAATG GATTGGAGGG	60 120
TCCCCCCCAG CTGACCAGAC CCTGGTCATC AAGACATTCC GCTTCCTGTC ACAGAAACTC	180
TTTATCTCCG TCTCAGTTCT CTCCAGCCTG GGCATTGTCC TAGCTGTTGT CTGTCTGTCC	240
TTTAACATCT ACAACTCACA TGTCCGTCTC GAG	273
(2) INFORMATION FOR SEQ ID NO:418:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 145 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:	
GAATTCGGCC TTCATGGCCT AAGCAGTTGC TAATGCCAGC AGTACATAAA TTGAGGATGG	60
AGCAAAAGGA TCGACACCAC CAATGGCTGC ATTGTGATAG GTGTGGACAG AGCCTGCCAG	
AATTAAACAC ACGCCAGGAC TCGAG	145
(2) INFORMATION FOR SEQ ID NO:419:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 290 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) IOLOBOOL. IIIICAL	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GGATTCGGCC TTCAT	GGCCT AGTGTTTATA AT	TTAATCCTT TAATATTATG	GTTATTAACC 60
TCTTAAACAT GAATG	AATTC TTGATTGTTT TA	AACACAGTA CCTAAGACTA	ATGCTTTCTG 120
TGGACACCAC TGAGC	TCTGC CTCAACTCCA CO	CCTCTGCGA CCGGAGGACT	ATGCCCCTAG 180
TAACTGCTGT CGGTG	TGGAC GCTGTGCTGG TI	CTGTTTTC TAAAGGAGCA	GAAGGACAGG 240
TCTCTGAGAC AGGAT	CGTTG TCCCTACAGG AG	GGAACAGTG GCCACTCGAG	290

- (2) INFORMATION FOR SEQ ID NO:420:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCCT	CCCAAAGTGC	TGTGATTACA	GGAGTGAGCT	60
GCCACGCCCA	GCCTACAAGT	TTTTCTTTAA	CTACTGCTTT	AGTCAACCAT	ATCCTCTAGC	120
TTCTGATATT	TTCATTGTTT	GTTGTCATTT	TCTAGATATT	CAACAATTTC	AAATTAGATT	180
TTCTCTTCGA	CTAAAGTGGA	AGAATTTTTT	CCCGTTTATT	TTCTACATGC	TAAAGATTTT	240
TATTTTCATT	TTGTTATTAA	TTTCTAGTGT	TACCGTATTG	TCATTAGAAA	ATATGGGCTG	300
GCTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:421:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GAATTCTGAA	AATATTAAGA	TTTATCCTAG	CACTTACGTT	CAACATACCA	TAATTTTTAT	60
ACTTCTCCAT	СТАААТАААА	CCAAGTTTGT	TCCTACACTA	GTCCAGCCTG	CATTCTCAAG	120
AACTCCAGTG	ATTATACATC	AACATCTAGA	GATCAGGTAT	CCCAATCCTT	TCTTCCTATA	180
TCTAAGCTAA	CTCCTTCTTA	GCCAAATGGT	ACCCTTTGAT	TTTGTGTTAA	TCCTTTCCTT	240
CCCTCCACTC	TTAACCCCTC	TCATTCCATC	TTCTCCCTCC	CTTTTCCACC	CCACTCTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:422:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GAATTCGGCC TTCATGGCCT AGGTTAAAGT TGTCTGGTAA TAAGGTGGAG TGGATTTGGG

60

GCAGGTTTTA TGTTTGTGTG CTTCTCTTAG AAGTCAAAGA GTTGGTGAGG TAACTGCAAT CCTGTCTATA TCAGTGTAGT GATAATGCAC TAGTGTAATG AAGAATGGAG CTGCACGTGT GAGGTTTTTC AAGTCCACAA AGATCAGGTA TTGTCTACGG TCAATAAAGA TTTTTTTAAA AAACCCTCTT AACTAAAGAG AGGTAACTTC CTTTTCAAAA CTCTGAAATT TACATGTGCT GACTTATAAT ATGTGTGATC CTCGCTGCTT TTCTGATCCC TGGTGGTTGG GGTGTGTG TGTGTGTGTC TGTGTGATGG GCTCTCGAG	120 180 240 300 360 389
(2) INFORMATION FOR SEQ ID NO:423:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 326 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:	
GAATTCGGCC TTCATGGCCT AATCTTAAGT GTTTTACATG CTCTACCTGC CGGAATCGCC TGGTCCCGGG AGATCGGTTT CACTACATCA ATGGCAGTTT ATTTTGTGAA CATGATAGAC CTACAGCTCT CATCAATGGC CATTTGAATT CACTTCAGAG CAATCCACTA CTGCCAGACC AGAAGGTCTG CTAAAAGGTC AGAGTAATGC AGAATGCGTG CCTTCATCTC AGATTTGTTC ATCACAGGTG GATCCCATGT GTCTTCAGTA GACAAGTCAC CTTTGTAGCT AGCACCAGTG CCAGCTCCAT GCCATTGCAC CTCGAG	60 120 180 240 300 326
(2) INFORMATION FOR SEQ ID NO:424:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 178 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:	
GCGATTGAAT TCTAGACCTG CCTCGAGCCA ATCATTTTTA AATCTAATCT	60 120 178
(2) INFORMATION FOR SEQ ID NO:425:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 127 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	-
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:	
GAATTCGGCC TTCATGTACA TAGATCTTCC TAGTGTCATT GACAAAGGTG ACATTTGCAA GGCTTTTTCT TCATCAGATG CAGGGATCTG GACTTCATGT GTATCCTTTT ATCCACTCCT CCTCGAG	60 120 127

ರ್ಷ ಸಂಕರ್ಣಗಳ ವಿಷ್ಣಾಗಿ ಮಾರುವ ಸರ್ಕಾರ ಕರ್ಮಾಣದ ಸಂಕರ್ಣಕರು ಕರ್ಮಕರು ಕರ್ಮನ ಕರ್ಮನಿಗಳ ಸಂಕರ್ಣಗಳ ಸಂಕರ್ಣಕರು ಕರ್ಮನಿಗಳ ಸಂಕರ್ಣಕರು ನಿರ್ದೇಶಕರು ನಿರ್ದೇಶಕ

- (2) INFORMATION FOR SEQ ID NO: 426:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GAATTCGGCC	TTCATGGCCT	AGAATTTAAT	TGCAGAAAAT	TATTCATATT	CTTATAATCC	60
TTTTAATGTC	TATAGGATTT	ATGATGATAT	CTCCCCTTCC	ATCCTGATTT	TTTCAAGTTT	120
${\tt TTGTTTTTC}$	TTTTTTTTTTA	TAAATTCTGG	TAAATGTTTA	TTAATTTTAT	TCATTTTTAA	180
AAAGAACCAG	CTTTTGGTTT	CATAAAGTTT	TATAATTTTT	TTGTTTTCAC	TTTCATTAAT	240
TCTACTCTTT	ATTATTTCCT	TCATTTTGTT	TACTTTGGGT	TTGTTTTGCC	ATTTTTTCC	300
TAGTTTCTTA	AGGTGCCAGC	TCGAG				325

- (2) INFORMATION FOR SEQ ID NO:427:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GAATTCGGCC	TTCATGGCCT	AGGCACACAG	GGCGGGCAGC	AACATAAACG	GCACCCATTA	60
AAAAGCAAGA	CTCGCTCTTG	AGACTAAAGG	AGAAGTTACC	TAAATTTCTG	TATAAACTCA	120
GTAATTCATT	CACTTTACTA	GTATTACATT	TATGAAATTC	ACCTTTGTGG	AAAAAGGAGC	180
GGGAGAGGGA	TAAGAAAATG	CCTGTTTCTA	GAAAACGCTC	GAG		223

- (2) INFORMATION FOR SEQ ID NO:428:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GAATTCGGCC	TTCATGGCCT	AAATTCATAC	AGAAGACCTT	ATTGTGATAA	AGTTCAACGG	60
TATAGGTAAA	CAACAACAAA	AAAACTATCA	ACCATAATTT	TTTCACCCTA	CCAACATTCT	120
CTGAACCTTT	CAGTAATATT	TTATACACAT	GTGCATATTC	TGCCTTTTTC	ATTTACTATA	180
TCATAAACTT	CTTTCTAGAT	CATTATTTTT	CTGCTGCATT	TTTTCAGGAT	TTATCACCTT	240
TATTTTTAGT	TTTAGTTTTT	GTGAGTGTAC	TCTCGAG			277

- (2) INFORMATION FOR SEQ ID NO:429:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AAATGAGCCC	TATCACTGAG	AAATACGTGT	TTCATGATTT	AACTCTGTGT	GTGTGTGTGT	60
GTGTATTTT	TTTTTGGTTG	TCTTCAGCTG	ACAGTATGAA	AAATGAAACT	GCTGAAAAAG	120
CTGAGCACCT	GGTCACCCTT	GGCCTTCCAT	TGCTTTGGCC	TTCAGTAAAA	AGCAGCCTCC	180
CTTCTAGGTC	AGGGAACCAT	GCCATTGAGA	CTAGTAACGG	GCGTTCTGGG	CACAGTCCCA	240
CTGTGCACAG	GTTTGAGAGG	ACAAGTTCAT	CAGAAGGAAG	GCAGTCCTTA	GAAGTCACAT	300
ACGTTGAGCC	CCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:430:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GAATTCGGCC	TTCATGGCCT	ACATTCAGAA	AACAGAAAAG	TTTCAAGAAG	CAGGAAGAAA	60
AGACTCACCT	ATGATCCCAA	CACCCAGAGG	TAATAATTTA	CCATTTTTGG	TGTATCTTCT	120
TTGTCTTTTC	CTATGTGTTG	CCTTATGTAG	ATATGTAACA	GGTTGTGGTT	TAAACCGAAG	180
CTATACCCAT	TGTTTGGAGT	CAGGCAGGTG	CGATAAATTT	GTAGGTGGCT	CACCAGAAAT	240
CTATTTGCAT	GATGAACCTA	CAGGACTCGA	G			271

- (2) INFORMATION FOR SEQ ID NO:431:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

GAATCATTTT	TGGTCACCAA	TCTCTCATAT	ACCACTACTG	GATATTTACA	ACATGCTTCA	60
GTGGAGGAGA	AGACACTGCT	GCTTTGCAAA	GATGACCTGG	AATGCCAAAA	GGTCTCTGTT	120
CCGCACTCAT	CTTATTGGAG	TACTTTCTCT	AGTGTTTCTT	TTTGCTATGT	TTTTGTTTTT	180
CAATCATCAT	GACTGGCTGC	CAGGCAGAGC	TGGATTCAAA	GAAAACCCTG	TGACATACAC	240
TTTCCGAGGA	TTTCGGTCAA	CAAAAAGTGA	GACAAACCAC	AGCTCCCTTC	GGAACATTTG	300
GAAAGAAACA	GTCCCTCAAA	CCCTGAGGCC	TCAAACAGCA	ACTCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:432:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GAATTCGGCC	TTCATGGCCT	ACCTGGATTT	CTCAATTTAT	TAAGTTGTAC	TTACCTGATG	60
CTGATGATGA	TTACTGTATT	TACACATTGT	CTCAGAGCTC	ACTCTTGCGG	AGGTTGTGGC	120
CTCGAAAATG	CCTTGTTGTC	CCTCTGGAAT	CTGTCTTTTC	AGCTTCATCT	CCTCCTCCTC	180
ACCTCCTGCT	GTGGTGCACA	GATACCTATA	GGCAGGCTCC	ATCTCCTCCT	CCCCAGCTCC	240
TCCCCTAGTG	CACACCTCGA	G				261

- (2) INFORMATION FOR SEQ ID NO:433:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GAATTCTAGA	CCTGCCTCGA	GTCCTACGGG	AAACCTCCAG	GGTTTTAGGA	AGCTGACGAT	60
GCAAGTTTAT	CCAAATGGGA	ATGATAATAA	TCATGTTTAT	TATCCTGGGG	TGCTTTCTCC	120
ATAGCAAGTA	CTCACTTAGG	TCCTGTTCAT	TAGTCAGTCT	TTTAATCTGT	ACTGAAATAG	180
GTGCTGTCGC	ATCCATGGGG	AATGAACTCG	AG			212

- (2) INFORMATION FOR SEQ ID NO:434:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

GGTTGCAGTG AGCTGAG	GATC GCACCACTGC	ACTCCAGCCT	GGGCAACAGA	GTGAGACTTC	60
ATCTCCAAAA AAAAAA	аааа аааааааада	CAACCACAAC	AAAAACGAAA	CACCACCACC	120
AAAAAAGTTT ACTGGT	AGAG TCTCCTCTAG	ATTGTTTTCT	TTTCAATACT	TGTTTCATAT	180
TCTCCAACTG CCCTCG	ICCC ATAATGTTGG	CTGTGCTTTT	CTTTGTGCTT	ACAGCTCATT	240
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GCTGGGATGG ATATGG	ፐር ልር ምምምርልተርጉል	CATTGACCAA	ልተልሮልልምርምር	CAC	202

- (2) INFORMATION FOR SEQ ID NO:435:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

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GAATTCGGCC TTCATGGCCT AGGCTTGAAA GGAAATGAGG GAAATTTCAG TGAGTTTGAG

GAATGCCAGA CTGGGTATGT GACAAATGAG TGGGTAAATA AGGAAATCTC AGATTGAGAA TCCTGGCAGA TCTTTCAATG GGTTAGACTG CAGGAATATT GATTTTAAAG CCAGACTGAA GCAAATTCTA GTGATAAAGG AAGGGGAAAG GGTGGCTGAA TCAAATGTTC TACCAATACT CCTTTTTTTA GTATTTGAGT TAAAATTCAG ATTANATGCT TGGCTTAGAA GAATGCAAAG CTTCACTGAG CCTAATAATA TGGATCCCAG TGGGTGAGTG GAGGTGAGTT CACTCGAG (2) INFORMATION FOR SEO ID NO:436:	120 180 240 300 358
(2) INFORMATION FOR SEQ ID NO:436:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 258 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:	
GCTCGAGAGA GCTTTTTTT TTTTTTTAA ACATTGTATC ATTAATTTAT CACGTGTATC CAAGCTCCTT TGAGTTTCCC TGCCCCATC CCTGTGTCAT TCCAGCCATA TCCAGCTACT CCTTCCATGC TTCCCCCATT CTTGTTTCTG ACTCTATTAC TCCCAGTCCA AATCTTGCTC TTCACTGCTC GCACCTTGTG CTCTCCTCTC	60 120 180 240 258
(2) INFORMATION FOR SEQ ID NO:437:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 299 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:	
CAAGCCGGCC ATATTAGAGA GATGGAAATA AAGCTTCCTT AATGTTGTAT ATGTCTTTGA AGTACATCCG TGCATTTTTT TTTAGCATCC AACCATTCCT CCCTTGTAGT TCTCGCCCCC TCAAAATCACC CTCTCCCGTA GCCCACCCGA CTAACCATCCT AGTCTCTGAA AATGCACAGA GATGCCTGGC TACCTCGCCC TGCCTTCAGC CTCACGGGGC TCAGTCTCTT TTTCTCTTTG GTGCCACCAG GACGGAGCAT GGAGGTCACA GTACCTGCCA CCCTCAACGT CCACTCGAG	60 120 180 240 299
(2) INFORMATION FOR SEQ ID NO:438:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:	
GAATTCCTAC TAAATAATAT TAAGCAGGAA TTTTTTAGGT GTTGCTTTTT AGCTCCTTTT TATCAGTTCT GGGAAGCAAA CAGTGCTGCA TCTCCTTTGC TCTCATAGAA TTCTGTAATT TTTATACCAC AGGTCTCTGC TAAAAGGGGG CATGTGTTTA GAAATCTAA AAATGAGGGC	60 120 180

TCTGAACTTT GTAACTGTCC TGATACGTTT TCCCTTTTTT AATCCCAACC CCCTCGAG

WO 08/45436

WU 98/4543	0	PCT/US98/06955	
	(2) INFORMATION FOR SEQ ID NO:439:		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 229 base pairs	•	
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double		
	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: cDNA		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:		
	GAATTCGGCC TTCATGGCCT ACAACTTGCA CTTCGCTCCA GCATCACTGC	G CCTCCTGCTG	60
	TTATTTAGGT ATACTAGGCA TTTCCTGTTT TAGGGCCTTT GTACCTCCAG	TTCCCTCTGT	120
	TTGGAATGCT TTTCCCCAGA TAGCCCTGTG GTTAAATCTC TTACTTCCT	TGGGTCTGTG	180
	CTCAGATGTT ACTTTCTCAG AGGGTCCCCC AAGCCCCCAT GCACTCGAG		229
	(2) INFORMATION FOR SEQ ID NO:440:		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 284 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double	÷ -	
	(D) TOPOLOGY: linear		
•	(ii) MOLECULE TYPE: cDNA		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:		
	GAATTCGGCC TTCATGGCCT AGAGTCTATT AACTATTTTT CTGTTATACC	· CTGCCAGAAA	60
	AGAATTTTAA AAGTTAGTTT ATGTTTTGTG TAACCATGTT CTTCAGAATC	CAGGTATGTG	120
	AGCATCATGG TTTCTGGGTA ATTCTGCTGC TCCTGTCTTT GAAAATGGAG	ATACCACTTG	180
	CAGCTTATCC CACTGCTGAG TATTCCAGCA TTGGTAGTGG TTTCACTCCA	A TTGCATCCAT	240
	CCAGAACTTT CACACAGGCC TCCCCATTAC CCAGCATCCT CGAG		284
	(2) INFORMATION FOR SEQ ID NO:441:		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 282 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: double		
	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: cDNA		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:		
	GAATTCGGCC TTCATGGCCT AATAAAATAA AAATTGGAAG AATGGCATT.	г таттасаста	60
	TAGTTAAGAG ATTGGCTAAG GCAGTAAATA AAACTTAGAA ATGCTCAAA		120
	TTGCTTTTAT AATCATTGAT ATATAAAGCA TGCTACTGCT AATCAATTA		180

- TAAGACCTAT CAGCATGTCT TTTTTTAGT ATCTGGTTGA CTTAAACATG ATGTTCTCTG 240 TACCATTTAA CATTTCAAG ACATATTCTC CCCAAACTCG AG 282
- (2) INFORMATION FOR SEQ ID NO:442:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs

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(B) TYPE: nucleic acid (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GAATTCGGCC TTCATGGCCT	ACTCACCTGC	AATCTATTGT	TTATATTGTT	GCTATGTATC	60
TCTATTCTTT CTGCATCAAA	TAATGAATAG	CTCATTTTGT	GTTGCCTTCA	AGTATGACAA	120
ATTCCTTTCC AAATGTGATT	CCAGACAGTA	TATCCAAACA	TGTCTTTCTT	TTCCCATTCC	180
TGATCATCCT ACATGTCAAG					240
G					241

- (2) INFORMATION FOR SEQ ID NO:443:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (E) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GCAAGCACAA	ATCTAACCAT	GAGCTTCAGC	AATCAGCTCA	ATACAGTGCA	CAATCAGGCC	60
AGTGTTCTAG	CTTCCAGTTC	TACTGCAGCA	GCTGCTACTC	TTTCTCTGGC	TAATTCAGAT	120
					AGTTCCTGGA	180
					TCAGACAGAT	240
CCTCTCGAG						249

- (2) INFORMATION FOR SEQ ID NO:444:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GAATTCGGCC TTCATGGCCT	AGGGATTTTT	TTTCTTTTTT	TTCCTCATAT	GTGAAGTAAT	60
AGTCTCTTCA CAACAGAAGA					120
AGGTTACGTA CCTCTTTGGT					180
TCATTTTCT ATTTCTTTGT					225

- (2) INFORMATION FOR SEQ ID NO:445:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

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GAATTCGGCC TTCATGGCCT AGTTTTGGAG AGCTCTACCT ACTAGCTGGT TATTTCTTAC ATTAAATTAA TACCTTTAAA AAGTATTATG AAAATAACAC ACTCAGTAAA AGAAATTTTA AAAAACAAAT GCAATAAAAA TGTGTTTCTT TTCAACCTTT GACTTGTCAC TTCCTCCAGC TTTTCCCTTA TTTAACTGTG AGAGGTATTC TCTATTAGCA GTTACTTATC CCCTTCCTCA AACTCGAG	60 120 180 240 248
(2) INFORMATION FOR SEQ ID NO:446:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:	
GGATTGAATT CTAGACCTGC CTCGAGCGAC CTCTAGAATC CTACATTTGA AATATTCTGG CAGTGAGGTG TTCATCCTAA CTCAGTCAGG TAGCTGTGGA CAGCCTTCAC CTGTTAGGAG CTCCTTAGAA ATAAATTCTG AATACCTTTG GTTTCTTTT ATCCTCCAGA GGAATTTCCA CTATCTCCGA AGCTGTTCCT TGTTCCACTG ACAATTCGCT TAGTTAATGT TCTTTTTTAG CCTGTACTAT CTCGAG	60 120 180 240 256
(2) INFORMATION FOR SEQ ID NO:447:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 250 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:	
GAAGGCAAGA AAATCTATGG AAAGAGAAGG CTACGAGTCC TCGGGCAATG ATGACTACAG GGGTAGTTAC AACACCGTGC TCTCACAGCC TTTATTTGAA AAGCAGGACA GAGAAGGTCC AGCCTCCACG GGAAGCAAAC TCACCATTCA GGAACATCTG TACCCCGCGC CTTCATCACC TGAGAAAGAA CAGCTGCTGG ACCGCAGACC CACTGAATGT ATGATGTCGC GATCAGTAGA TCACCTCGAG	60 120 180 240 250
(2) INFORMATION FOR SEQ ID NO:448:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 198 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:	
GAATTCGGCC TTCATGGCCT AGCTGGGGG AATAGGTTAT GTGATAAGGA GTCAGTCGGA CAGAGTGGGG TGAAAGATGT TCAGACAGGG AAACACACAT GCAANAGAGG GAAGGTGGGA CACAGCATAT GCNTCCAACA TTTGGTAGGG CCGAGGCCCC ACATGGGAGC AGTGAGAGGT TAGGGATCGA CGCTCGAG	60 120 180 198

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(2) INFORMATION FOR SEQ ID NO:449:

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 163 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:	
GAATTTTCCT TACCAGGAAA ATTCATGCTT TACAATTTGT CAGAGGTGCA CATTACTAAT TACAATAGGT CACACTTTTT CTATGCGCTT CATTATAATA TTGGCAACTT TATTATGCCC CATTACATAC TGTATTATGC TCTTACTTTA TATGCATTTT GAG	60 120 163
(2) INFORMATION FOR SEQ ID NO:450:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 122 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:	
GAATTGCTGA TATCTTATAA AGGGGACCTT TTTTCTTTAC ATTTCTGACG GTTTTTATCA GAATGTATGT ATTAATGCTA TTTGTCTTTG TATATTTATT TTATTTCCAG CCACTTCTCG AG	60 120 122
(2) INFORMATION FOR SEQ ID NO:451:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 302 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:	
GAATTCGGCC TTCATAGCCT AACTCAAGAT CTCCCATCTA TTAAAGCAGA GGAATAACTT TTGTAGGCTT AATACTGCTT TCTCACTTAG GAAAAGTTGA AATTAAGAAC ACACAGGAAG GGATCATTTC CTAAGGTTTA TGTCCTCAAC ATCAAATTGA GTTGAAACTT GACTACAGGC CATCTGCTCA TTCAAAGCAT TACAATAAAT CTGTCCTATT GATGATCAAA ATGAGAGCTG AATTGGATGC AGGATTGGAC ATTGCAAGCT GTTCTCCCAA GTGGGATGGA AAGGTGCTCG AG	60 120 180 240 300 300
(2) INFORMATION FOR SEQ ID NO:452:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 265 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GAATTCGGCC	TTCATGGCCT	ACAAAAATAT	TTATTTGACT	GAATGATTTA	ATATGCAGTT	60
ATGGTGTTTA	ATATATCATG	TGTTATTTGT	TTGTTTAAAT	ACAGACATAA	CCCACAGTTA	120
TCTTGAACAA	GAAACTACGG	GGATAAATAA	AAGTACGCAG	CCAGATGAGC	AACTGACTAT	180
GAATTCTGAG	AAAAGTATGC	ATCGGAAATC	CACTGAATTA	GTTAATGAAA	TAACATGTGA	240
GAACACAGAA	TGGCCCGGAC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:453:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GAATTCGGCC	TTCATGGCCT	ACTITAATTT	CTCTGAGCAG	TATTTTACAG	TTTTGATGTA	60
TAAACCTGGC	ACAGATTATG	TTCAGTTTAT	TTCTAAGTTT	AAGTCATGTT	TTTGAATGTT	120
ATATTAAAGG	ATATTTTCTT	TTTTAAAAAA	TCTACAATGT	TTATTTTATT	ATTATTATTT	180
TTAATCTCGC	TTCATCACCA	AGGCTGGAGT	AAAGTGACGC	GACCTCAGCT	CGAG	234

- (2) INFORMATION FOR SEQ ID NO:454:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GAATTCGGCC	TTCATGGCCT	ACGCACATCC	GCAGTCAGCC	ACCTCGCGCG	CGCCTCCAGG	60
AGCAAGGATG	GAGAGGCTGG	TGATCAGGAT	GCCCTTCTGT	CATCTGTCTA	CCTACAGCCT	120
GGTTTGGGTC	ATGGCAGCAG	TGGTGCTGTG	CACAGCACAA	GTGCAAGTGG	TGACCCAGGA	180
TGAAAGAGAG	CAGCTGTACA	CACCTGCTTC	CTTAAAATGC	TCTCTGCAAA	ATGCCCAGGA	240
AGCCCTCATT	GTGACATGGC	AGAAAAAGAA	AGCTGTAAGC	CCAGAAAACA	TGGTCACCTT	300
CAGCGAGAAC	CATGGGGTGG	TGATCCAGCC	TGCCTATAAG	GACAAGATAA	ACATTACCCA	360
GCTGGGACTC	CAAAACTCAA	CCCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:455:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GAATTCGGCC	TTCATGGCCT	AGCTGATATT	ATTTCTGAGT	TTTTGCTTAT	TTGCTTTCTA	60
CATAGAATCA	ATAAAATTGA	CAACTAGCAT	TGCCTATATA	TGCAGGTGTG	ATACTATTCA	120
GGGTACTAGT	ATATTGGCCA	CTCATTATGA	AACTTTCAGG	TECTCATATA	TTTTCTTTTA	180
TTACAATGAT	CTACTTATTT	CTGATAAATA	TTGGATTCAT	AGAGGCTAAA	GGGCTGGGAA	240
AGGAAAACAT	TCGTGACTAC	TTACAACCAT	TTGATACGAG	TTGTGTCAAT	ACAGACCTCA	300
CACAGCAGCA	CCTCGAG					317
				•		

- (2) INFORMATION FOR SEQ ID NO:456:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GAATTCGGCC	TTCATGGCCC	ACAAAATGGT	AATACAAATA	AACCACTACT	TACTGCTTTT	60
AATGGTAGTT	${\tt TGTTTTTTT}$	TTTTTGAGAC	AGAGTCTCGC	TGTGTCGCCC	AGGCTGGAGT	120
GCAGTGGCGC	GATCTTGGCT	CACTGCAAGC	TCCGCCTTTC	GGGTTCACAC	CATTTTCCTG	180
CCTCAGCCTC	CCGAGTAGCT	GGGACTGCAG	GCGCCCGACT	CCCGGGTTCA	CACCATTCTC	240
CTCCCTCAGA	CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:457:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GAATTCGGCC	TTCATGGCCT	AGGAGAATCG	TGAGACCTCT	ATTTCCATAT	CTTTTTCTAC	60
TACTGGAATT	TTTATTTTTA	CCATACCCAT	AAATTACTTT	CTATTTTAAG	AAGCAAATAT	120
ATAATTCCTC	AGTTTAGTAA	AAAGTTCTCA	CTTGAAAAGC	TGGTATATGA	ACTTTAGAGG	180
GCAGATTAAT	CAACTGCTAA	ATATTATTAA	TCTTTCTTCT	TGGAACTTTC	CAACACAAAA	240
GACAGTTTAT	AGAAAACAAA	GTCAGTGTTC	AAAACAGCTG	AATGAACTAT	CTTTTGATAT	300
TTTATTTGTT	TTTGTTTTGT	TTTGTTTTGT	TGAGACAGAG	TCTTGCTCTG	TTGTCCAGGC	360
TGGAGAGTAA	TGGCACGATG	ACTGCAACCT	CTGCCTCCCG	GGCTCAAGTG	ATTCTCCTGC	420
CTCAGTCTCT	CGAG					434

- (2) INFORMATION FOR SEQ ID NO:458:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

GAATTCGGCT TCATGGACGA GGAGATCGTG TCCGAGAAGC AAGCCGAGGA GAGCCACCGG

CAGGACAGCG	CCAACCTGCT CATCTTCATC CTGCTGCTCA CCCTCACCAT TCTCACAATC AGCACCGCCG GGCCCGCTTC CTGCACGAAA CCGGCCTGGC TATGATTTAT	120
CCTCTTCA	AGACCACCA GACCACCATC CIGCACGAAA CCGGCCIGGC TAIGATTTAT	180
GGTCTTTTGG	TGGGCCTTGT GCTTCGGTAT GGCATTCATG TTCCGAGTGA TGTAAATAAT	240
GTGACCCTGA	GCTGTGAAGT GCAGTCAAGT CCAACTACCT TACTGGTAAA TGTTAGTGGA	300
AAATTTTATG	AGTATATGCT GAAAGGAGAG ATACTCGAG	339
	ATION FOR SEQ ID NO:459:	333
	SEQUENCE CHARACTERISTICS:	
127		
	(A) LENGTH: 256 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:459:	
	•	
GAATTCGGCC	TTCATGGCCT ACTTATTTT GTTTCTGTGT GTTTGTTTTA AATGTGTGTG	60
CGCTCATGTG	AGTTTGAAGG GAGTTAGATG CAACAGCAGG AGCTGTGCTC AGGGCAGTGG	120
TGTTAATTAT	GGAGGGCGTG GGAAGGGCTG GGAAGAGGAG GGGGTTGTAA GACTCCCCTT	180
TTCCCTCGCA	TGTAAACAGA TGCTGGTGAC TGAAAGTCTG TCTGCGGTTA TTGGCAAGAG	240
TGACGGAAAG	CTCGAG	256
		230
(2) INFORM	ATION FOR SEQ ID NO:460:	
(i)	SEQUENCE CHARACTERISTICS:	
, ,	(A) LENGTH: 320 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(nei)	CDOVIDAGE PROGRESS OF THE CO.	
(X1)	SEQUENCE DESCRIPTION: SEQ ID NO:460:	
GAATTCGGCC	TTCATGGCCT AATTTGAAAA TTCATAAGTT TCTACCAATA CTTCCAATTT	60
CAATCCAACA	TCTGAGGATC TCCCTAGATT TCCTATTTCC ATGATTATAA CTCTTGTACC	120
AGATGATAAG	AAACATGGAT CTGACTATAC TCAATTTATT CACATATTTT CTCAGTGAAC	
TAACTTATT	CCTCAATATA ACCACTATAC TCAATTTATT CACATATTTT CTCAGTGAAC	180
OTOTO CONTROL	GCTGAATATA ACCAGTCCCC AGCCTTCCAA CTGCCTCTCT CACTTGCCAC	240
CICIGCATCI	TCCCCCACTG TCTTCCTCAG CAATCAGACT GCCTCTTGCC AAGTCATCAC	300
CACAGCACCC	CACTCTCGAG	320
(2) INFORMA	ATION FOR SEQ ID NO:461:	
(i)	SEQUENCE CHARACTERISTICS:	
,-,	(A) LENGTH: 307 base pairs	
	• • • • •	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:461:	
GAATTCGGCC	TTCATGGCCT ACCCTCTACT ATTTTTGAAC CAAATCAACA ACAACCTATT	60
TAGCTGTTCC	CCAACCTTTT CCTCCGACCC CCTAACAACC CCCCTCCTAA TACTAACTAC	
СТСАСТССТА	CCCCTCACAA TCATGGCAAG CCAACGCCAC TTATCCAGTG AACCACTATC	120
	CTCTACCTCT CTATACTAAT CTCCCTACAA ATCTCCTTAA TTATAAAATT	180
	· SASSASSES ELECTROPHENT OFFICE TO A A A TOTO CONTRATA TOTAL TOTA	240

CACAGCCACA GAACTAATCA TATTTTATAT CTTCTTCGAA ACCACACTTA TCCCCACCCA TCTCGAG	300 307
(2) INFORMATION FOR SEQ ID NO: 462:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:	
GAATTCGGCC TTCATGGCCT AGTACAATTT AATATAATTT CTTACAAGTT TATTACCTAA AACTTTGCAA ATAATTGAAG TTAGAAGCTT TGGATTTGT TTTTAGAGCT TAATCCTTTT CTGTAAGTGG AAATCCTTTC CACTGGTTTA TTTTCCTTTT GATTTTATTT TACTTTGACA CCCTAAAGGT TTAGTGTTCC TGTTTTTAAA TCTACTGATC GTTTCTTATG AGATTCCTTA GAGTACCCCT CGAG	60 120 180 240 254
(2) INFORMATION FOR SEQ ID NO:463:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 283 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:	
GAATTCTAGA CCTGCCTCGA GAGGACGCCG GAGAGAAATG AGTAGCAACA AAGAGCAGCG GTCAGCAGTG TTCGTGATCC TCTTTGCCCT CATCACCATC CTCATCCTCT ACAGCTCCAA CAGTGCCAAT GAGGTCTTCC ATTACGGCTC CCTGCGGGGC CGTAGCCGCC GACCTGTCAA CCTCAAGAAG TGGAGCATCA CTGACGGCTA TGTCCCCATT CTCGGCAACA AGGTAGCGCA GCTGCTTTGG GGAGCTCCTC CCTACTGCCC AGCAAAACTC GAG	60 120 180 240 283
(2) INFORMATION FOR SEQ ID NO:464:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 233 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:	
GAATTCGGCC TTCATGGCCT AAAAAGTGGT TCCTATTTTC CTGGTTGAAC CTTGAGTGAT ACACCCAGTA TTGTACCACC CAATTAGTAG ACATTATTTC TTCTTAGGTC ATATTATTCT CAGCTTATAG AGCAAGAAGT TGAAGCTTAA AGGGTTAGAT TACTTGCCCA AGGTAATACA GCAAGAATCT TATTTCATCC AACCTAGAGT GAATATTTCC CCCACATCTC GAG	60 120 180 233
(2) INFORMATION FOR SEO ID NO:465:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 497 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:465:	
AGATATTGAA GCATTTGTCC GAAACTTGTC ATAACCACTT ACATTTCAAA TGTCTGCTGC	TTCATGGCCT ACTGATGTTG AAGACGACAC CACGGCTTTG ATGGAATATC AATGTCTCTC TGCCTGTTCA TCCTTCTGTT TCTCACACCT GGTATTTTAT TCTCCAATGT ATATGCACAG AGAGGCACAG GCATGTGGAC TGTTCAGGCA TACATTACCA TCTGGACTGC AAGAGAATAT TATACATTTA AACCTGTCTT TACTGATCTG CATAACCAGT TAACCCAATA TACCAATCTG AGGACCCTGG CAACAGGCTT GAAAGCCTGC CTGCTCACTT ACCTCGGTCT CTGTGGAACA TAACAACAAC ATTAAACTTC TTGACAAATC TGATACTGCT TATCAGTGGA TCTGGATGTT TCTAAGAACA TGCTGGAAAA GGTTGTCCTC ATTAAAAATA	60 120 180 240 300 360 420 480 497
(2) INFORMA	ATION FOR SEQ ID NO:466:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:466:	
CCCCCGCCAG AGCTTGCCTG ACCCCTCCAT	TTCATGGCCT AGCCCCGACT AGCTTTGCCC TAACTCCTTC ATCAAAAGAC CTTCCCACAC CTCATACGCA GCCACATCTG CCCTATTCTC CATGCTTTCC CCCCTTCCTCA TCTCTCCCTG CCTGTGCAGA CCTCCACCCT TCTTTCCTCC CCCCCAATGC TTGTAGACCT TCCATTCATT CCGTCTCATC GTGCGTGGTC CATCACCTGA CCTCGAG	60 120 180 240 267
(2) INFORMA	TION FOR SEQ ID NO:467:	
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 152 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:467:	
TCACACCTCA	ATATTATACT AGCATTTACC ATCTCACTTC TAGGAATACT AGTATATCGC TATCCTCCCT ACTATGCCTA GAAGGAATAA TACTATCGCT GTTCATTATA TAACCCTCAA CACCCACTCG AG	60 120 152
(2) INFORMA	TION FOR SEQ ID NO:468:	
(i) s	GEQUENCE CHARACTERISTICS: (A) LENGTH: 198 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

CAATATTTCA	AGCTATACCA	AGCATACAAT	CAACTCCAAG	CTCGGAATTT	TAACTTCATG	60
GCAAACAGAA	AAGCTAGACT	GAGTTATCAG	TGTTGTGAGA	${\tt GGAATATTTG}$	GCCCAACAAG	120
AGTTGTTGGG	GTGGGAGGAG	GGAGAGACAA	AAGGAAAGGA	CTGCCAGCTC	TCAGAGGGTG	180
GAGATGGGGG	ACCTCGAG					198

- (2) INFORMATION FOR SEQ ID NO:469:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - () STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GAATTCGGCC	TTCATGGCCT	ACTGCTATAT	TCAAGTTTCT	CCCACTACTG	TGGTTTCTTT	60
TTTTTTTTT	TTTTTTTTT	TTTTGAGACA	GGGTCTTGCT	CTGTCACCCA	GGCTGGGGTG	120
CAGTGGTGCG	ATCTCGGCTC	ACTGCAAATT	ACACCTCCTG	GATTCGAGCA	ATTCTCATGC	180
CTCAGCTTCC	TGAGTAGCTG	GGATAACAGG	TATGCACCAC	CACCCCTGGC	TAATTTTTGT	240
GTTTTTAGTA	GAGACAAGTT	CTCACCATGT	TGTCCAAGCC	ACCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:470:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

GAATTCGGCC	TTCATGGCCT	AAAAGAAGAA	TACTAATTAG	AATTTGAGTT	CTAGGGGTTT	60
TTCCTAGGTT	TTTCATTCTA	GACTTAGCTT	TTATTCAAAC	CTGTTGATCC	TGCATAGGGG	120
TAGTCTAGCT	TTAAAAAATA	AAACAATAAA	CATAAATGAG	CCTATTGAGT	TCAATCAGAG	180
TAGGGAGCAG	TTTTATTGAA	CAGCACATTT	TCAAATTCTT	CAGTTGTGTT	TTGTTTTTCA	240
GCTACGTGTC	TCTCTGTGAT	AATGAAAAGA	CAGGTTGCAA	AGCCCGGGAA	CTAAAATCAG	300
TTTATGTGGA	TGCAGTAGGA	CTCGAG				326

- (2) INFORMATION FOR SEQ ID NO:471:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

ATTTAATGGT GTCTTGCTCT ACCTCCCAGA TGAACAAACA	TTCATGGCCT AGTGTAAAGT GTTTTTGCAC AGTGCCCAGA AATTTGCAGT CCTTCCTCCT TATTTATTTT TATTACTTGT TTTTGTTTTT TTGAGACAGT GTCGCCCAGG CTGGAGAGCA GTGATATTAT CGTGACTCAC GGCAGCCTCG CTCAGGTGAT CCTTCACCT CAGCCTCCCA GGCAGCTGG ACCATAGCTA CGTCCAACTC CTCGAG	60 120 180 240 300 326
(2) INFORMA	ATION FOR SEQ ID NO:472:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:472:	
TTGGTTTGGC GTGATCCTAG	TGTCCCTTGT AACATTTTGG TTGGCTATAA AGCTGTATAT CGTTTGTGCT TATGTTCTAT CTTCTTCTCT CTTTACTAAT GATCAAAGTG AAGAGTAGCA AGCTGCAGTG CACAATGGAT TTTGGTTCTT TAAATTTGCT GCAGCAATTG TGGGGCATTC TTCATTCCAG AAGGAACTTT TACAACTGTG TGGTTTTATG CGAG	60 120 180 240 254
(2) INFORMA	ATION FOR SEQ ID NO:473:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 286 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:473:	
TTTAAAATAC TTTCAAGACT ACATATTTAC	TTCATGGCCT ACAGAAATCT AATTCCTGGT GCTATTTGCA ACTACATATA AAGGAGATAA ATACCCAGAA CACATTAAGC CTACTGATTT AAACAGAACA GCTACACAGA AAGGGAAGGA AGCTGTTAAC CCAGCACAGC AGCACACCTC GTCTCAGAGA TTAAATGGAA AGAAAGGATC AATCAAAACC TTTAATGCTC AACACAGTCA AGTCTATCAA ATTTCCAGAT TTACAG	60 120 180 240 286
(2) INFORMA	ATION FOR SEQ ID NO:474:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 380 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:474:	
	TTCATGGCCT ACAATTAAAA GGTTCTGTTA AATTACGTCT TTCAGTCTGA	60
	AGAATTTACT TAAAATTTTT CCATTTAAAA ACAGGTATAA AATTAATTGC AATCACCCAG TATAAAGATA GAAAAGACCT GTAAGACAAC TGTGTGGTTA	120 180

AATACATGAT AACACATTTA CGTGCCTTTT ATAGAAATCC ACTTATTATG TACATACTGG	240
CTTGTTTTTT TTCCCACTTC TCCAGTACAC TATTTCAGGC ACAGGCTCAA AATTTGAACC	300
CAAATGGTCT GTTAGGTCTC TTGACTTTTT CAGTTCAAAG CTCTGCTAAT CTGCTAAACC	360
TAGCCCCAAA CCCACTCGAG	380
(2) INFORMATION FOR SEQ ID NO:475:	
(') apprinted cuapa comparante	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 254 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:	
G110000000 GG0GGGGGG AGGGCGG AGGGGGGG GG1401GG AMGG111GG	
GAATTCTAGA CCTGCCCGGA GCCCTGACCT AGTCCGGCGT GGAGAGAGGA ATGGAAAGCA GTGTCCCTTT TGAGAAGGCA AATTTACAGC TGGCTTTTGT AATCCTAGCT ATTTTTTGTT	60 120
TGTTTGCTAA GTCTTTGATA GTCCCCAGTG TGGTTTGTCT GCCAGTGATC TCAGCACCAC	180
CAGAGAGCTT GTTAGAAATG CGGCATCCCA ACCCCACCAC AGCCCTCCCA AGTCAGATAC	240
TCCCCCCTCT CGAG	254
(2) INFORMATION FOR SEQ ID NO:476:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 389 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:	
GAATTCGCTG TGGAGCTGGG CGTGCTGTTC GTCCGGCCCC GGCCCGGAAC CGGGCTGGGT	60
AGAGTGATGC GGACCCTCCT GCTGGTGCTG TGGCTGGCGA CGCGCGGAAG CGCGCTCTAC	120
TTTCACATCG GAGAGACGGA GAAGAAGTGC TTTATTGAGG AGATCCCGGA CGAGACCATG	180
GTCATAGGAA ACTACCGGAC GCAGCTGTAT GACAAGCAGC GGGAGGAGTA CCAGCCGGCC	240
ACCCCGGGGC TTGGCATGTT TGTGGAGGTG AAGGACCCAG AGGACAAGGT CATCCTGGCC	300
CGGCAGTATG GTTCCGAGGG CAGGTTCACT TTCANTTCCC ATACCCNTGT GTGAGCACCA	360
GATCTGTTTT CANTCCAATT CCACTCGAG	389
(2) INFORMATION FOR SEQ ID NO:477:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 431 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:	
CANDROCCOCC DECARGOCCOE ACANGGANAE ANACCOCCOC AMERICANOS DECARGOS	60
GAATTCGGCC TTCATGGCCT AGAAGGAAAT AAAGGCCCCG ATTTCTGGAG TTCTGAGCCT ACTTTTTTTG GGTGCATTTT GAAACATACG GATTTTACCG CTAGTATATT CAGTGAGGAA	120
GGAAGGCTTC TGAAGGATTG ATGATCCCCA AACTGGATTA TGTGTTCATG ATAATGGTGT	180
ATTTGGTGGC CTAGCATAGT GAGGTGAGGT AGGTCTTTAA AATGGCTCAT TATAAACATC	240

CCTCATCAAT (AGCTCACTTG CCCTTGCATC TCCTGCCAGA GT GCTTGTAGAT TTTAAATTCG GAGGCACACT TG ATCAGGGTTA GCAACTTCAT TTCTGCTNAC GC G	GGAAGACAA	TGGTGGCTGG 360
(2) INFORMA	TION FOR SEQ ID NO:478:		. 431
	GEQUENCE CHARACTERISTICS: (A) LENGTH: 426 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:478	8:	
CCTGAGTTCT (CTGCTTTGTC T ATCAGCATCT T TTTCCATGTG (CTCTGGATTG (TTAATTCATT GGCAACTGTT ACGATGGAAG ACCTGAAGCCCG GGCCATCATG CTTTCCAGAG GCTAGGAATGGC CTATATTTCC TCCCAGATGG GACTGGCATGGT TGGGGATGGT TGGGGACTGT TGGCATCGGAG CATCGTGACC AGCATGGGCT TCCCAGGTTCT CCCAGCTTCT CCCAGCTTCT CCCAGCTTCT CCCAGCTTCTC CCTGCCCACC AATCTAACCG TTCCAGCTTCTC CCTGCCCACC AATCTAACCG	CTTGCCTT CCTGTGCT CTTCTGCCT GCTGGGCT AGCATGCC	TGGCTATGGG 120 GCAGGCAGCA 180 TGGAATGTTC 240 CGTCATGGCC 300 ACCCTCTCCC 360
(2) INFORMAT	TION FOR SEQ ID NO:479:		
(i) S	EQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		•
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:479	9:	
NTTGAAATCA T NATACTAAAA T TTTTTCCAGT G NACATTTTAT A	TCATGGCCT AAATTTTCAG GCAGTTTGAA GT TGGGACGTT GATTTTTAAA TTACCTAGAA GC TTCTCCTCT CTCTTTTCTT TACCTCTC TC GCCAGTTCAG ATCTTGGCAA CAGTTGTTTT GA AAAGTAAAGT ATTCAGGAAC TGACAGAACT GG ATGGACAACC TCGAG	AATCCCAA 1 CCCTGAAA 1 AAAAGTAC (TGCTTTATGT 120 ATAATCATTT 180 CTGAACAAAA 240
(2) INFORMAT	CION FOR SEQ ID NO:480:		
(i) S	EQUENCE CHARACTERISTICS: (A) LENGTH: 406 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear		
(ii)	MOLECULE TYPE: cDNA		
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:480	0 :	
GCAAGTAAC A	AGGTTGCAAG AATTGGAGGC AGAGCAACAG CA AGACAAAAGG AAGCTATGAA AGCAGAGGCA GG	GATCCAAG A	AAGAAAGAGA 60 AACAACAATT 120

AGTACGTGAT	ACAGACAAAT TAATGAAGGA AAAACTAGAA GTACAATGTC AAGCTGAAAA GACCTTCAAA AACAAGTGAA AGCTCTAGAA ATAGATGTGG AAGAACAAGT ATAGAGCTGG AACAAGAAAA AAATACTGAA CTAATGGATT TAAGACAGCA	180 240
AAACCAAGCA	TTGGAAAAGC AGTTAGAAAA AATGAGAAAA TTTTTAGATG AGCAAGCCAT CATGAGAGAG ATGTATTCCA ACAGGAAATA CTCGAG	300 360 406
(2) INFORMA	ATION FOR SEQ ID NO:481:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 357 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:481:	
	AAAGAGGCCT AGTCGGTGCC TCATTGGTAT AAATGTTATG TCTGCATGGG	60
	AATTTCTTTC TAAGATTATT TCTCCCCAAA GCTCAGCACT TTTGGAATTT	120
	TCCAAAAATG GAAGCAATTT TATGTAAATG TCTCTTGGAA GCAGTGTTGG	180
	TTGGGTAGCA GAAGCAGTAG TTACAAGGGT AGTGGTGTCT TTTGTGGTGG TGCTGCAGTT GTTCATATTT GGGGTGCAGG AGTAGGAGG GTAGGATCAG	240 300
	TACAGGGAAA AATGGAGGTC CAGGTGGATA GGGTCTAGAA TTCAATC	357
(2) INFORMA	ATION FOR SEQ ID NO:482:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 303 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:482:	
CTGTCAGTGG GAAGAATCTC AAACCTCAAG	AAAGAGGCCT AAGTGACTCC AGAGCCTCCT GCAAGATGCT GTTGATTCTG CCTTGCTGGC CCTGAGCTCA GCTCAGAACT TAAATGAAGA TGTCAGCCAG CCTCCCTAAT AGCAGGAAAT CCACAAGGAG CACCCCCACA AGGAGGCAAC GTCCCCCATC TCCTCCAGGA AAGCCACAAG GACCACCCC ACAAGGAGGC AAGGTCCCCC ACCTCCTCCA GGAAAACCAC AAGGACCACC CCCTATTCTC	60 120 180 240 300 303
(2) INFORM	ATION FOR SEQ ID NO:483:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 469 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: CDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:483:	
	AAAGAGGCCT AAGCAGACAC AATGGTAAGA ATGGTGCCTG TCCTGCTGTC	60
	CTTCTGGGTC CTGCTGTCCC CCAGGAGAAC CAAGATGGTC GTTACTCTCT TACACTGGGC TGTCCAAGCA TGTTGAAGAC GTCCCCGCGT TTCAGGCCCT	120
GWCCINIAIC	INCHCIGGGC IGTCCAAGCA TGITGAAGAC GTCCCCGCGT TTCAGGCCCT	180

TGGCTCACTC	AATCACCTCC	ACTOC TOTAL	7 T7 C1 1 C1 CT		AGTCTCAGCC	
TOUCICACIC	MIGACCICC	AGIICIIIAG	ATACAACAGT	AAAGACAGGA	AGTCTCAGCC	240
CATGGGACTC	TGGAGACAGG	TGGAAGGAAT	GGAGGATTGG	AAGCAGGACA	GCCAACTTCA	300
					ATTACAACGA	360
CAGTAACGGG	TCTCACGTAT	TGCAGGGAAG	GTTTGGTTGT	GAGATCGAGA	ATAACAGAAG	420
CAGCGGAGCA						160

- (2) INFORMATION FOR SEQ ID NO:484:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GAATTCGGCC	AAAGAGGCCT	ACTACTTCTG	TAGTCTCATC	TTGAGTAAAA	GAGAACCCAG	60
CCAACTATGA	AGTTCCTTGT	CTTTGCCTTC	ATCTTGGCTC	TCATGGTTTC	CATGATTGGA	120
GCTGATTCAT	CTGAAGAGTA	TGGGTATGGC	CCTTATCAGC	CAGTTCCAGA	ACAACCACTA	180
TACCCACAAC	CATACCAACC	ACAATACCAA	CCTGCCTCAA	GGTCCTCCAC	CTCCTCCAGG	240
AAAGCCACAA	GGACCACCCC	CACAAGGAGG	CAACAAACCT	CAAGGTCCCC	CACCTCCAGG	300
AAAGCCACAA	CGACCACCCC	CACAAGGAGG	CAGCAAGTCC	CGAAGTTCTC	GATCTCCTCC	. 360
AGGAAAGCCA	CAAGGACCAC	CCCCACAAGG	AGGCAACAAA	CCTCAAGGTC	CCCCACCTCC	420
AGGAAAGCCA				TCCCGAAGTG	CCCGATCTCC	480
TCCAGGAAAG	CCACAAGGAC	CATCCCACAA	CTCGAG			516

- (2) INFORMATION FOR SEQ ID NO:485:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GAATTCGGCC AA	AGAGGCCT	ACTTCACTTC	AGCTTCACTG	ACTTCTTGAC	TCTCCTCTTG	60
AGTAAAAGGA CT	CAGCCAAC	TATGAAGTTT	TTTGTCTTTG	CTTTAGTCTT	GGCTCTCATG	120
ATTTCCATGA TT	AGCGCTGA	TTCACATGAA	AAGAGACATC	ATGGGTATAG	AAGAAAATTC	180
CATGAAAAGC AT	CATTCACA	TCGAGAATTT	CCATTTTATG	GGGACTGTGG	ATCAAATTAT	240
CTATATGACA AT	TGATATCC	TTAGTAATCA	TGGGGCATGA	TTATAGAGGT	TTGACTGGCA	300
AATTCACTTT TA	CTCATTTA	TTCTCATTCA	TCACACCGCA	AGTCTAGGCC	TCTCGAG	357

- (2) INFORMATION FOR SEQ ID NO:486:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

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GGTTACCATC	CTCAAAGGAT	TGGCTAAAAG	CAAGCAACTG	GATTGAACAC	CCTAAGAAGA	60
AAGATTCACA	CTGCACCAGG	AGACATCAGA	AAGAATGAAA	ACTCTGCCGC	TGTTTGTGTG	120
CATCTGTGCA	CTGAGTGCTT	GCTTCTCGTT	CAGTGAAGGT	CGAGAAAGGG	ATCATGAACT	180
ACGTCACAGG	AAGGCATCAT	CACCAATCAC	CCAAATCTCA	CTTTGAATTA	CCACATTATC	240
CTGGACTGCT	AGCTCACCAG	AAGCCGTTCA	TTAGAAAGTC	CTATAAATGT	CTGCACAAAC	300
GCTGTTAGGC	CTAAGCTTCC	ACCTTCACCT	AATAACCCCC	CCAAATTCCC	AAATCCTCAC	360
CAGCCACCTA	AACATCCAGA	TAAAAATAGC	AGTGTGGTCA	ACCCTACCTT	AGTGGCTACA	420
ACCCAAATTC	CATCTGTGAC	TTTCCCATCA	GCTTCCACCA	AAATTACTAC	CCTTCCAAAT	480
GTGACTTTTC	TTCCCCAGAA	TGCCACCACC	ATATCTTCAA	GAGAAAATGT	TAACACAAGC	540
TCTTCTGTAG	CTACATTAGC	ACCCAGTGAA	TTCCCCAGCT	CCACAAGACA	CCACAGCTGC	600
CCCACCCACA	CCTTCTGCAA	CTACACCAGC	TCCACCCCTC	GAG		643

- (2) INFORMATION FOR SEQ ID NO:487:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GAATTCGGCC	AAAGAGGCCT	ACAAGATGCT	GCTGGTCCTG	CTCTCAGTGG	TCCTTCTGGC	60
TCTGAGCTCA	GCTCAGAGCA	CAGATAATGA	TGTGAACTAT	GAAGACTTTA	CTTTCACCAT	120
ACCAGATGTA	GAGGACTCAA	GTCAGAGACC	AGATCAGGGA	CCCCAGAGAC	CTCCTCCTGA	180
AGGACTCCTA	CCTAGACCCC	CTGGTGATAG	TGGTAACCAA	GATGATGGTC	CTCAGCAGAG	240
ACCACCAAAA	CCAGGAGGCC	ATCACCGCCA	TCCTCCCCCA	CCTCCTTTTC	AAAATCAGCA	300
ACGACCACCC	CAACGAGGAC	ACCGTTCATC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:488:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GAATTCGGCC	AAAGAGGCCT	AGACACATTG	CCTTCTGTTT	TCTCCAGCAT	GCGCTTGCTC	60
CAGCTCCTGT	TCAGGGCCAG	CCCTGCCACC	CTGCTCCTGG	TTCTCTGCCT	GCAGTTGGGG.	120
GCCAACAAAG	CTCAGGACAA	CACTCGGAAG	ATCATAATAA	AGAATTTTGA	CATTCCCAAG	180
TCAGTACGTC	CAAATGACGA	AGTCACTGCA	GTGCTTGCAG	TTCAAACAGA	ATTGAAAGAA	240
TGCATGGTGG	TTAAAACTTA	CCTCATTAGC	AGCATCCCTT	CTACAAGGTG	CATTTAACTA	300
TAAGTATAAC	TGCCAACCTC	GAG				323

- (2) INFORMATION FOR SEQ ID NO:489:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:489:
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GAATTCGGCC	AAAGAGGCCT	AGTGACACCA	GAGCCTCCTG	CAAGATGCTT	CTGATTCTGC	6
TGTCAGTGGC	CCTGCTGGCC	TTCAGCTCAG	CTCAGGATTT	AAATGAAGAT	GTCAGCCAGG	120
AAGATGTT						12

- (2) INFORMATION FOR SEQ ID NO:490:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GAATTCGGCC	AAAGAGGCCT	AATTTTGACC	AGCAGATTAA	TCAACTGTAA	GACGGATCCT	60
CACACAAAGA	GGCAACTGAA	AGGATGAAAT	CACTGACTTG	GATCTTGGGC	CTTTGGGCTC	120
TTGCAGCGTG	TTTCACACCT	GGTGAGAGTC	AAAGAGGCCC	CAGGGGACCA	TATCCACCTG	180
GACCGCTGGC	TCCTCCTCAA	CCTTTTGGCC	CAGGATTTGT	TCCACCACCT	CCTCCTCCAC	240
CCTATGGTCC	AGGGAGAATC	CCACCTCCTC	CTCTGCAGAG	AAAACCTTTG	AAGAAAAGCA	300
GGAACAGAGA	TCGATGGCGA	TCTATTTCCC	TGTACTATAC	TGGAGAGAAA	GGTCAAAATC	360
GTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:491:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GGTTTCCCGT	TTGTCCCTCC	TTCAAGGTTT	TTTTCAGCAG	CTGCAGCACC	CGCTGCCCCA	60
CCTATTGCAG	CTGAGCCTGC	TGCAGCTGCA	CCTCTTACAG	CCACACCTGT	AGCAGCTGAG	120
CCTGCTGCAG	GGGCCCCTGT	TGCAGCTGAG	CCTCCTGCAG	AGGCACCTGT	TGGAGCTGAG	180
CCTGCTGCAG	AGGCACCTGT	TGCAGCTGAG	CCTGCTGCAG	AGGCACCTGT	TGGAGTGGAG	240
CCAGCTGCAG	AGGAACCTTC	ACCAGCTGAG	CCTGCTACAG	CCAAGCCTAG	GCCTCT	296

- (2) INFORMATION FOR SEQ ID NO:492:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

CTCGAGTCCT	TGTGGCTTTC	CTGGAGGTGG	GGGACCTTGA	GGTTTGTTGC	CTCCTTGTGG	60
GGGTGGTCCT	TGTGGCTTTC	CTGGAGGAGG	TGAAGGACCT	TGAGGCTGGT	TGCCTCCTTG	120

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TGGGGGTGGT	CCTTGTGGCT	TTCCTGGAGG	AGATCGGGGA	CTTCGGGGAC	TTGTCTCCTT	180
GTGGGGGTGG	TCCTTGTGGC	TTTCCTGGAG	GTGGGGGACC	TTGAGGTTTG	TTGCCTCCTT	240
GTGGGGGTGG	TCCTTGTGGC	TTTCCTGGAG	GAGGTGGGG	ACCTTGAGGC	TGGTTGCCTC	300
CTTGTGGGGG	TGGTCCTTGT	GGCTTTCCTG	GAGGAGATGG	GGGACCTTGA	GGTTTGTTGC	360
CTCCTTGTGG	GGGTGCTCCT	TGTGGATTTC	CTGCTATTAG	GGAGGGAGAT	TCTTCCTGGC	420
TGACATCTTC	ATTTAAGTTC	TGAGCTGAGC	TCAGGGCCAG	CAGGGCCACT	GACAGCAGAA	480
TCAACAGCAT	CTTGCAGGAG	GCTCTGGAGT	CACTTAGGCC	TCTTTGGCCG	AATTC	535

- (2) INFORMATION FOR SEQ ID NO:493:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GAATTCGGCC	AAAGAGGCCT	AGTCGGTAAT	CACAACAAAC	ACGGAGCAAT	CTCAATGCTG	60
TTTATCCGGA	${\tt GGACAGTCTG}$	CGGGGTCGTG	ACGATTCTTT	TCTTCTTGAA	GTTTTTCCTT	120
TTCCTGAATC	TCATAATGAT	TCTTGGCCAT	GATTCTGTCT	TTTCAATGAC	TGTGGCTTCT	180
ACTCGAACAA	GATCCTTTCC	GAGGAGTGGC	TTGCCAAGCA	GCGTGAAGTT	GTCTGCCCCA	240
ACCAGCAGGA	CCTTCTCCAG	TCGAATTCTC	TCTCCACACG	CAAGGTCTAG	TTCATTTCCA	300
ATTAAGATCA	GGTCTTCAGA	G				321

- (2) INFORMATION FOR SEQ ID NO:494:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GAATTCGGCC	AAAGAGGCCT	AACCTGCCTT	GGTTCTTGCT	CCTCTTTCCA	CGTTGGATAA	60
CAATTTTTTG	GTTGTTTTGT	TTAAGTTGGT	GCTCTGAAGC	TTAATCTCAG	TACCCTTTAC	120
TCTGAATTGT	CAAATTTTGA	TAAAACGTGC	CATTTTCTTT	GGTAAGAGAA	AGCAGGTCTT	180
AATGTCTGCC	AGAACACAAT	TTATATGCCT	TATTGGCTTC	ATTAAACTTT	TAGAAAACTT	240
TAGCATTTGT	TACTTTTTTC	CATTGCATTT	ACTTTCAAAT	GCACCTAATG	AATTCGTCAC	300
CCAGTCGCAA	CTTTTCCCTT	CTCTGTCCCA	TTGCTTTCTC	CTTTCCCCAA	CGCAGCTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:495:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

GAATTCGGCC AAAGAGGCCT AAAGCGACCA AGATAAAAGT GGACAGAAGA ATAAGCGAGA

CTTTTTATCC ATGAAACAGT CTCCTGCCCT CGCTCCGGAA GAGCGCTACC GCAAAGCCGG

60

120

•	GTCCCCAAAG CCGGTCTTGA GAGCTGATGA CAATAACATG GGCAATGGCT GCTCTCAGAA GCTGGCGACT GCTAACCTCC TCCGGTTCCT ATTGCTGGTC CTGATTCCAT GTATCTGTGC TCTCGTTCTC TTGCTGGTGA TCCTGCTTTC CTATGTTGGA ACATTACAAA AGGTCTATTT TAAATCAAAT GGGAGTGAAC CTTTGGTCAC TGATGGTGAA ATCCAAGGGT CCGATGTTAT TCTTACAAAT ACAATTTATA ACCAGAGCAC TGTGGTGTCT ACTGCACATC CCGACCAACT AGGCCTCTTT GGCCG	180 240 300 360 420 435
	(2) INFORMATION FOR SEQ ID NO:496:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 122 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:	
	GAATTCGGCC AAAGAGGCCT AGAAATATAT TTTCTAGTGA ATTCTTATTG GAAGCCAGGT CTCTCCTCTC	60 120 122
	(2) INFORMATION FOR SEQ ID NO:497:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:	
	GAATTCGGCC AAAGAGGCCT AAGAAAATCA GCCTGTCTGC TCTCTCCTTG GCTCAACAAG GCCTCTAACA GTCTTCTGCC CTCTATTCTG CACACGGCAT ATTTGGGAAC GAGAAACAAA AGTTTTCCCA AATGAAGAGA ACTCACTTGT TTATTGTGGG GATTTATTTT CTGTCCTCTT GCAGGGCAGA AGAGGGCCT AATTTCCCCA CATATGATGG GAAGGACCGA GTGGTAAGTC TTTCCGAGAA GACCCTCGAG	60 120 180 240 260
	(2) INFORMATION FOR SEQ ID NO:498:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:	
	GAAAGAGGCC TACCAACATG CCAGAGGCCG TACCCATATC CGCAGCAG	48
	(2) INFORMATION FOR SEQ ID NO:499:	

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 276 base pairs

 (B) TYPE: nucleic acid

 (C) STRANDEDNESS: double

 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

GAATTCGGCC	TTCATGGCCT	ACCCTGTCAA	AATTTTGCCT	CCTCTTGATT	TTCAATATAT	60
ATATATTTT	TTGTCTTACT	CTGTTGCCCA	GGCTAGAGTG	CAGTGACGTG	ACCTTGGCTC	120
ACTGCAACCT	CTGCCTCCTG	GGCTCAAGCA	ATCCTCCCAC	CTCAGCCTCC	TCAGTAGCTG	180
GGACCACAGG	CATATGCTAC	AAAGCCCAGA	TTATTTTTTT	ATAGAAACAG	GGTTTCACCA	240
TGTTGCCCAG	GCTTGTCTCG	AACCCCAGAA	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:500:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

GAATTCGGCC	TTCATGGCCT	ACAAATGCCC	ATCAAAGACT	GGATAAAGAA	AATGTAGTAT	60
ATATATATAT	ACCATGGAAT	ACTGTGCAGC	CATAAAAAAG	GAATGAGATC	ATGTGTTTCA	120
CAGGGATGTG	GATGAAGCTG	GAAGCCATCA	TCCCCAGCAG	ACTAACACAG	GAACAGAAAA	180
CCAAACACTG	CATGTTCTCA	CTCATAAGTG	GGAGCTGAAC	AATGAGAACA	GGTGGGCACA	240
GGGACGGGAA	CAACACACAC	CAGGGCCTGT	TGTGTGGTGG	GGGTGAGGGT	TGGAACTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:501:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

GCGAGGCAGG	GAAACTCACT	TCACGTCTCT	TTCCTTGTAG	AGCATCATGC	TTATTTCTGG	60
CTCACTCACA	TCTTTGTCTC	GGGAGTTCTC	TGCCGAGCCA	TTGCCCCCTA	CAGCAGAGAG	120
CACAGCTGGC	TGCACTAGTG	CTGAAGGAGC	CAGCCCCAGA	GCAGGGCATT	TCCAGGGGCT	180
CTTGTCCCAG	AGCGGCAGGC	GTTGTGTGCA	GAGAACGCCC	CTCCCACGCA	GCACAGAGAA	240
CGCGGGGTGG	GTGTGTGGCT	CCGGGCCTGT	GGGGCTTAGG	CTGCCTGAAC	CACCGCCGAC	300
TGGCACCATG	ACTCGGCATT	CCTGGAAGTG	CCTTACCAAG	TTGTTGTTGT	TGTTTTGTTG	360
TTTTTTAAGA	GACGGGCTTG	CTCTATCATC	CAGGCTCGAG			400

(2) INFORMATION FOR SEQ ID NO:502:

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(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 286 base pairs

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:	
GAGATAAACA AAATTGATTG CCCCATTCTC TCACTTCCCC ATCTTGTCTT CCTAGACCCC	60
ACAGAGTTAA AACTTGGGAT TCCCCTGGCC CCCCCAGAAC ACTTGTATAT TGTTTGTTTG	120
AGGTTCGTGC CGCAGTAACA GACACAGTAT TTAATTGCAC ATACAGATGT TTGCTGGGTA	180
TATTCACTGT AAATTTTATT TAATCTGTTT TTTTGTTTGT TTGGGGGGTTA TTTGGGGGGA GGTTGGTTTT GTTTTTAAAT ATAAAAAAA AAATCTGTCA CTCGAG	240
TOTAL TOTAL TOTAL TOTAL TOTAL CICARO	286
(2) INFORMATION FOR SEQ ID NO:503:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 279 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:	
(1000m01 CCP, T) (1000) (1)	
GGCCTCACCT TACCCCAGGA CTCCGCTATG ACACCGCCTC TGCCCCTACA AGACACAGAT CTCTCGTCAG CCTCAAAGCC TGTGGCTGCA GCCACGCCTG TGTCCCAGCA GGCTGAAGAG	60
GGCCTCACCT TACCCCAGGA CTCCGCTATG ACAGCACTC TGCCTCTGCA AGACACAGGC	120
CCCACCTCAG GTCCAGAGCC TCTGGCTGTG GCCACCCCTC AAACCTTGCA GGCAGAAGCA	180 240
GGCTGTGCCC CAGGGACAGA GCCTGTGGCC ATACTCGAG	279
(2) INFORMATION FOR SEQ ID NO:504:	
(i) apouring any account	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 306 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
4.40.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:	
G0117G001G G117F00111 F1-F1-F1	
GCAATGGCAG GAATTCGAAA TATTGGCATA TGGTTCTTTT GGATTAGATT ATATAAAATC AGAAGAGGTA GAACCAGGCC CCAAGCACTC CTTTTTCTCT GCATGATACT TCTGCTTATT	60
GTCCTTCACA CTAGCTACAT GATTTATAGT CTTGCTCCCC AATATGTTAT GTATGGAAGC	120
CAAAATTACT TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCTT	180 240
TCTGTGCCAA AGAGATGTGA TGCAGAAGCT CCTGAAGATC AGTGTACTGT TACCCGGACG	300
CTCGAG	306
(2) INFORMATION FOR SEQ ID NO:505:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 361 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GAATTCGGCC TTCATGGCCT	AAGGAGAATG	GCGTGCACCC	GGGAGGCGGA	GCTTGCAGTG	60
AGCCAACATC ACGCCACTGC	ACTCCAGCCC	GGGCGACTGA	GCGAGACTCT	CTCTCNAAAA	120
AAAAAAAAA AAAGAAAAAG	AAAAAGAAAA	AGAAAAAGAA	AAGAAAATAT	ATANATACAC	180
ACAGAGAGTG AGAGAGAGAG	AGAGAGAGAG	ACCAGAAAAA	GAGAGAAGGA	GAAAGAGAGA	240
ATGCAAAAAC CAAGAGGANA	GÀATGATCCA	CTCTCCAACT	AGAAAGGTAG	CTCTCAATCT	300
GAAAAGTCAC TTGATTACTT	TGTCTATTTT	GCTTATCTGC	TACATCAATG	GTTCCCTCGA	360
G					361

- (2) INFORMATION FOR SEQ ID NO:506:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GAATTCGGCC	TTCATGGCCT	AGGCCTTTTC	TTTTTAAAGG	AATTCAAGCA	GGATACGTTT	60
TTCTGTTGGG	CATTGACTAG	ATTGTTTGCA	AAAGTTTCGC	ATCAAAAACA	ACAACAACAA	120
AAAACCAAAC	AACTCTCCTT	GATCTATACT	TTGAGAATTG	TTGATTTCTT	TTTTTTATTC	180
TGACTTTTAA	AAACAACTTT	TTTTTCCACT	TTTTTAAAAA	ATGCACTACT	GTGTGCTGAG	240
CGCTTTTCTG	ATCCTGCATC	TGGTCACGGT	CGCGCTCAGC	CTGTCTACCC	GCAGCACACT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:507:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GGGGCTGCGG	GGATTGACCT	CCTCACTTCT	GGGTTGCCAC	TCGAAGCTTG	CTCCGGGCAA	60
CGACCCTGCT	GCTTCCCAGA	GGGAAACTGT	AGCCCACAGA	CCAGGAGAGA	AGCCAAAGCA	120
CCTGCTCCAC	GTCCACATCA	CCCCAGGCTT.	CTAGCCCCCA	GGGGCTTCAT	CAGTGCTTCA	180
GCGCTCTCTC	CCATCCCCCA	CTCCCCATGT	CCCTCGTGAT	CCGAACTCCT	AGGGCTCCGT	240
GTCCCACAGG	TCACCACTTC	CGGCTGTCTC	GAG			273

- (2) INFORMATION FOR SEQ ID NO:508:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GAATTCGGCC TTCATGGCCT ACA	ATCAATAA AATACATTCT	ACACAGAATA	CGCCAACCAT	60
ACACTACTCT TTTTTGATAA TAA	VAAAATGT ATTTACTGAG	CCAGTTGTGG	TGGCTCGCGC	120
CTATAATCCC AGCACCTTGG AAC	GCCAATG GGAGTGGATC	GGTTGAGGCC	AGGAGTTTGA	180
GACCGGCCTG GCCAACATGG TGG	SAATGCCG TCTCTACTGA	GAATGCAGAA	ATGAGCCGGG	240
CACGGTGGCA CGCACCTGTA GTC				287

- (2) INFORMATION FOR SEQ ID NO:509:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

AAGAGGCGAT GCCGGCGATG GCATCTCTCG GCGCCCTGGC GCTGCTCCTG CTGTCCAGCC	60
TCTCCCGCTG CTCAGCCGAG GCCTGCCTGG AGCCCCAGAT CACCCCTTCC TACTACACCA	120
CTTCTGACGC TGTCATTTCC ACTGAGACCG TCTTCATTGT GGAGATCTCC CTGACATGCA	180
AGAACAGGGT CCAGAACATG GCTCTCTATG CTGACGTCGG TGGAAAACAA TTCCCTTGTC	240
CACTCGAG	248

- (2) INFORMATION FOR SEQ ID NO:510:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

GGCGATGATT AGGCCAGACC	CTCCCCATCC	TCGTGAGGGC	CAGAAGCTGT	TGCTACACTG	60
TGAGGGTCGC GGCAATCCAG	TCCCCCAGCA	GTACCTATGG	GAGAAGGAGG	GCAGTGTGCC	120
ACCCCTGAAG ATGACCCAGG	AGAGTGCCCT	GATCTTCCCT	TTCCTCAACA	AGAGTGACAG	180
TGGCACCTAC GGCTGCACAG	CCACCAGCAA	CATGGGCAGC	TACAAGGCCT	ACTACACCCT	240
CAATGTTAAT GACCCCAGTC	CGGTGCCCTC	CTCCTCCAGC	ACCTACCACG	CCATCATCGG	300
TGGGATCGTG GCTTTCATTG	TCTTCCTGCT	GCTCATCATG	CTCATCTTCC	TCGGCCACTA	360
CTTGATCCGG CACAAAGGAA					397

- (2) INFORMATION FOR SEQ ID NO:511:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

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GCCTGCCTCC AGGCCTTTGC TCCCACTGTT GCCTCCACTT AGAATAACAT TCCACCCCAT CTCTATAAAT ATCCTACAGA CAAATACTAC CTTCCCCTTA AGGCCAGTTC TAACCCTAAC	60 120
TGACAACAAA TCATCTCTAC ATGATCTTTT CCTTCTGGGA ATGCCTGCAG CACTGTTTAA	180
TCCTGCCCCA CCACCATCCC CTCACCCAGC ACCCTCTCCC AGACCAGACA GGGTGGCTCA TGCCTGCAAT CCCAGCACCT TGGGAGGCTG AGGCAGGAGG ATTGCTCGAG	240 290
TGCCTGCAAT CCCAGCACCT TGGGAGGCTG AGGCAGGAGG ATTGCTCGAG	290
(2) INFORMATION FOR SEQ ID NO:512:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 304 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) Torollog1. Tilleg1	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:	
GAATTCGGCC TTCATGGCCT ACTATGCCGT CATGATAGAG AAGATGATCC TGAGAGACCT	60
GGGCCGTTC ATGTTTGTCT ACGTCGTCTT CTTGTTCGGG TTTTCCACAG CGGTGGTGAC	120
GCTGATTGAA GACGGGAAGA ATGACTCCCT GCCGTCTGAG TCCACGTCGC ACAGGTGGCG	180
GGGGCCTGCC TGCAGGCCCC CCGATAGCTC CTACAACAGC CTGTACTCCA CCTGCCTGGA	240
GCTGTTCAAG TTCACCATCG GCATGGGCGA CCTGGAGTTC ACTGAGAACC ATGAACTTCT	300
CGAG -	304
(2) INFORMATION FOR SEQ ID NO:513:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 314 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:	
GAATTCGGCC TTCATGGCCT AGGAACCTGG ACCGCGGCGG CGCCGGGTTT CCCTCATGAT	60
CCCGGGCGGG CGGCGGCGC GGCAGAGGCG GCGGGAGGAT GACCTCTTAC CGGGAGCGGA	120
GTGCCGACCT GGCCCGTTTC TACACTGTCA CCGAGCCCCA GCGACACCCG AGGGGCTACA	180
CAGTATATAA GGTCACCGCC CGGGTTGTTT CACGAAGAAA TCCAGAGGAT GTCCAGGAGG	240
GAGAATCCTG AACCAACCTA TCCATGAACA TACTCTCTGC CATTTTCTTA GTCCTTTTTT	300
CGGAAAAACT CGAG	314
(2) INFORMATION FOR SEQ ID NO:514:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 529 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:	
GAATTCGGCC TTCATGGCCT ACGAACTTAA GAAAATGAGA CTGAGCAATC TCATGGTTCT TGGACAGTTA GTCTATGGCC AATTGATGGA ACCAGTAAAT CGAGAGAACT TTACGCAGAC	60 120

180

CTTGCCCAAA ATGCCAATTC ATTCTCATGC ACAGCCCCCA GATGCCAGGG AAGAGGATAT

CATACTTGAA	GGTCAACAGA	GCCTGCCATC	CCAGGCTTCA	GATTGGAGCC	GATACTCAAG	240
					TAATGACTCC	300
	GAACTTCAAG					360
	CATCCCAGAG					420
					ACACCAGTCT	480
GGACTCTGGG	GTGGACATGA	ATGAGCTTCA	CTCAAGTAGA	AAGCTCGAG		529

- (2) INFORMATION FOR SEQ ID NO:515:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GGAGATGAAA	GTTAAAAGTG	AAAACCTTAA	AGAGGAGCCT	CAGTCTTCTG	AAGAAGAATC	60
TATGTCTTCT	GTGGAAACCA	GGACACTAAT	AAAATCTGAG	CCTGTAAGTC	CAAAGAATGG	120
	CAGGCTACTG					180
CATGGTTGCA	GCCAGAACAG	AACCCCTAAC	TCCAAACCCA	GCTTCTAAGA	AACCAAGAGT	240
	${\tt GGATCAGAAT}$					300
TTCTTCCAGA	TCATCTTCTT	CCTCATCATC	CTCTTCTTGT	CCCACTCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:516:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GTCTACACCN	TTCCGAGTTG	GCTGCAGATT	TGTGGTGCGT	TCTGAGCCGT	CTGTCCTGCG	60
CCAAGATGCT	TCAAAGTATT	ATTAAAAACA	TATGGATCCC	CATGAAGCCC	TACTACACCA	120
AAGTTTACCA	GGAGATTTGG	ATAGGAATGG	GGCTGATGGG	CTTCATCGTT	TATAAAATCC	180
GGGCTGCTGA	TAAAAGAAGT	AAGGCTTTGA	AAGCTTCAGC	GCCTGCTCCT	GGTCATCACT	240
AACCAGATTT	ACTTGGAGTA	CATGTGAAAG	AAAACGTCAG	TCTGCCTGTA	AATTTCAGCA	300
AGCCGTGTTA	GATGGGGAGC	GTGGAACGTC	ACTGTACACT	TGTATAAGTA	CCGTTTACTT	360
CATGGCATGA	ATAAATGGAT	CTGTGAGATG	CACTGCTACC	TGGTACTGCT	TTCAGTGTGT	420
TCCCCCTCAG	CCCCTCCGGC	GTGTCAGGCA	TACTCTGAGT	AGATAATTTG	TCATGCAGCG	480
CATGCAATCA	GAATCTCGAG					500

- (2) INFORMATION FOR SEQ ID NO:517:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GAATTCGGCC	TTCATGGCCT	AGATGCTCAA	CACCTCCTCC	TTGGTGGAGC	AGCTGAACGA	60
GCAGTTTAAC	TGGGTGTCCC	GGCTGGCAAA	CCTCACGCAA	GGCGAACACC	AGTACTATCT	120
${\tt GCGGGTCACC}$	ACGGTGGCTT	CCCACACTTC	TGACTCGGAC	${\tt GTTCCTTCCG}$	GTGTCACTGA	180
${\tt GGTGGTCGTG}$	AAGCTCTTTG	ACTCTGATCC	CATCACTGTG	ACGGTCCCTG	TAGAAGTCTC	240
CAGGAAGAAC	CCTAAATTTA	TGGAGACCGT	GGCGGAGAAA	GCNCTGCAGG	AATACCGCAA	300
AAAGCACCGG	GAGGAGTGAG	ATGTGGATGT	TGCTTTTGCA	CCTACGGGGG	CATCTGAGTC	360
CAGCTCCCCC	CAAGATGAGC	TGCAGCCCCC	CAGAGAGAGC	TCTGCACGTC	ACCAAGTAAC	420
TCTCGAG	•					427

- (2) INFORMATION FOR SEQ ID NO:518:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GAATTCGGCC	TTCATGGCCT	AATCTTAAGG	GACCTTTCCT	TACTACAGAT	TCAAATGCGA	60
GATCTTGAGG	GTTACAGGGA	AACGAGGTAT	CAGTTACTTC	AGCTTCGACC	TGCGCAGAGA	120
GCATCATGGA	TTGGTTATGC	TATTGCTTAC	CATTTATTAG	AAGATTATGA	AATGGCAGCA	180
AAGATTTTAG	AAGAATTTAG	GAAAACACAA	CAGACATCCC	CTGACAAGGT	GGATTATGAA	240
TATAGTGAAC	TACTCTTATA	TCAGAATCAA	GTTCTTCGGG	AAGCAGGTCT	CTATAGAGAA	300
GCTTTGGAAC	ATCTTTGTAC	CTATGAAAAG	CAGATTTGTG	ATAAACTTGC	TGTAGAAGAA	360
ACCAAAGGGG	AACTTCTGTT	GCAACTATGT	CGTTTGGAA			399

- (2) INFORMATION FOR SEQ ID NO:519:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GAATTCGGCC	TTCATGGCCT	ACTTATCTTA	ATCCAATGGG	TGACATCTTC	AACAACCCTG	60
TTCCAAATAA	GGCTGCATTC	TAAACACTAG	GGATTAAGAC	ATCAACATGT	GAATTTTGGA	120
GGAATGTAGT	TCTAACCATA	ACAGCAGTGA	ATGAGATGAC	AGACTATTGC	TCTCAAAAGA	180
TAGCCAGGTT	TCTAGTTTCC	TTAGGCATTT	TCTGGAGGTT	TGCGAGCAGT	TCATTATTAT	240
CTTAAAAATA	TTATCCAGAG	CTGTGGTCTA	TCAGCAGCTC	ATTACCAGAC	TGGCAGATAC	300
ATTTAATCAG	CAAAAGAGTT	GTTCCTGTGA	TTAGCATCCT	CCTGGTTTCC	CAGCTCAAGA	360
GTTCTTCTGA	GTAATAGTAA	TCCTTCCCCC	ATGCTCGAG			399

- (2) INFORMATION FOR SEQ ID NO:520:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

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CAGAAAGGAG GCGAATAGTT ATAAAAACTC	TGACTTTTGA GAGAGGACAC AAAATTATCA TCAGCTCCAG TCGGAGAATC AAGAGGTAAG AGTGTGAGAG ATTGCATCTG CCATGTTGTT CAGATCCTGG CCCTCCTCAC ACAGGTCACT TACTCACTTG TTTCCCAATT CTTTGTTGTG TGTCCATAAT AGGCCAGATG TTCCCACCCT GCAGTATCTC ACCCTTCAGG CACCTTCCTC CACATCCCTC GAG	120 180 240 273
(2) INFORM	MATION FOR SEQ ID NO:521:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:521:	
TGAGTCTAAG ATGATTATGA GTAACTGCCC TACCAATGGT	TTAACGAAAG CAGTGTCAAG ACAGTAAGGA TTCAAACCAT TTGCCAAAAA TGCATTTACT CTCTTCCTGG CATTGATTGG TGGTACCAGT GGCCACTACT TTTTCCCCTA TCAATTTATG GGCAATCATC ACCAAACTGT GCACCAGAAT TGAAAGCTAC CCAAGTGCCA TGTACTGTGA TGAGCTGAAA TTGAAAAGTG GCCTCCTGGA ATCAAGTATC TTTACCTTAG GAATAACCAG ATTGACCATA GGCCGCACTC GAG	60 120 180 240 300 323
(2) INFORM	ATION FOR SEQ ID NO:522:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 274 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:522:	
ACACAGATAC ICAACAGAAA ATTTGTCGCA GGTTGAAGGA	GAGAAAGCCA AGGAAGACAA GGGCAAACAA AAGTTGAGGC AGCTTCACAC GGAGAACCAG AAGTGCCAGA GTCAGCATTC TGGAAGAAAA TCATAGCATA CTTCTAAACT ATTTGCTCG CAACTTTTAC AACATGAGAA TGTTAGCCTT TTTGCTATCA ATTTCATCTT GCTCTTTTAT AAGGTCTCCA CTTCTTCTGT AAGGAGCTCC CCACGAGGCT CGAG	60 120 180 240 274
(2) INFORMA	ATION FOR SEQ ID NO:523:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:523:	
CTCCTGCTAA	AGATCCAGGA CTGAGATCCC AGAACCATGA ACCTGGCCAT CAGCATCGCT CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG TGACCAGCCT AACGGCCTGC AGAGCCTTCG TCTGGACTGC CGCCATGAGA ATACCAGCAG TTCACCCATC	60 120 180

CAGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCACG TGCTCTTTGG CACTGTGGGG GTGCCTGAGC ACACATACCG CTCCCTCCTC GAG	240 273
(2) INFORMATION FOR SEQ ID NO:524:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 456 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:	
GAATTCGGCC TTCATGGCCT ACTCTCCTAT AAAGCAGACG CCGCGCCGCG	60 120 180 240 300 360 420 456
(2) INFORMATION FOR SEQ ID NO:525:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 452 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:	
GAATTCGGCC TTCATGGCCT AATGGGACAA CTCCTCGCCC TCTACCTGTC CCCTCCCCT TTGGTTGTAT GATTTCTTC TTTTTTAAGA ACCCCTGGAA GCAGCGCCTC CTTCAGGGTT GGCTGGGAGC TCGGCCCATC CACCTCTTGG GGTACCTGCC TCTCTCTCTC CTGTGGTGTC CCTTCCCTCT CCCATGTGCT CGGTGTTCAG TGGTGTATAT TTCTTCTCCC AGACATGGGG CACACGCCCC AAGGGACATG ATCCTCTCCT TAGTCTTAGC TCATGGGGCT CTTTATAAGG AGTTGGGGGG TAGAGGCAGG AAATGGGAAC CGAGCTGAAG CAGAGGCTGA GTTAGGGGGC TAGAGGACAG TGCTCCTGGC CACCCAGCCT CTGCTGAGAA CCATTCCTGG GATTAGAGCT GCCTTTCCCA GGGAAAAAGT GTCCGACTCG AG	60 120 180 240 300 360 420 452
(2) INFORMATION FOR SEQ ID NO:526:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 366 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:	
GCGATTGAAT TCTAGACCAG ACTCGTCTCA GGCCAGTTGC AGCCTTCTCA GCCAAACGCC GACCAAGGAA AACTCACTAC CATGAGAATT GCAGTGATTT GCTTTTGCCT CCTAGGCATC	60 120

ACCTGTGCCA TACCAGTTAA ACAGGCTGAT TCTGGAAGTT CTGAGGAAAA GCAGCTTTA	AC 180
AACAAATACC CAGATGCTGT GGCCACATGG CTAAACCCTG ACCCATCTCA GAAGCAGAI	AT 240
CTCCTAGCCC CACAGACCCT TCCAAGTAAG TCCAACGAAA GCCATGACCA CATGGATGA	AT 300
ATGGATGATG AAGATGATGA TGACCATGTG GACAGCCAGG ACTCCATTGA CTCGAATCO	A 360
CTCGAG	366

- (2) INFORMATION FOR SEQ ID NO:527:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

CCCCAGTCC	AGATCCAGGA	CTGAGATCCC	AGAACCATGA	ACCTCCCCAT	CACCATCCCT	60
						60
TCCTGCTAA	CAGTCTTGCA	GGTCTCCCGA	GGGCAGAAGG	TGACCAGCCT	AACGGCCTGC	120
TAGTGGACC	AGAGCCTTCG	TCTGGACTGC	CCCCATCAGA	ATACCACCAC	TTC A CCC A TC	180
		reredictor	COCCATONON	ATACCAGCAG	TICACCCATC	180
AGTACGAGT	TCAGCCTGAC	CCGTGAGACA	AAGAAGCACG	TGCTCTTTGG	CACTGTGGGG	240
						300
TCTACTTAT	CCGCCTTCAC	TAGCAAGGAC	GAGGGCACCT	ACACGTGTGC	ACTCCACCAC	360
					,,createate	500
CIGGCCATT	CCCCACCCAT	CTCCTCCCAG	AACGTTACAG	TGCTCGAG		408
	TCCTGCTAA TAGTGGACC AGTACGAGT TGCCTGAGC TCTACTTAT	TCCTGCTAA CAGTCTTGCA TAGTGGACC AGAGCCTTCG AGTACGAGT TCAGCCTGAC TGCCTGAGC ACACATACCG TCTACTTAT CCGCCTTCAC	TCCTGCTAA CAGTCTTGCA GGTCTCCCGA TAGTGGACC AGAGCCTTCG TCTGGACTGC AGTACGAGT TCAGCCTGAC CCGTGAGACA TGCCTGAGC ACACATACCG CTCCCGAACC TCTACTTAT CCGCCTTCAC TAGCAAGGAC	TCCTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG TAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA AGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCACG TGCCTGAGC ACACATACCG CTCCCGAACC AACTTCACCA TCTACTTAT CCGCCTTCAC TAGCAAGGAC GAGGGCACCT	TCCTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG TGACCAGCCT TAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA ATACCAGCAG AGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCACG TGCTCTTTGG TGCCTGAGC ACACATACCG CTCCCGAACC AACTTCACCA GCAAATACAA	CCCCAGTCC AGATCCAGGA CTGAGATCCC AGAACCATGA ACCTGGCCAT CAGCATCGCT TCCTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG TGACCAGCCT AACGGCCTGC TAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA ATACCAGCAG TTCACCCATC AGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCACG TGCTCTTTGG CACTGTGGGG TGCCTGAGC ACACATACCG CTCCCGAACC AACTTCACCA GCAAATACAA CATGAAGGTC TCTACTTAT CCGCCTTCAC TAGCAAGGAC GAGGGCACCT ACACGTGTGC ACTCCACCAC CTGGCCATT CCCCACCCAT CTCCTCCCAG AACGTTACAG TGCTCGAG

- (2) INFORMATION FOR SEQ ID NO:528:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GTAGGTCACA	GCAGAAGCAG	CCAAAATGGA	TCCCCAGTGC	ACTATGGGAC	TGAGTAACAT	60
TCTCTTTGTG	ATGGCCTTCC	TGCTCTCTGG	TGCTGCTCCT	CTGAAGATTC	AAGCTTATTT	120
CAATGAGACT	GCAGACCTGC	CATGCCAATT	TGCAAACTCT	CAAAACCAAA	GCCTGAGTGA	180
GCTAGTAGTA	TTTTGGCAGG	ACCAGGAAAA	CTTGGTTCTG	AATGAGGTAT	ACTTAGGCAA	240
AGAGAAATTT	GACAGTGTTC	ATTCCAAGTA	TATGGGCCGC	ACAAGTTTTG	ATTCGGACAG	300
TTGGACCCTG	AGACTTCACA	ATCTTCAGAT	CAAGGACAAG	GGCTTGTATC	AATGTATCAT	360
CCATCACAAA	AAGCCCACAG	GAATGATTCG	CATCCACCTC	GAG		403

- (2) INFORMATION FOR SEQ ID NO:529:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

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GAATTCCTCT TCTTTACCCT CGTCCTGCCG GGCACTTTCC TTAGGTTTGG TTTCATCTAC

259

AGCTTCTATG	TTCTCTTCAG	CTTGGCTGCT	CTCCCCAGTC	TCCGTTGGAG	GCTGGGCTGT	120
TGCCTTGGCA	GCAGCATCCT	CTGCGGCAGG	${\tt GGTGGTGGCA}$	GCAGCAGCAG	TGACAGCAGC	180
AGGCACATCG	GCTTGTTTAG	GCTCCTCCTT	GGCTGGGGCA	TCTTCAGCCT	TGGAGGACGG	240
CGAGTTATCA	GTGGAAGCTT	TAGTGGCACT	TTCTGTCTCA	GCTGAGCCGG	CCTTCTCCTC	300
TGAGGATGCA	GGAGCCTGGG	${\tt GGGCTACCTG}$	CTCTGTGGCA	GCATCACCCT	CCCCCTTTTT	360
CTCCTCGGAA	GGAGTTTCTC	CTGCTTTGCC	GGGCTCATCA	GGCTTGGAGC	CAGTGGCTGG	420
GGCTGCTTCG	${\tt GCAGTAGTGG}$	TGCCTTCTCC	CTTCTTCTCC	ACCCCATCGC	TCGAG	475

- (2) INFORMATION FOR SEQ ID NO:530:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GTGCTGGCGG	ACATGGACGT	GGTGAATCAG	CTGGTGGCTG	GGGGTCAGTT	CCGGGTGGTC	60
AAGGAGCCCC	TCGGCTTTGT	${\tt GAAGGTGCTG}$	CAATGGGTCT	TCGCCATCTT	CGCCTTTGCC	120
ACATGCGGCA	GCTACAGTGG	GGAGCTCCAG	CTGAGCGTGG	ATTGTGCCAA	CAAGACCGAG	180
AGTGACCTCA	GCATCGAGGT	CGAGTTCGAG	TACCCCTTCA	GGCTGCACCA	AGTGTACTTT	240
GATGCACCCA	CCTGCCGAGG	GGGCACCACC	AAGGTCTTCT	TAGTTGGGGA	CTACTCCTCG	300
TCAGCCGAAT	TCTTTGTCAC	CGTGGCCGTG	TTTGCCTTCC	TCTACTCCAT	GGGGGCTCTG	360
GCCACCTACA	TCTTCCTGCA	GAACAAGTAC	CGAGAGAATA	ACAAAGGGCC	CATGCTGGAC	420
TTTCTGGCCA	CGGCTGTGTT	CGCCTTCATG	TGGCTAGTTA	GCTCATCGGC	ATGGGCCAAG	480
${\tt GGGCTGTCAG}$	ATGTGAAGAT	GGCCACAGAC	CCAGATGAAC	TCGAG		525

- (2) INFORMATION FOR SEQ ID NO:531:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

GCAAACAGAC AAGGCTTACA GGTTAGTTCA GGATC	TGCGC CTTATCAAGC AAATTGTTTT 60
GCCTATCCAA CCTGCGGTGC CAAACCCATA TACTC	TCCTA TCCTCAATAC CTCCCTCCAC 120
AACCCCTCCA TAACCCATTA TTCGGTTCTG GATCT	CAAAC ATGCTTTCTT TGCTATTCCT 180
TTGCATCCTT CATCCCAGCC TCTCTTTGCT TTCAC	TTGGG CTGGCCCTGA CACCCATCAG 240
CCTCAGCAAC TTACCTGGGC TGTACTGCCA CAAGC	CTTCA CGGACAGCCC CCATTACTTC 300
AGTAGCCCTC GAG	313

- (2) INFORMATION FOR SEQ ID NO:532:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GAGACTATCG	CCTATACTTT	ATTTGGGTAA	ATGGTTTGGT	TAAGGTTGTT	TGGTGGTAGC	60
TGGTTGGGŢT	GCTGGGGCTC	GGTTGTTGTA	GTCGCGATGT	TCTTCTCCGA	GGCCAGAGCC	120
AGGTCGCGGA	CGTGGGAAGC	CAGTCCCTCG	GAACACAGGA	AGTGGGTGGA	AGTATTTAAA	180
GCATGTGATG	AAGATCACAA	AGGATATCTC	AGCAGAGAGG	ACTTTAAAAC	TGCTGTTGTA	240
ATGCTGTTTG	GGTACAAGCC	CTCCAAGATA	GAAGTGGATT	CTGTGATGTC	TTCAATAAAT	300
CCAAATACTT	CTGGTATATT	ACTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:533:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GCCTGCCCCC	ACCTTACAGG	TCTGGGATGT	ACCTTTCCAT	CTGTTGCTGC	TTTCTTCTAT	60
GGGCCCCTGC	CCTCACTCTC	AAGAACCTCA	ACTACTCCGT	GCCGGAGGAG	CAAGGGCCG	120
GCACGGTGAT	CGGGAACATC	GGCAGGGATG	CTCGACTGCA	GCCTGGGCTT	CCGCCTGCAG	180
AGCGCGGCGG	CGGAGGGCGC	${\tt AGCAAGTCGG}$	GTAGCTACCG	GGTGCTGGAG	AACTCCGCAC	240
CGCACCTGCT	GGACGTGGAC	GCAGACAGCG	GGCTCCTCTA	CACCAAGCAG	CGCATCGACC	300
GCGAGTCCCT	GTGCCGCCAC	AATGCCAAGT	GCCAGCTGTC	CCTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:534:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

GGTAGGACCG	GCGAGGAATA	GGAATCATGG	CGGCTGCGCT	GTTCGTGCTG	CTGGGATTCG	60
CGCTGCTGGG	CACCCACGGA	GCCTCCGGGG	CTGCCGGCAC	ATTCTTCACT	ACCGTAGAAG	120
ACCTTGGCTC	CAAGATACTC	CTCACCTGCT	CCTTGAATGA	CAGCGCCACA	GAGGTCACAG	180
GGCACCGCTG	GCTGAAGGGG	GGCGTGGTGC	TGAAGGAGGA	CGCGCTGCCC	GGCCAGAAAA	240
CGGAGTTCAA	GGTGGACTCC	GACGACCAGT	GGGGAGAGTA	CTCCTGCGTC	TTCCTCCCCG	300
AGCCCATGGG	CACGGCCAAC	ATCCAGCTCC	ACGGGCCTCC	CAGAGTGAAG	GCTGTGAAGT	360
CGTCAGAACA	CATCNACGAG	GGGGAGACGG	CCATGCTGGT	CTGCAAGTCA	GAGTCCGTGC	420
CACCTGTCAC	TGACTGGGCC	TGGTACAAGA	TCACTGACTC	TGAGGACAAG	GCCCTCATGA	480
ACGGCTCCGA	GAGCAGAGTT	CTCGAG				506

- (2) INFORMATION FOR SEQ ID NO:535:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

GAATTCCTCT	TCTTTACCCT	CGTCCTGCCG	GGCACTTTCC	TTAGGTTTGG	TTTCATCTAC	60
AGCTTCTATG	TTCTCTTCAG	CTTGGCTGCT	CTCCCCAGTC	TCCGTTGGAG	GCTGGGCTGT	120
TGCCTTGGCA	GCAGCATCCT	CTGCGGCAGG	GGTGGTGGCA	GCAGCAGCAG	TGACAGCAGC	180
AGGCACATCG	GCTTGTTTAG	GCTCCTCCTT	GGCTGGGGCA	TCTTCAGCCT	TGGAGGACGG	240
CGAGTTATCA	GTGGAAGCTT	TAGTGGCACT	TTCTGTCTCA	GCTGAGCCGG	CCTTCTCCTC	300
TGAGGATGCA	GGAGCCTGGG	${\tt GGGCTGCCTG}$	CTCTGTGGCA	GCATCACCCT	CCCCCTTCTT	360
CTCCTCGGAA	GGAGTTTCTC	CTGCTTTGCC	GGGCTCATCA	GGCTTGGAGC	CAGTGGCTGG	420
GGCTGCTTCG	GCAGTAGTGG	TGCCTTCTCC	CTTCTTCTCC	ACCCCATCGC	TCGAG	475

- (2) INFORMATION FOR SEQ ID NO:536:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GAATTCGCCT	TCATGGCCTA	CAAGCTCTAG	CCTAGACCTT	TAGTGTGCCA	TGCAGTCACA	60
GGTCTGAAAA	GCAGCATCAT	CCAAACCTTA	CTTAATCTCT	AAAATCTCAG	CTGGTGGACA	120
GCTCATGATT	AGTTCAGCCC	ACTTCCTCCC	CCTTAGTTGA	GTTTGCAGCA	GGACGCAGGA	180
GATAAGCACT	TCCAAGCAAG	TCTGATTTAT	ATATCAAACT	CGGTCTCCAT	CCCAGGCCAG	240
CTGACCCTCA	GAGCCAGCAA	TGCTCTGTGC	TTCCTCCCTG	CGTCACGGCT	TGGCAAGAGC	300
TGCCTCTGCT	GAGCAGTGTG	TGTGATGGAG	ACGGAGGCCG	CTGAAGGCCG	AGTGCTTGCA	360
${\tt GGCTTGTGAA}$	CTGCCATCGA	ACACAATCCA	AACTCTGGAA	ATGTTCCTGA	CCACCTAAGC	420
CCTCAACAAC	GTAATGCCTG	TATGTGCTNT	TTNTCAGTAA	ACTCCTTGCT	CATGTCNATA	480
AAGTATCCCT	GAACACTCGA	G				501

- (2) INFORMATION FOR SEQ ID NO:537:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

GCGGGCACCA	TTTCCAGTAT	GTACCAAACC	AAAGCCGTCA	TCATTGCAAT	GATCATCACT	60
GCGGTGGTAT	CCATTTCAGT	CACCATCTTC	TGCTTTCAGA	CCAAGGTGGA	CTTCACCTCG	120
TGCACAGGCC	TCTTCTGTGT	CCTGGGAATT	GTGCTCCTGG	TGACTGGGAT	TGTCACTAGC	180
ATTGTGCTCT	ACTTCCAATA	CGTTTACTGG	CTCCACATGC	TCTATGCTGC	TCTGGGGGCC	240
ATTTGTTTCA	CCCTGTTCCT	GGCTTACGAC	ACACAGCTGG	TCCCGGGGAA	CCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:538:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GCTCCACCAG CTACTGAGAA A	ATGGCCTGT	AAAGATCCAG	AAAAACCCAT	GGAGGCCTGT	60
GCCTCAGCAC ATGTGCAACC C					120
AGCCCAGAAA CAGGGGAGAA G	GTAGTAGCA	GGAGAGGTAA	ACCCACCCAA	TGGCCCTGTG	180
GGGGACCCAC TGAGCCTCTT G	TTTGGGGAT	GTGACATCCC	TGAAAAGCTT	TGATTCATTG	240
ACAGGTTGTG GTGACATAAT A	GCAGAACAA	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:539:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GAATTCGGCC	TTCATGGCCT	AGCCAGACAA	CTTGTACTGA	TCTTTCTTTG	CTTTGCCTAC	60
					ACGGATGAAG	120
GTTTCAGTGT	CCCAAGGCCC	CATACCGTAT	CTGATTTTAC	TTTATTTTTG	TTTGTTAAGC	180
CTAACAGCTT	CTGAGGAGCC	ACGTAGAGCT	CAAGAAGCAA	AAGCTACTGA	GAGTAGATGC	240
TATGTAAACT						267

- (2) INFORMATION FOR SEQ ID NO:540:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

GAATTCGGCC TTCATGGCC	ACAAAAAGAT	GCTGGACAAG	GCGTTTGCAG	AGCGGATCAT	60
CCATGACTAC AAGGATATT					120
ACTGCCCTAT TTTGAAGGT	ATTTCTGGCC	CAATGTGTTA	GAAGAGAGCA	TTAAGGAACT	180
AGAACAAGAA GAAGAGGAG					240
GGGCAGTCAG GGCGACAGC	AGAATGCCNA	GAAGAAGAAC	NACNAGAAAA	CCAACAAGAA	300
CAAAAGCAGC ATCAGCCGCC	CCAACAAGAA	GAAGCCCAGC	ATGCCCAACG	TGTCCAATGA	360
CCTGTCCCAG AAACTCGAG					379

- (2) INFORMATION FOR SEQ ID NO:541:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

(A) LENGTH: 295 base pairs

(i) SEQUENCE CHARACTERISTICS:

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:585:	
•		
GAATTCGGCC	TTCATGGCCT AGAGAAACTG AGAGGAAGTT AAAGATTTGT CTTACAAAG	G 60
CTGTGTAGTG	ATAAGACCTA AGGTTTTCTC TGAGATTCAA AATGGGTATT ATTTGTTCT	T 120
	GATTATTCTT TTGGAAAAAA GGGAAGTAGA GGAAAGGAAG TAGAAAAAT	
	TACTTATTAT GTACCAGACA TGGTGCTAAG TTCATTTAAA ACACTGCCT	C 240
ATTTAATCTT	TGCAACCAAT TTATACCCAT ACACATAAGG CCACAAAAGC TCGAG	295
(2) INFORMA	ATION FOR SEQ ID NO:586:	
(i)	SEQUENCE CHARACTERISTICS:	
•	(A) LENGTH: 325 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)) MOLECULE TYPE: cDNA	
(xi)) SEQUENCE DESCRIPTION: SEQ ID NO:586:	
	TTCATGCCTA AGGTAAGGGA AAGTGAGAAG CAGCAGGATA GTCAGCCTC	
	GATGTGCTAG AGATGGTTGA GAATGTCAAA CATGTAATTG CTGACCAGC	
	ACTAATCGAG TTGAAAGTGT AGAACCTTCA GAAAATGAAG CTAGCAAAA	
	GAAATGGAAT TTGAAATTGA GCCAGATAAA GAATGTAAAT CCCTTTCTC	
	; AATGTCAGTG CTTTAGACAT GGAAAAGGAG TCTGAGGAAA AAGAAGAA; ; CCCCAACCAC TCGAG	AA 300 325
(2) INFORM	NATION FOR SEQ ID NO:587:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 272 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)) MOLECULE TYPE: cDNA	
(xi	SEQUENCE DESCRIPTION: SEQ ID NO:587:	
GAATTCGGCC	C TTCATGGCCT ACAAGGACGT TAAAGGCATT TTATTCCAGC GTCTTCTA	GA 60
	TATACAGATG AGGGTGTCCG CTGCTGCTTT CCTTCGGAAT CCAGTGCT	
	I AGCCTGTAGC TTATATTTGA CATTCTTCAC TGTCTGTTGT ATACCTAC	
	A CCGTTCACTT CCCCTTCCAA CTATGTCCAG ATGTGCAGGC TCCTCCTC	
	T CCAAAGGCAC TGGACCCTCG AG	272
(2) INFORM	MATION FOR SEQ ID NO:588:	
(5)	SEQUENCE CHARACTERISTICS:	
(1)	(A) LENGTH: 243 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GAATTCGGCC	TTCATGGCCT	AGCATCCCTG	AAACTGTGTA	ATTTTGAGGA	TCCTTCTGGT	60
CTTAAAGCCA	ATTTAGAAGG	TGCTAATCTG	AAAGGTGTGG	ATATGGAAGG	AAGTCAGATG	120
ACAGGAATTA	ACCTGAGAGT	GGCTACCTTA	AAAAATGCAA	AGTTGAAGAA	CTGTAACCTC	180
AGAGGAGCAA	CTCTGGCAGG	AACTGATTTA	GAGAATTGTG	ATCTGTCTGG	GTGTTAGCTC	240
GAG						243

- (2) INFORMATION FOR SEQ ID NO:589:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAATTCGGCC	TTCATGGCCT	AAATTATACT	CCAAATGTTT	TATCTAAAAT	GCATTTTCTG	60
					GTGTCTTTAC	120
ATCCAAAATG	CAAAGCAGAC	AAATGGGCAT	ATCAGGGAAG	AACATGACAA	AAAGCACCAG	180
					ACACTGCAGT	240
					AAATGGTAGC	300
TATCGTTGGT	CTGTCACGGA	AAAGTCGCAG	TGCTTCTCAG	CTCAGCGGAC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:590:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

CAATTCAAAT	CCTTCACCTA					
GAATICAAAT	GCTTCAGGTA	AATGTTGAAG	CTCGGTGTAC	CGCGGGACAA	ATCCTGAGTC	60
ACCCCTGGGT	GTCAGATGAT	GCCTCCCAGG	AGAATAACAT	GCAAGCTGAG	GTGACAGGTA	120
AACTAAAACA	GCACTTTAAT	AATGCGCTCC	CCAAACAGAA	CAGCACTACC	ACCGGGGTCT	180
CCGTCATCAT	GAACACGGCT	CTAGATAAGG	AGGGGCAGAT	TTTCTGCAGC	AAGCACTGTC	240
		ATGGAGCCCA				300
TCCCTGTGCC	TGGGGAAGCA	GTCCCGGCCC	CCACCCCTCC	GGAATCTCCC	ACCCCGCTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:591:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

GAATTCGGCC	TTCATGGCCT	ACTCAGTCTG	CACAACCTTT	TTGCTGTGTG	TCGGAATATG	60
TATAACTGGC	TACTGCAGAA	TCCCAAAAAT	GTCTGTGTTG	TCCACTGCTT	GGATGGACGG	120
GCGGCATCAT	CAATTCTGGT	TGGTGCTATG	TTCATTTTCT	GTAATCTCTA	CTCTACTCCT	180
GGCCCAGCCA	TTCGATTGCT	ATATGCAAAG	CGACCAGGAA	TTGGACTTTC	ACCATCCCAT	240
AGGAGATACC	TGGGCTATAT	GTGTGACCTA	CTGGCAGACA	AGCCCTACCG	CCCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:592:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

GAATTCGGCC	TTCATGGCCT	ACCGTAAGCA	GATGAAGCTG	CTGCTGCTGC	TGCTGCTGCT	60
GAGCTGCGCC	GCGTGGCTCA	CCTACGTGCA	CCTGGGCCTG	GTGCGCCAGG	GACGCGCGCT	120
GCGCCAGCGC	CTGGGCTACG	GGCGAGATGG	TGAGAAGCTG	ACCAGTGAGA	CCGACGCCG	180
GGGGGTCCAC	GCTGCGCCAT	CCACACAGAG	GGCTGAGGAC	TCCAGTGAGA	GCCGTGAAGA	240
GGAGACCAGC	GCAGACATGC	TGCGGCCAGA	TCCCAGGGAT	TACCTCGAG		289

- (2) INFORMATION FOR SEQ ID NO:593:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

GAGAGATGGT GACTGAGGCA	GAAGCTAATA	GGGAAGATGA	TAGGAAAGAA	ATTTTACCCA	60
AGGAATTAGA TTTAGCAAGA	GAGCGAAGGA	AAGCTGAGAG	GCCAAAAACA	TCTCTGAGGA	120
AAACTGACTC TGAGAGAGAA	GAGGTGACAA	GGGCAAATGC	ACTCAAGGAT	GAAGATGCTT	180
TTAAAGAAGA GCAAAAACTT	AAAGCGGAAG	AAGGGGAAAC	AGAGACAGAA	GTAAGAGCTG	240
AGGAAGAGAC AAAAGCTCCC	CCAAATGAAA	TGGGATCTGA	TGCTGAGAAC	GAAACACTCG	300
AG					302

- (2) INFORMATION FOR SEQ ID NO:594:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

GAATTCGGCC TTCATGGCCT AGGATATTTA AACCTCTATT ATTTTAGACA AGACTGTCTA GAACTTAAGT TTGATCTGTC AGCCAGTACT CCCCATTAAAT TCAGTGTAGT TTCACTTGAT AGAATCAGAT ATGTTATCGA AATGTTAGCA GCAGCTTCAT CCTCCTTCTG ATTAAAGTAA GTAGAAATGG GATGTTTTGT TTAATAACAG CCATAGTGTG TGTTTAGACC ACAGCGGATG TTGTAGACCA GGACCCTCGA G	60 120 180 240 261
(2) INFORMATION FOR SEQ ID NO:595:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 370 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:	
GAATTCGGCC TTCATGGCCT AGGGCTTTT GTCAAGATAG AAGGGTATCA ACGGTTTCTG TACAGCACAG ATTATGACAG CGTCTTTCTT AAGACTTATC ATTTGGAGCA CTGGCTCAGG AGTCGAAATC ACCAATGGCT CATCCATCAA TCAACCAGAA GTGAAGACGA AAGCTTCAAA GAAGAGAATG TTTAAATTTC ATCAAATGAA ACATATTTTT GAAATACTTG ATAAAATGAG ATGCCTGAGA AAACGTTCTA CAGTGTCATT CTTGGGAGGT CTTGTCATTT TTCTCCTTTT TATGAACTTG TACATTGAAG ATAGCTATGT TCTGGGAAGGA GACAAACAAC TTATAAGGGA AACTCTCGAG	60 120 180 240 300 360 370
(2) INFORMATION FOR SEQ ID NO:596:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 240 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:	
GAATTCGGCC TTCATGGCCT ACTAACGACT CATCTTTGTT TTTAGTTTTT TTAATTAACA ATCGTTCTGT TCACAATTTT TAATTCCTT TCTTCCCCCT TCTCCGCAAA GCACTCAGGC ATCGGACACG CTATGGTAAA CAAACTACAT TGTCTGGTAG ATATCATTCT TATTGTCTCT TTTTTTGGGT TTGCCCTGTG TTGCCCCCCT TTTCCTCTCC AACCCCCCC ATTCCTCGAG	60 120 180 240
(2) INFORMATION FOR SEQ ID NO:597:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 224 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:	
GAATTCGGCT TCATGGCCTA GTGTATTGGT TGTGTGTGTT TTCCTTTTTG CATAAGAAAT ATGTCCATTT AGTCCAGAGG CTCTTGCTTT ATCCGGATGA CGGAGGGTAC ACGGGCCGTC CGCCTCAGTT CCCGCCGAAG GACGTATTCG CTGAACTGGG ACGAGTCTAC TCCTCCCCCA CAGGAGCCCA CGATTTCAAA TCCTCTTTGC TGCAACCTCT CGAG	60 120 180 224

(2) INFORMATION FOR SEQ ID NO:598:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 272 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:	
GAATTCGGCC TTCATGGCCT AGATATTTTA AAGGAGTGAT GACATCTTTT TCCTATCATG	60
TGAAGAGGGG AAAGAGAAAG GAAAGGGCCC ATATTATTGT GTTCCTGCTT GTGCCAGCTG	120
TTCTATATCT GTTGATCTCA TTTAGTCCTC ATGACAGTTC TATGAGGAGG GCACTGTCAT	180
CATCACCATT GCACAGATGC AGAAACTGTG GCTCACAGAG GATAAAGCTA GGTCACTCAC	240
ACAACCCCCT GACTCCAGAG CCACCACTCG AG	272
(2) INFORMATION FOR SEQ ID NO:599:	
(') CROUDING CHARLES CONTRACTOR	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 351 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:	
GAATTCGGCC TTCATGGCCT AGTAAGGGAG AAACTGAATG GTGATTCAGA GCATAGAGAT	60
TATGTTTTTT TATGCACAGG GCTTCATCAG AAAAATGGAA GGAATTGTCA ATAACAATAA	120
AATGTTCAGC TAGATCAACT CAGTATATAG TATGTATTAT ACAATTATTC AAAATAGTGT	180
TTAACAGTAC TGTAATAACA TGAATAAATG TTTTGTCATA TTAAGTGAAA AAGAGCTATA	240
TAAAATTATC TAAGTTTATG GTATATGTAG ATTGTTGCAA AAATGTCTTC AATTCTTTAT	300
CCCTCCCTGT ATCCACACCT GTATCAGTTT TCTCGGGGCA GCTGCCTCGA G	351
(2) INFORMATION FOR SEQ ID NO:600:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 107 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:	
GAATTCGGCC TTCATGGCCT AGAATATTTT TATCATCCCA AAGCTAAAAC ATTAAAAAAT	60
TTAAAGTTTA TTCTTAGAGA TTGATGCAAC TTGCATATCT AATCGAG	107
(2) INFORMATION FOR SEQ ID NO:601:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 277 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

GGAAAATTAC	TTAAACGTTG	CACACAACGT	TTCACAAAAT	CTTTTGTGAA	AGAAGAAAAG	60
GAAATTCAGT	GTGTGAGTCT	CAGCAGGAGT	TAAGCTAATG	CAGCTTAACA	TCATGCCGAC	120
AAAGAAGCGC	TTATCTGCGG	GCAGAGTGCC	CCTGATTCTC	TTCCTGTGCC	AGATGATTAG	180
TGCACTGGAA	GTACCTCTTG	ATCTGGTACA	GCCTCCAACC	ATCACCCCGC	TAAATCCCCT	240
AGAAGTCCCA	CTCCTAAACA	CATCCGTATT	ACTCGAG			277

- (2) INFORMATION FOR SEQ ID NO:602:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GAATTCAAAT	TAACATTTTA	CCTTGAAATA	GTTGGCTTCA	GATTAATATC	AACTTAGTTT	60
CAATAGCATA	GGAAATTTGC	TTCACTATAT	TTCCATTTTC	TCCCCGTCCT	TTGTGCTATT	120
ATTACTATAC	·CAATTAGATC	TCTACACAAT	ATAGGCATAT	CAACACATTT	TGTAATTATT	180
TCCTTATCCA	GTTGTCTTTT	AATATAGATC	TGTGAAGAAA	AGTATTACAC	AAATAGATCT	240
ATTCTGTTTT	TTATAATTAT	TTAATTACCT	TTGGTGGTGC	TGTTTATTTT	TCATGCATTT	300
GAGTTACTGT	CTAGTATTCA	TTCATTTCTC	TCTGAATCAC	TCCCCGGTAT	TGCTCGAG	358

- (2) INFORMATION FOR SEQ ID NO:603:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GAATTCGGCC	TTCATGGCCT	AGCCATCTTA	TTTGAACTAT	ATTTTTCCTT	CAAAGAAGCA	60
ATAGGTCTCA	ACATAGTGTA	GGTAGCATCA	GGTGACAGAA	AGCCAATTTT	ATTTTCAAAT	120
TTAAGTTAAT	TATCTTCGTG	ATCCTATTTA	TCCACAATTT	CTTTCAGAAA	AGACTGAAAA	180
AACACATTAT	ATTCAGGAGA	TATAATGAAA	TTATTGGAAG	GCATCACTCG	AG	232

- (2) INFORMATION FOR SEQ ID NO:604:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GAATTCGCCC	TTCATGGCCT	AAATATTTTC	CATCTTCCTC	TCCAGTAAAC	ATTCTTTTGT	60
CATCACAGTC	TGTCTCTGAC	ACCTTCGTTA	AAGAGGTCTT	AAAATGGAAA	TATGAAATGT	120
TTTTGAACTT	TGGTCAGTGT	GGGCCCCCTG	CAAGTCTTTG	TCAGTCCATC	TCAAGACCTG	180
TGCCTGTCAG	ATTTCACAAT	TATGGAGATT	ATTTTAATGT	TTTTTTCCCT	TTGATGGTAT	240
TGAATACTTT	TGAAACAGTG	GCACAAGCGG	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:605:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GAATTCGGCC	AAAGAGGCCT	AAAAATATAA	TTTAAAAATA	CATTGCGTAT	TTTCTAAAAC	60
AATAAATTTA	TAGTGTTAAT	ATTCATAGGG	TCAATCAAAA	TGAAGCTTCT	CCTTTGGGCC	120
TGCATTGTAT	GTGTTGCTTT	TGCAAGGAAG	AGACGGTTCC	${\tt CCTTCATTGG}$	TGAGGATGAC	180
AATGACGATG	GTCACCCACT	TCATCCATCT	CTGAATATTC	CTTATGGCAT	ACGGAATTTA	240
CCACCTCCTC	TTTATTATCG	CCCAGTGAAT	ACAGTCCCCA	${\tt GTTACCCTGG}$	GAATACTTAC	300
ACTGACACAG	GGTTACCTTC	GTATCCCTGG	ATTCTAACTT	CTCCTGGATT	CCCCTATGTC	360
TATCACATCC	GTGGTTTTCC	CTTAGCTACT	CAGTTGAATG	TTCCTCCTCT	CCCTCCTAGG	420
GGTTTCCCGT	TTGTCCCTCC	TAATCTCGAG				450

- (2) INFORMATION FOR SEQ ID NO:606:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 614 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GAATTCGGCC A	AAAGAGGCCT	ATCAGGTGAT	AATAATAA	TTTAAAACTA	CTATAGAAAC	60
TGCAGAGCAA A	AGGAAGTGGC	TTAATGATCC	TGAAGGGATT	TCTTCTGATG	GTAGCTTTTG	120
TATTATCAAG T	TAAGATTCTA	TTTTCAGTTG	TGTGTAAGCA	AGTTTTTTT	TAGTGTAGGA	180
GAAATACTTT 1	TCCATTGTTT	AACTGCAAAA	CAAGATGTTA	AGGTATGCTT	CAAAAATTTT	240
GTAAATTGTT T	CAAATTTTAAAC	TTATCTGTTT	GTAAATTGTA	ACTGATTAAG	AATTGTGATA	300
GTTCAGCTTG A	AATGTCTCTT	AGAGGGTGGG	CTTTTGTTGA	TGAGGGAGGG	GAAACTTTTT	360
TTTTTTTTTAT A	AGACTTTTTT	CAGATAACAT	CTTCTGAGTC	ATAACCAGCC	TGGCAGTATG	420
ATGGCCTAGA T	rgcagagaaa	ACAGCTCCTT	GGTGAATTGA	TAAGTAAAGG	CAGAAAAGAT	480
TATATGTCAT A	ACCTCCATTG	GGGAATAAGC	ATAACCCTGA	GATTCTTACT	ACTGATGAGA	540
ACATTATCTG (CATATGCCAA	AAAAATTTTA	AGCAAATGAA	AGCTACCAAT	TTAAAGTTAC	600
GGAATCACCT (CGAG					614

- (2) INFORMATION FOR SEQ ID NO:607:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GCGAAGACCA	TCAAATGAAT	TGTCACAATA	CTCGAATAAT	GCAAGACACA	GAAAAGGATG	60
ATAACAATAA	TGACGAATAT	GACAATTACG	ATGAACTGGT	GGCCAAGTCA	TTGTTAAACC	120
TCGGCAAAAT	CGCTGAGGAT	GCAGCCTACC	GGGCCAGGAC	TGAGTCAGAA	ATGAACAGCA	180
ATACCTCCAA	TAGTCTGGAA	GACGATAGTG	ACAAAAACGA	AAACCTGGGT	CGGAAAAGTG	240
ልርተተርልርተተዋ	ACACTTAGAC	AGTGATGTTG	TTACACAAAAC	ACTOCCOCTO	GAG	293

- (2) INFORMATION FOR SEQ ID NO:608:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs(B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (C) SIRANDEDNESS: GOUDTE
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GAATTCGGCC	TTCATGCTTA	CTCAGAAAGC	CACTGCCCCA	AACAAGCCAC	CTGCATTATC	60
AAACACAGAG	AAGAGGAATC	ATTCCGCCTT	TTGGGGACCA	GAGAGTCAAA	TCATTCCTGT	120
GATGCCAGAT	AGTAGTTCCT	CAGGGAAGAA	CAGAAAAGAG	GAAAGTTATA	TATTTGAGTC	180
AAAGGGTGAT	GGAGGAGGAG	GGGAACACCC	AGCCCCAGAA	ACAGGTGCAG	TGCTACCCCT	240
GGCGCTGGGT	TTGGCTATCA	CTGCTCTGCT	GCTTCTCATG	GTTGCATGCC	GACTACGACT	300
GGTGATCCTC	GAG					313

- (2) INFORMATION FOR SEQ ID NO:609:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GCCCATTCCG	GCCCCCATCT	CACCCAAGAT	CCCCCAGAGT	CCAGGAGCTG	GACGGGGACA	60
CCCTCAGCCC	TCATAACAGA	TTCCAAGGAG	AGGGCACCCT	CTTGTCCTTA	TCTTTGCCCC	120
TTGTGTCTGT	CTCACACACA	TCTGCTCCTC	AGCACGTCGG	TGTGGGGAGG	GGATTGCTCC	180
TTAAACCCCA	GGTGGCTGAC	CCTCCCCACC	CAGTCCAGGA	CATTTTAGGA	TAAAAAAAA	240
GAAATGTGGG	GGGCTTCTCA	TCTCCCCAAG	ATCCTCTTCC	GTTCAGCCAG	ATGTTTCCTG	300
TATAAATGTT	TGGATCTGCC	TGTTTATTTT	GGTGGGTGGT	CTTTCCTCCC	TCCCCTACCA	360
CCCGTCCTCG	AG					372

- (2) INFORMATION FOR SEQ ID NO:610:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GGAGCTAAAT TTAAGAAATG CAACTAGCCA GGTGCTAAGA AGCTCAGTTA CACGTTTCTC AAAAGTTGGC TGTTAGTTCC ATGACTCAGA GTGCACTCAA ATCATTTTAA TTACTCGAG	119
(2) INFORMATION FOR SEQ ID NO:611:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 474 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:	
GAATTCGGCC TTCATGGCCT AGGTCCTGTT TGCCTATTTG AGCTGCTATT AGTGTGAGAA GAAACTCAGA TGATAGTAGC AGAAACAGAA AGAGGAAGAG GCTACAAGAG ATGGTAGATG CTGAACTTAA GGCATTTGAT AACCAATGGA TATAGAAAGA AAAGGAAATG AATGGCTCTA AGTTTTCAAA CTTGACTGAT GAGGAAAATA TTCACATCAA GAATGGACTG AAGAAATAAG GAGGAGATGC TGGGTTAGGG TGAAAGGAGA TGAGCCCCAT TTTACATTGG AAAGCTCTAT GGAACAACGG AAGTAGTAGT AGCTTTATAT TCCAGTATGC CAAATTCTCA GCTCCAAGAC TCCAGCACTG TGTGCTCTAC AGTATGTTTT GTGATTGCC TGAGTTTTGG TTTCTTTATT TCAATTAGGG ACTCTTCATA CCAGGGTCAG GGGTTATGCT CGAG	60 120 180 240 300 360 420 474
(2) INFORMATION FOR SEQ ID NO:612:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 283 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:	
GAATTCGGCC TTCATGGCCT AGTTCCTGTG CTCTTGAAAG AACAAGTTGA TGCTTGTAAA GCTGTTTTGA TTATTTTTAG GCGCATGATA ATGGAGCTTA CAATGAATAA AAAGACATGG GAACAGATGT TGCAAATACT ACTCAGGATA ACAGAAGCTG TCATGCAGAA GCCAAAGGAT AAACAAATAA AGGACTTGTT TGCCCAGAGC TTGGCAGGGT TACTATTTAG GACGCTCATG GTAGCTTGGA TCCGAGCAAA CCTCTGTGTG TACATTTCTC GAG	60 120 180 240 283
(2) INFORMATION FOR SEQ ID NO:613:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 280 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:	
GAATTCGGCA CGAGGGCCG CCGTTTTTT TTTTTTTTT TTTTCAGGTG CACATAAAGT TAGTTTATTA ATGACTATAT TTTGAAGCCA GCCATTTTGT CCAATATTTA AATAACAAGC TGTTTAATAT TAAAGCAGAA AGTACTGCCA CATTGTGACA GAAGTACAGC TTTATCCATA AACCCTTCAC ACAATTATAC ATTAAATGCT ATTTTTATTT AAGCAAGGCA CCCCTACTTG TTCTAAAATA TGGGATGTAC TACACCATGT ATTACTCGAG	60 120 180 240 280

- (2) INFORMATION FOR SEQ ID NO:614:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

GAATTCGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAACCA	AGAATTCGGC	ACGAGGGAAT	60
GAAATTAGCT	AACAGCCTTC	AGCTACAGAA	ACTTTGGGAT	CCAGACAGCA	TTTGAGCTGA	120
CGCCACGCCC	TTCTCAGGCA	GCCCCCACAG	TGAAGGAGGA	GGATCTAGAA	GGGCCTGGCC	180
ATTTTTCCTC	AATGTAGGGT	CCCTCTGATG	GGAATTCTTT	GTCTGGAGAC	CCGAGCTGAG	240
ACTTTGTCAG	ATTGGCATCT	CTGTCCCTGC	TCAATGCTGC	TTTCCATGCT	CCCTTTTCTA	300
TCACAGACAT	CATAGCCTGA	AATCTTTCCA	CACCCAATAC	TGCTTCCTAT	ACCCCTTAGC	360
CTTTCCTGAT	CTCATTGAGG	TTACCATTTT	TCCTCCGTCG	CTCGAG		406

- (2) INFORMATION FOR SEQ ID NO:615:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GAATTCGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	AGAATTCGGC	ACGAGGCTTT	60
TTTAGGTAAT	TCTTTGTACT	CCTGCTGTCT	ACCTCTCCTC	ACACCCCAGC	ACCCCCCATT	120
TTTTCAAACC	TTGGTATCTG	TTGGGTGAAC	AGTATAATCT	TTTCATCTGC	TTTTAGAATG	180
TGGGATATTT	CCAGTACCTA	CTTTTTTTT	TTTTTTTTGC	TGAATCCAAA	GATATATAAA	240
TAAAATATAT	ATATTTTATA	AAGATCAGAA	TGATATAAAG	GAGATACATG	TTTCTTCCTT	300
AATAAAAAT	ACGGAAGTTA	CATTGTTAAT	GTTCATATTA	TGATGCGAAT	TCTCTGGTTC	360
CTCCTCGAG						369

- (2) INFORMATION FOR SEQ ID NO:616:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GAATTCGGCC	TTCATGGCCT	AGGATGTCTG	AGGTCTTAAC	CTGCCCAGTC	CTGAATTCCT	60
GGGACTTCAA	CGACTCTCTC	TCTGCCAAAT	GATGTGAGTC	TTTAGGTAGA	GTTATAGCGC	120
AAAGGGCTAC	TATCAATGTT	ATTAAGCATA	AATTATGACT	AGAGCCACAG	AATGATTTCC	180
TCATTAATCC	ааааааааа	AAAAAGCAAA	CCACTCTTTT	ACTTTATGAT	GAGCACATAA	240
ACAGTTTTTT	TTTCTTTTTA	TTTATCTACT	TTTACTTACT	TAAATTTTAG	AGATGGGGTC	300
TTGCTATGTT	GCCCAGACTA	GACTCAAACT	CCTGGGCTCA	AGTGATCCTC	TAGCCTCAGC	360
CTCCCAAGTA	GCTGGGACTA	CAGGAAGGAG	CTACTGCACC	TGACTCAATT	TTTTTTTTT	420

CTGAGATGGA GTCTCACTCT GTGACCCAGG CTTGTCTCGA G

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:617:

461

(A) LENGTH: 391 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:	
AATTCGGCC TTCATGGCCT ACATCAATAA CAGCCAAACT GAGACACATA ATGTTTTCTA	60
CTCCAAGAG GCTAAATGTG AGAATCCAGA ATTTGAGAGA AATGTGGAGA ATACATCTTG	120
TTCATGGTC CCTGGTGTTC TTCCTGATAC TTTGAACACA GTCAGAATAA GAGTCAAAAC	180
AATAAGTTA TGCTATGAGG ATGACAAACT CTGGAGTAAT TGGAGCCAAG AAATGAGTAT	240
AGGTAAGAAG CGCAATTCCA CACTCTACAT AACCATGTTA CTCATTGTTC CAGTCATCGT	300
COCAGGTGCA ATCATAGTAC TCCTGCTTTA CCTAAAAAGG CTCAAGATTA TTATATTCCC	360
CCAATTCCT GATCCTGGCA AGAATCTCGA G	391
(2) INFORMATION FOR SEQ ID NO:618:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 306 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:	
GAATTCGGCC TTCATGGCCT ACGTGAAGAC AAGATGAAGT TCACAATTGT CTTTGCTGGA	60
CTTCTTGGAG TCTTTCTAGC TCCTGCCCTA GCTAACTATA ATATCAACGT CAATGATGAC	120
AACAACAATG CTGGAAGTGG GCAGCAGTCA GTGAGTGTCA ACAATGAACA CAATGTGGCC	180
AATGTTGACA ATAACAACGG ATGGGACTCC TGGAATTCCA TCTGGGATTA TGGAAATGGC	240
TTTGCTGCAA CCAGACTCTT TCAAAAGAAG ACATGCATTG TGCACAAAAT GAGCAAGGAA	300
CTCGAG	306
(2) INFORMATION FOR SEQ ID NO:619:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 370 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:	
GAATTCAAGG CCACGCCGGA GCTGTACCTT GGAAGGAGGA GCCAAAAATT ATGCTGAGAG	60
TGATCACAGT GAAGACGAGG ACAATGACAA CAATAGCCCC ACCGCAGAGG AGTCCACGAA	120
GAAGAATAAG AAGAAACCAC CGAAAAAAAA GTCTCGTTAT GAAANGACAG ATACCGGTGA	180
GATAACATCC TACATCACTG AAGATGATGT GGTCTACAGA CCAGGAGACT GTGTGTATAT	240
CGAGAGTCGG AGGCCAAACA CACCGTATTT CATCTGTAGC ATTCAAGACT TCAAACTGGT AAGCGTTTTT AATGTGCTGT TCACTCTGCT CTGTATTCTC TCTTTTTCCA GTTCCATTGG	300 360
ANGESTITE ANTOISEIGE FENETEIGE CIGIATICIC TETTITICA GITCATIGG	500
288	

370 CGCTCTCGAG (2) INFORMATION FOR SEQ ID NO:620: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 183 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:620: GAATTCGGCC TTCATGGCCT AAAAACCTTA CAACTAAAGC AAATAGACTT TTCAAGAATT 60 TAAATAGGAT TCCTTCCCTT TAATCAATTA ATTATCCACT TTGTCATGGT GTCAACCTGT 120 AATTTCATGG TTTTGTGTGT GTGTGTGTGT GTGACAGAAA TTTACAAACA ATGTGATCTC 180 183 GAG (2) INFORMATION FOR SEQ ID NO:621: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 565 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:621: GAATTCGGCC TTCATGGCCT ACAACTAATT TGATCATATT AACAAGAGGT TGGTTTTTAA 60 ACCAAGCAGT ATAAATATAA ATACAGCCTT GGGTAGATCA TAGTCAAACT ATCCAAATGC 120 AACCTCAGCT TCAAAGATTG TAAAGTCTTT TCTTTCCCCT TTTCTCCTTT CCTTTTTTTT 180 240 TCCTCCAAAT ATTTATTTAC TACCTACCAT GTGCCAGGCA CTGTGATGGG CTATGAGGAT GCAGTGGGGG ATAGGACAGA TGCCATCCCT GCCCTGAGGA GACTTGCAGT TTATTGGAAA 300 AGATGGACAT CGTAAAATAT ACAATCATAC AAATAAAAAT TACATAAATA ATTCAGTACT 360 420 TCAACTTGTG GGAGGTACAG CAGTTTATAA TAATAACATC CCTCCCACCT TCTTGAGAGA GTCATTGGTT GCCCCACTTC TCTTCATGAA TGAGAGGACA TGATTAAACC TATCATTTCA 480 GGTAGGAGTT TACTGTGGGA TGGATATCAA TCTTCTATTA ATATGTTTGT GCTCATGCTC 540 TCCATTTTGC AATGGACGTC TCGAG 565

- (2) INFORMATION FOR SEQ ID NO:622:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

60	AAAGTGCAAC	GAACCAATGA	CTATGTCTTA	AAAATGAAAG	TTCATGGCCT	GAATTCGGCC
120	CATGTGGATC	GTCCGGGGAT	GCTGAAAAGC	CAGCGAAGAA	AAACTCTTCC	CAACAGATAC
180	CTCAGACATG	CCACCACCCT	GAATGTGTTT	TCGCTGCAAA	ACACCAAACC	ACATCACAAC
240	TGGTGATCGT	TATGTGGAGC	GGCAACTAAG	AGACCCTCAA	CATAAAAGAG	GGCAAGAAGG
294	CCAC	GAAAAAGTCT	DADAGATOTO	AGAGGGAAGG	CCACACTTTC	CCCACACAAC

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GAATTCGGCC	TTCATGGCCT	AGCTTCTGGT	AATGGCGGAC	TAGATGATTT	AGAGCAACCC	60
ACCCATTGAA	AAGAACTACA	AAACGTCAGA	TCTCTAAAAG	GCTACAAAAT	TAATACAATT	120
GTGAGGAATT	GCTAGGTTAT	ACTACAAGAG	AACAGAAGCA	TCCAGAGAGG	TAAGCCTAGG	180
ACTTAAAACT	ATATTTTTAT	TGAAGGTATC	TGTGGTTGAG	TAATAAGCCT	GTGCTAAACT	240
GCGTGGAACT	TATGGCACAT	TCAAGGCACT	ATAGTAACAG	AAGTCAGAGC	CCAAGGCCCA	300
TCAAAAGGGG	TGGAGTGTTT	CCTGACAAAC	CATCACCCAT	AGTATGCTGG	GAACCGCAAA	. 360
TGTTTATACC	TTCAGGGTAA	TTGTAATCAA	AAAATATACT	AGCCCTTACA	AAGTCTTGTA	420
GCTTGGCTTT	GCATCATCTG	GGTGGACTAG	TGAACTGTAA	GTTCTGAACA	AATATTATGG	480
AGGCAACTCG	AG					492

- (2) INFORMATION FOR SEQ ID NO:624:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GAATTCGGCC	TTCATGGCCT	ACTTCCCTGA	GCTGGGGTTT	CCCTGCTTGT	CCAGTTGTGA	60
GCTGTCCTCG	GTGTTACCGA	GGCTGTGCCT	AGAGAGTGGA	GATTTTTGAT	GAAAGGTGTG	120
CTCGCTCTCT	GCGTTCTATC	TTCTCTCTCC	TCCTTGTTCC	TGCAAACCAC	AAGATAAAGG	180
TAGTGGTGTG	TCTCGACCCC	ATCAGCCTCT	CACCCACTCC	CAGACACACA	CAAGTCCTCA	240
AAAGTTTCAG	CTCCGTGTGT	GAGATGTGCA	GGTTTTTTCT	AGGGGGTAGG	GGGAGACTAA	300
AATCGAATAT	AACTTAAAAT	GAAAGTATAC	TTTTTTATAAT	TTTTCTTTTT	AAAACTTGGT	360
GAAATTATTT	CAGATACATA	TTTTAGTGTC	AAGGCAGATT	AGTTATTTAG	CCACCAAAAA	420
AAAGTATTGT	GTACAATTTG	GGGCCTCAAA	TTTGACTCTG	CCTCAAAAAA	AAGAAATATA	480
TCCTATGCAT	CTCGAG					496

- (2) INFORMATION FOR SEQ ID NO:625:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GAATTCGGCC	TTCATGGCCT	ACAAAATTGA	TTATGACAAG	ATTGTCTACT	ATGAAGCAGG	60
GATTATTCTA	TGCTGTGTCC	TGGGGCTGCT	GTTTATTATT	CTGATGCCTC	TGGTGGGGTA	120
THEFT	ATGTGTCGTT	CCTCTAACAA	ATCTCCTCCA	CANATCCACC	ACCCACACAA	180

GGAAAATGGG CCCTTCCTGA	GGAAATGCTT	TGCAATCTCC	CTGTTGGTGA	TTTGTATAAT	240
AATAAGCATT GGCATCTTCT	ATGGTTTTGT	GGCAAATCAC	CAGGTAAGAA	CCCGGATCAA	300
AAGGAGTCGG AAACTGGCAG					360
TCCAGAGCAA ATCAAATATA	TATTGGCCCA	GTACAACACT	ACCAAGCTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:626:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GAATTCGGCC	TTCATGGCCT	AGTTAGGTGG	CTTTTAGTGT	ATTGACAAAG	TTGTGAACCC	60
ATTATCACAA	TCTAATTTTA	GAACATTTTT	ATCAGCCTCC	TTGCCCCCTA	AAAAAACCCA	120
GTACTTTTTA	CCAATCCAGT	CATTTAAAAC	TTACTACATA	TTTAATAGAT	GGATAGATAG	180
ACAGGAGGAT	GGACAGACTG	AAGGAAGAAT	GGATGATTAT	GTATAAATAA	ATGAAAAAAC	240
AAAAACTATC	CCCAAATCAT	AAGGGTATAC	GCAATGCTTT	CCTGTGGCAA	AAGATTCGGA	300
ACATGTACAG	CAGATTTTTT	TTCAAATGTT	CATAATTCTA	AATTCCCAAA	ATGGTCTACA	360
CAACTTCTCG	AG	•				372

- (2) INFORMATION FOR SEQ ID NO:627:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 575 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GAATTCGGCC TTC	ATGGCCT AGGAGAAAG	AAGGGAAGCA	TTACTGGGTT	ACTATGCACT	60
TGCGACTGAT TTC	TTGGCTT TTTATCATT	TGAACTTTAT	GGAATACATC	GGCAGCCAAA	120
ACGCCTCCCG GGG	AAGGCGC CAGCGAAGA	A TGCATCCTAA	CGTTAGTCAA	GGCTGCCAAG	180
GAGGCTGTGC AAC	ATGCTCA GATTACAATO	G GATGTTTGTC	ATGTAAGCCC	AGACTATTTT	240
	AATTGGC ATGAAGCAG				300
	TCGATAT CCAGATATA				360
ATACCTGTTT CAA	CAAAAAT TTCTGCACAA	A AATGTAAAAG	TGGATTTTAC	TTACACCTTG	420
	CAATTGC CCAGAAGGG				480
	CTGTGAG GTCAGTGAA		GAGTCCATGC	ACGAAGAAGG	540
GAAAAACATG TGG	CTTCAAA AGAGGGGATG	CTCGAG			575

- (2) INFORMATION FOR SEQ ID NO:628:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GAATTCGGCC	TTCATGGCCT	AACAGGGTCT	TGCTCTGTCA	CCCGGGATGG	AGTGTAGTGG	60
					CCACCTCAGC	120
			CCATCATGCC			180
TTGTAAAGAC	AGGTTTCACT	GTGTTACCCA	GGCTGATCTC	GAACTCCCGT	ACTCAAGCAA	240
CTCCCCACCT	CAGCCTCCCA	AAGTGCTGGG	ATTACAGACG	TGAGCCACAG	CGCCGGGCCC	300
CAAAATCTAT	TTTAAATGTA	AAGAAACCCA	AAAGTAACAG	TTTTGTAAAA	GAAAATTCAC	360
${\tt GTACTGTTTT}$	GTAGTAAATT	CTAAACACTG	TGTATCTTTG	TGTCTAGTTA	AATCCTAGGC	420
TTACAGCTAA	AATTCAATGA	GAAGGCAAGT	ACTCGAG			457

- (2) INFORMATION FOR SEQ ID NO:629:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

GAATTCGGCC	TTCATGGCCT	AGAAAGCTAT	CATTTATTGA	GAGTTAATTG	TATATTAAGT	60
ACCATGCTAA	GTGCTTTGTA	TGTATTATTT	ATCTTTATAA	AAATCCTATG	AAATGAATAC	120
TGTTATTTTC	CCCCATTATA	CAGATGAAGA	TAGAGAAAGG	AAGAAAAGGG	AGGGAAAGAG	180
GAATACCATT	TCACTGAGCA	ATTTTACTGA	AATATTTTAT	GGAGCATTTG	TGGGTTTTGT	240
TTGTTTGCTT	GTTTTGTTTT	TTTGTTTGTT	TTTTTTTTTG	AGACAGAGTC	TCACTTTGTC	300
GCCCAGGCTG	GATCTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:630:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 557 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

ACGGTGAAAC	CCTGTCTGTA	CTAAAAATAC	AAAAAATTAG	CGGGGCATGG	TGGTGGGCAA	60
CTGTAGTCCC	AGCTACTCGG	GAGGCTGAGG	CAGGAGAATG	GCATGAACCC	AGGAGGCGGA	120
GCTTGCAGTG	AGCCGAGATC	ACGTCACTAC	ACTCCAGCCT	GGGCGACAGA	GCGAGACTCC	180
GTCTCAAAAA	AAGAAAAAC	CAAGACAAAA	CCAAAAATAA	CTTTGTCTGT	TAAGTACAAT	240
ATCTGTGTTC	CTCAGGGACA	GTTTCTATTG	ACCATTGTTT	TTCTTGTGCA	TAGACTATCC	300
TTTCCTTTTT	TTGTACATCT	TGTAATTTTT	GTTTTATTAA	AACTGGAATT	TTAAAAATAA	360
TGCAGTGTGG	CAACTCTACT	GCTTGATTTG	GCTCAAAGGT	ATATTATTTA	TTTTTTAATA	420
TAACAAACCA	ATATTTGGGT	TCTCTATTCT	ATAGTTTTAG	CATTTTGAAT	GCAACAACTG	480
TCTTATTCAC	CATTTAATTC	TCAGTACTAC	CGTTTCTAGT	ACACAATATG	CACTTAATGA	540
ATATGAGGGT	CCTCGAG					557

- (2) INFORMATION FOR SEQ ID NO:631:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GAATTCGGCC	TTCATGGCCT	AGACCGTGCC	AGGTATTGAG	AGCGACCCTC	ACATTCCTAC	60
AGTGCTCTGT	GTGGCATCTT	AATGAAACTT	TATTCTCTCC	CCTTAAATGA	GAAAGAATAG	120
CTAGTTGTCA	TCCTTTCTGA	ACCGATTTTG	TCTTTCAAAG	GTAGTAGTGT	ACCAGGCCTG	180
CTATTTTGCA	AAACGGTCTC	CACCAAAATC	GAATTACCTG	CCTCGCGGGG	CAGGCGTGTT	240
GACCAGGTGG	ACTCTAGAAG	TAGGTGGTTT	GCTTGGTTTC	TTTTCCTTTT	AAGGTTTCCC	300
TTTCTTCTTC	TTCTTTTCTG	TGTTTTTTT	TTTTTTTTT	TTTTTTCAAT	ATAGAAACTG	360
TCCCTAAGAG	AGGAAACCTT	TCTGGCCATG	TTATTCCAGG	AATCTTTTGT	CCCCTAAGTT	420
TGACCTTGTT	CTTTCGTTCA	CCCTTTACTC	TTGCATCTCG	AG		462

(2) INFORMATION FOR SEQ ID NO:632:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOFOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GAATTCGGCC	TTCATGGCCT	ACATAAAATC	AGTTGACTAT	TGTGCAACAT	AGAATTATTG	60
TTTGTGTGAA	ATTACCGCTG	AAGGACCTTG	CCTACATTCA	AGGGTCTATT	TTTATTTTTC	120
CAGGTATTCT	TTCACATTAG	TGACATTATA	GTCTAGTACA	ACTGCTTGAT	AATTTGGAGA	180
AACTAACATT	AATTTTAGAT	AGTGATTGAT	AAAATTTGGC	CTGCCAAATG	CATTTTAAAA	240
ATAATTCTAG	GATTTATCTA	TGCTCATTTC	TAGTATACCT	CATGATATAT	AAGACATCTT	300
TCTTTTGTCA	TATCAGTTCT	TCAGATACTA	AGACAGAGGT	CCTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:633:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GAATTCGGCC	TTCATGGCCT	AGGTGGTGCA	ATATTATAA	ATGTTGCCAG	TCAATGCCAA	60
CCAGTGTCTG	ATTGGCTTCC	TGTGCATGTC	CAATTTCCTC	TGTGACACTG	TGTTGGTGCC	120
AGAGCTTCTG	AATCTTCTTG	AATCGCTCTT	TGCATAAATG	TAAAGGATTT	CCCCGTCTGA	180
GTCCCTGGTC	GGTCTCCCCA	TAATCATCAA	GGTAAGGAGG	AGAATAAAAA	CAGCCTTTGG	240
TTTTGCCAGC	TAAAAATAGC	ACCTGACATT	CCCGTACTCT	CAGGAAGATG	CCCACTCCAG	300
AGCCACAGGA	GTAGGTGTGA	GCTGTGCAGG	CTCCTACATC	CTCCCCTTCC	AGTTCAGTCT	360
GGCAGCAGTA	ACTCTGGGAG	CACAGCAGAG	ATCCGCACAC	AAGGCACAGA	GTTGGGGCTC	420
TGCTCTTATC	ACCACCTGAT	TTCGGGCACC	TCGAG			455

- (2) INFORMATION FOR SEQ ID NO:634:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GCATGAAGGC CGGCCTTCAT	GGCCTACAGG	CTATGTACTG	TATGATTCCA	AATATGACAT	60
TCTGGAAAAG GCAAAACCAG	GGACACAGTG	AAAAGATCAG	GGGTTGAGAG	GGGAAAAAAG	120
GAGGGATGAG TAATCAGAAC	ATACAAGATT	TTTTTAAGGC	AGTGGAACCG	CTCTGTATAA	180
TACCATAATA GTGGATACGT	GTCATTATGC	ATTCATCCAA	ACTCCTAGAA	TGTACAGCAC	240
AAATAGTGAA CTGTAATGTA	AATGCAGTGT	GTAGGTGTTT	ATACAAAAAA	ACAGATGGAA	300
AGATTTTGTA CATAGCTCTA	TGTGAAAATG	TATTTATTTA	TTAAGAGCAA	AAATATGCTT	360
ATTTCAAATT TCCACGTACG	ACTTTTTCAA	AAAGACACGA	TCCACTGAAA	TAACCCTCCA	420
AAAGAATTTC TATAATCTAT	AGCAGGTGTA	CATGTTGTTA	ATCAAGTGCT	TAATGTTACT	480
CGAG					484

- (2) INFORMATION FOR SEQ ID NO:635:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GAATTCGGCC TTCATGGCCT	ACCCCACCAG	AGGACAGACG	TTGAAAGATA	CCACGTCCAG	60
TTCTTCAGCA GACTCAACTA	TCATGGACAT	TCAGGTCCCG	ACACGAGCCC	CAGATGCAGT	120
CTACACAGAA CTCCAGCCCA	CCTCTCCAAC	CCCAACCTGG	CCTGCTGATG	AAACACCACA	180
ACCCCAGACC CAGACCCAGC	AACTGGAAGG	AACGGATGGG	CCTCTAGTGA	CAGATCCAGA	240
GACACACAAG AGCACCAAAG	CAGCTCATCC	CACTGATGAC	ACCACGACGC	TCTCTGAGAG	300
ACCATCCCCA AGCACAGACG	TCCAGACAGA	CCCCCAGACC	CTCAAGCCAT	CTGGTTTTCA	360
TGAGGATGAC CCCTTCTTCT	ATGATGAACA	CACCCTCCGG	AAACGGGGGC	TGTTGGTCGC	420
AGCTGTGCTG TTCATCACAG	GCATCATCAT	CCTCACCAGT	GGCAAGTGCA	GGCAGCAGTC	480
TCTCGAG					487

- (2) INFORMATION FOR SEQ ID NO:636:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

GAATTCGGCC TTCATGGCCT	AATTTTATTT	AAATTTTTAT	TATATATA	TTTATTTAAA	60
ATTTTCATGA AATGGCCAAG	CAGGGTTTAA	TATAAAATGG	AAACAGGGTT	TATCTCAGAA	120
ATTTGGTGGC TAAATTCCTT	GTATCCCGTC	TTATCTAGGG	ATGTTGTTTG	TTTCAAGGTT	180
CTACCTTGAG AGGAGCCTGT	CATTTTCTTT	TTTGTGTGCT	GCTTTGCCTA	GTTGACATCT	240
TGGCTTTATG TGCTCCTGTT	GAATGCATTG	GGAAATTTTC	TTTCTTCTTT	CTATGTCCTG	300
AAATAGCTTA TATAAGAGGG	AAACTCTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:637:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 625 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GAATTCGGCC	TTCATGGCCT	ACAAAAATAC	TTTCATTTGT	TTTGCTATTA	CTAGTTTCTC	60
ATTTTTTATT	GCACTTGCAA	TCATTTTAGG	AATATCCTCA	AAATATGCTC	CAGATGAAAA	120
TTGCCCAGAT	CAAAATCCTC	GTCTCAGGAA	TTGGGATCCA	GGACAAGATT	CTGCAAAGCA	180
AGTTGTTATC	AAGGAGGGG	ATATGCTCCG	TCTGACCTCA	GACGCCACCG	TGCATTCTAT	240
AGTCATTCAG	GATGGAGGAC	TGCTTGTATT	TGGGGACAAT	AAAGATGGAT	CCAGAAATAT	300
TACTTTGAGG	ACTCATTACA	TCCTGATCCA	GGATGGTGGG	GCGCTTCATA	TTGGAGCAGA	360
AAAATGCCGC	TATAAATCCA	AAGCGACAAT	TACCTTGTAT	GGCAAGTCAG	ATGAAGGTGA	420
AAGTATGCCA	ACATTTGGCA	AAAAGTTTAT	TGGTGTGGAA	GCTGGCGGGA	CACTGGAGTT	480
ACATGGGGCA	CGGAAGGCAT	CGTGGACGTT	GTTGGCAAGG	ACCCTGAATT	CCTCAGGCTT	540
GCCGTTTGGG	TCCTATACCT	TTGAAAAGGA	CTTTTCCCGG	GGCCTCAATG	TGAGGGTCAT	600
TGACCAAGAC	ACGGACGCTC	TCGAG				625

- (2) INFORMATION FOR SEQ ID NO:638:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

GAATTCGGCC	TTCATGGCCT	AGAGAACTTT	TTGAGGGCTT	TTTTTTTCC	CCTTTTAAGC	60
TATTTTGTAT	GTAGACTTAA	TTTTTCTAAT	TTTGCCACTT	CTGGCAATCT	GAAATCATTA	120
AAAAGGACAC	AATTCAAATT	TATGTTAAAG	GTCATAAATT	TTGCCCAGGA	CTCAATATTT	180
TCTCATTTTT	CCAAAAATAA	AATCTTATTT	ATGCATTATA	GCGACTTGGT	TTTCACTTTA	240
TCTTGAATTA	TAGCTTTTAA	GAGGCAGAAA	GAATCCTTTT	TATAAGGACA	GTCTCAAGTG	300
TACACACAGA	TTAAATATTA	CAAATATAGG	TTGCAAATAA	AACTTTCAAA	ATGTGGGATT	360
ATAGGAAGCA	AAAGAGAACC	AACCAAAGCA	TCAACAAATT	TACCTTTTTG	TTTTTTTTAA	420
AGATTTTTCT	TATTTCCTTA	GCTGCTTTTG	CATTAGCATT	AAATAACATT	CTTATTGGAG	480
TGGTATGTGC	ATGGCCCAAG	CTCGAG				506

- (2) INFORMATION FOR SEQ ID NO:639:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GAATTCGCCC TTCATGGCCT ACTC	CAGCTT TATTATCTCA	GCTACCATCA	AACTATATTA	60
CATCAAATTA TCATCATTAC TCTC	CTGCAC AGTAACTTTC	TTTCTGCTCC	ACTAAGAAGC	120
TTACTCCCAT CCTGTTTATT CTCT	ATATCG TAGCTGGACT	AATCTTTTCA	AAGTGCAAAG	180
CCAATCACAA TACCACCTGC TTAA	AATCCA TCAGTGGCTA	ACTTTTCATT	CTAGGACGAA	240
AAGAAAATTC TATAACATGA CTTC	AAAGGC TCTGCATGTC	CTTCTATTTC	TCTTGTCCTC	300

TCACCCACAA CCCGTCACGC CACTCGAG

TCTAGTCTTT TCTTTGATGG TCTCCACTCC AGCCCTACTG GCTTCTTTCT GGAATCAATG

360

388

(2) INFORMATION FOR SEQ ID NO:640:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 385 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:	
GAATTCGGCC TTCATGGCCT ACTCCGCTCT GGCCCAGAAG GAGGCCAAGA AGGACGAGCC CAAGAGCGGC GAGGAGGCC TCATCATCCC CCCCGACGCC GTCGCGGTGG ACTGCAAGGA CCCAGATGAT GTGGTACCAG TTGGCCAAAG AAGAGCCTGG TGTTGGTGCA TGTGCTTTGG ACTAGCATTT ATGCTTGCAG GTGTTATTCT AGGAGGAGCA TACTTGTACA AATATTTTGC ACTTCAACCA GATGACGTGT ACTACTGTGG AATAAAGTAC ATCAAAGATG ATGTCATCTT AAATGAGCCC TCTGCAGATG CCCCAGCTGC TCTCTACCAG ACAATTGAAG AAAATATTAA AATCTTTGAA GAAGAAGAGC TCGAG	60 120 180 240 300 360 385
(2) INFORMATION FOR SEQ ID NO:641:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 392 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:	
GAATTCGGCC TTCATGGCCT AGCAAGGAGA ACTATTGTCT TATGATCACG TTTGCCATCT TTCTGTCTCT TATCATGTTG GTGGAGGTGG CCGCAGCCAT TGCTGGCTAT GTGTTTAGAG ATAAGGTGAT GTCAGAGTTT AATAACAACT TCCGGCAGCA GATGGAGAAA TACCCGAAAA ACAACCACAC TGCTTCGATC CTGGACAGGA TGCAGGCAGA TTTTAAGTGC TGTGGGGCTG CTAACTACAC AGATTGGGAG AAAATCCCTT CCATGTCGAA GAACCGAGTC CCCGACTCCT GCTGCATTAA TGTTACTGTG GGCTGTGGGA TTAATTTCAA CGAGAAGGCG ATCCATAAGG AGGGCTGTGT GGAGAAGATT GGGGGGCTCG AG	60 120 180 240 300 360 392
(2) INFORMATION FOR SEQ ID NO:642:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:	
GAGTTGAAGT GGCCAAAAAA TTATAACACT CTCCTACTTT CATATCTTGA TTTTAATTTT TTCCCTTACT TGTATTTTAT TTCTGAGTGG CTAATGGATC TTAGTCTAAG AACTGGAGGT GGAGAACTCG AG	60 120 132
296	

WO 98/45436

PCT/US98/06955 (2) INFORMATION FOR SEO ID NO:643: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:643: GCACAAAGAC GCATTTCATC TGAGTTTCCC TGAAAGCTAG AATAAGTTTG CTGGTGTCAG CTGGGATCCT GTCTTCTATA GCTTTGTATC AAGCAAACTC AGCATTGTGT CTTGAATGCA 120 TGTCATGTGC AGCCTGCGTT TATGTGCGAC TGAGCACTTG GGTGGGGACA TCTTAAGGCT 180 GTTTATATTT CTTTTTCATG TGTTGTTGTT GTTGTTGTTG TTGTTGTTTT GGAGAGAGTC 240 TCGCCCAAAG CTCGAG 256 (2) INFORMATION FOR SEQ ID NO:644: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 447 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:644: GTGCTCGCAG CCNTGGTGGC CTGGCGCTCG GCGTNCCTTG TCTGCCTCGC TTTCTCCTTG 60 GCCACCCTGG TCCAGCGAGG ATCTGGGGAC TTTGATGATT TTAACCTGGA GGATGCAGTG 120 AAAGAAACTT CCTCAGTAAA GCAGCCATGG GACCACCAC CCACCACCAC AACCAATAGG 180 CCAGGAACCA CCAGAGCTCC GGCAAAACCT CCAGGTAGTG GATTGGACTT GGCTGATGCT 240 TTGGATGATC AAGATGATGG CCGCAGGAAA CCGGGTATAG GAGGAAGAGA GAGATGGAAC 300 CATGTAACCA CCACGACCAA GAGGCCAGTA ACCACCAGAG CTCCAGCAAA TACTTTAGGA 360 AATGATTTTG ACTTGGCTGA TGCCCTGGAT GATCGAAATG ATCGAGATGA TGGCCGCAGG 420 AAACCAATTG CTGGAGGATG GCTCGAG 447 (2) INFORMATION FOR SEQ ID NO:645: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 285 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:645: GCTCAGCAAC ATTTTAGGAA CAACATTGGT GAGTATATGA GAATAGCCGT GACCTCCATA 60 TTTCATCAGC CGGGTTTTCG TATGTATGTC ATGTGCTACC AGAATTCGAT CTTCACAGCC 120 CTCTTCCACC AGGAGACGCA CCCTGTGAAA AATGTTAACT CATTAGATGT CATTTGTCTT 180

(2) INFORMATION FOR SEQ ID NO:646:

. AAAGATACTG ACTTCTACTG TGGCGTGTGT ACTGAGAGAC TCGAG

240

285

TCATTTCGC TTTTCAGGAT GCTTTCAACT TTTTACTCAT TAACCTATTG TGCTTGTCGT

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:	
GGAGATTTGA AGAAGAATTG AATGAAAGGA TGATTCAAGC AATTGATGGG ATTAATGCAC AGAAGCAATG GCTCAAGTCT GAAGACATTC AGAGAATCTC ACTGCTTTTC TATAACAAAG FACTAGAAAA AGAGTACCGG GCCACGGCAC TGCCAGCGTT CAAGTATTAT GTGACTTGTG CCTGTCTCAT ATTCTTCTGC ATCTTCATTG TGCAGATTCT CGTGCTGCCA AAAACGTCTG FCCCGGGCTA TCTCGAG	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:647:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 296 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:	
GGGGCAGCAG TAAAATCCAG GCCCGAATGG AACAGCAGCC CACTCGTCCT CCACAGACGT CACAGCCACC ACCACCTCCA CCACCTATGC CATTCAGAGC TCCAACGAAG CCTCCAGTTG GACCCAAAAC TTCTCCCTTG AAAGATAACC CGTCACCTGA ACCTCAGTTG GATGACATCA AAAGAGAGCT GAGGCTCAA GTTGACATTA TTGAACAAAT GAGCAGCAGC AGTGGAGCA GCTCTTCAGA CTCTGAGAGC TCTTCGGGAA GTGATGACGA TAGCTCCAGA CTCGAG	60 120 180 240 296
(2) INFORMATION FOR SEQ ID NO:648:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 324 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:	
GTGCANATGT ACGGTGACCA CCTGGCCCTT GACCGGGCGG CTCGAACCTG GCGGCCCTGG GACCAGCGTC TTCTTCCTCA ACAGCCCGTT CCCCAGAATG TCCAGCCACT CTTCTGGGGC CGGGGCTGGG GCTCCATGGC AGCAAGGAAC TCTCGGGCCA GGGCCCCAGG CTGCTCANCC TCCTCCGCCG GGGGTTGTCC CATGTCCTCC AGCGGTGGCA GCTCACTCAG GTCATCCTCT TCCTCCTCTT CCTCCTCCTC TTCCTCCTCA CCCTCTGCAT CCTCAACCCC ATCCAGTACC TCGAAGTCCT CGAG	60 120 180 240 300 320
(2) INFORMATION FOR SEQ ID NO:649:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 309 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
298	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

GAATTCGGCC TTCATGGCCT ACT	TCCTGAT ACAGATACAT	TTACTACAGA	AAATTTCCTT	60
TATAGGTGTA AATTTCTGTT TACK	AACAGGC GAGTCGAAAA	ATAATAAGAA	CAAAAGGAAA	120
AAAAGCAGTC ATACTTTATT TTAC	GGCAGTT GAGGGGTAGC	TGAATAAGTT	ATCCTGTGTT	180
GTTTGGTTCT GTTACTTATA GCT	CAAAGTC ATCAATATGC	CAGGGTGGCA	TGTTTGGGGA	240
TGGTGCATTC TTGTCTTTTG CAG	TCATTTA TCAGGGTGGC	GTTTCCTAAA	TTCTAACACA	300
GACCTCGAG				309

- (2) INFORMATION FOR SEQ ID NO:650:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GGTGACGCCT	GCTTCACATC	TCTAATGAAC	ACCCTCATGA	CGTCGCTACC	AGCACTAGTG	60
					CCTCATGGCC	120
CGGCTCCTTA	GCACCTCTCC	AGCTCTTCAG	GGAACACCAG	CATCCCGAGG	GTTCTTCGCA	180
GCTGCCATCC	TCTTCCTATC	ACAGTCCCAC	GTGGCGCGGG	CCACCCGGG	CTCAGACCAG	240
GCAGTGCTAG	CCCTGTCCCC	TGAGTATGAG	GGCATCTGGG	CCGACCTGCA	GGAGCTCTGG	300
TTCCTCGAG						309

- (2) INFORMATION FOR SEQ ID NO:651:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

GCAAGGGCAG	GCGGGTCCCC	CAGTCCCGCC	ATTACGGGTT	GTCAGACCGT	CTGCGTGTGG	60
CAGGGCTCCC	AAGGGCAGGC	GGGTCCCCCA	GTCCCGCCAT	TACGGGTTGT	CAGACCGTCT	120
GCGTGTGGCA	TTTTTTGGCT	TATAAGCTTC	ACCCACTCAC	CCCCAACCCA	CACCCCACAT	180
CCCCCTGCCG	GCAGCCCCTC	AACCTAAGAA	GGCCAGAGCA	TATTTATTTT	CGGAGGGAGC	240
AGATTACTTC	TCCCAGAGAA	AGGAAAATCT	TGGAAAAGAT	TTAAAAACAC	AAATCTAAGC	300
CTTGACGGTT	TTTTTTTCCC	TTTTGACCCC	CTTCCCATCT	CTTCAGAATT	TATTCCCATG	360
GCTTTTTTTT	TTCTTGTGCG	TGTTCTCGAG				390

- (2) INFORMATION FOR SEQ ID NO:652:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

GAATTCGGCC	TTCATGGCCT	ACCAAATTCC	CTGCCTGTGC	CTGCTGGGAC	CAGACTCCGC	60
TGTCATGAGG	GTGACATCCG	CCACCTGTGC	TCTTCTGCTG	GCTCTGATCT	GCAGCGTCCA	120
GCTGGGGGAT	GCCTGCCTGG	ATATCGATAA	ACTGCTTGCG	AATGTTGTGT	TTGATGTGTC	180
CCAAGACCTC	CTGAAGGAGG	AGCTTGCTCG	TTACAACCCC	AGTCCCCTGA	CAGAGGAGTC	240
CTTCCTCAAT	GTCCAGCAAT	GCTTTGCCAA	TGTCCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:653:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

GGTGTTTGGC	CACAGTTCGG	GACCTATGGT	AGAAAAATAC	TCAGTAGCTA	CCCAGATTGT	60
AATGGGTGGC	GTTACTGGCT	GGTGTGCAGG	ATTTCTGTTC	CAGAAAGTTG	GAAAACTTGC	120
AGCAACTGCA	GTAGGTGGTG	GCTTTCTTCT	TCTTCAGATT	GCTAGTCATA	GTGGCTATGT	180
GCAGATTGAC	TGGAAGAGAG	TTGAAAAAGA	TGTAAATAAA	GCAAAAAGAC	AGATTAAGAA	240
ACGAGCTCTC	GAG					253

- (2) INFORMATION FOR SEQ ID NO:654:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCGGCCTCCC	AAAGTGCTGG	60
GATTACAGGG	GTGAGCCACC	GCACCCAGCC	TGTGAAATAC	${\tt TATTTTTATG}$	GTAAGCTAGA	120
ATTTTAAAAC	TATTTCTTGC	AAGTTTAGGA	TTAAATGAAT	TACATTATGT	AAAATTACAT	180
CTTTGTCTGT	ATTACGTATT	TGTATACAGT	TGAATAGTTT	TGGTAACACG	TACCTTAGTG	240
CTTTACATTG	ATTGGCTCAT	TAATTTTATA	TTTTGAGTAA	TAATCATCTA	TATTATTAT	300
TGTACAATTC	AGTCTTAAAT	TATGTTATGA	TGTGAAAATG	GTAGCTTTCT	TGAGTGTATT	360
TATTTTTGTA	GTAGTGGGCA	ATGTAATTAT	CACACATAAA	ATGAACTGTG	AGACTTTTGA	420
GCCTGAAATA	TTATTCATAT	TATAATGCTC	CTCGAG			456

- (2) INFORMATION FOR SEQ ID NO:655:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GAATTCGGCC	TTCATGGCCT	AGTATATACA	TGCATTTAAT	TGTGATTTTA	TCACCTTTCC	60
CATTTCTTTC	CCCACAAGCT	GGCATTTCAG	TAGTTGCTTT	TGAATAATGG	TTTTGGTTAC	120
CTGGGAAGGC	AGGCCCAGAA	CCCATTTCCT	TGACTTGCAG	TTCCGGGCTG	TGTTCACATG	180
ACTGCTGTCT	AGCTGATGCA	TTTTTCACAT	TTGTCAACTC	TGGTTAGAAA	CAGGTCCTCA	240
GGAGTATTCT	CTAACCTGAT	ATTTTCTAAA	AAGATATGTT	GATTCAACTT	TGTTTAGCAT	- 300
CCTACTTTCT	AGATTGTGGG	GCTCATTTTG	CCAGGGCCAA	GCTACCAGAA	AAGTAGAAGT	360
GGAGATTACC	TGGTATGTAT	CTCTCTGGGT	GCCCCAGTTA	GAGCTGCCAC	AGCTCAGGAA	420
AAAGATGAGG	CATAACGACC	TTGAATGTAA	TTGGAGTAAG	TGACAAAATA	AGAACTACCC	480
TGGGAAACTC	GAG					493

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

GAATTCGGCC	TTCATGGCCT	ACTTGGCCTT	TGTTTGTGTT	TGCCTTTGTC	AGTCTCCTGC	60
CTCTGGATGG	GTTTCTGTTT	GTTTCCAAAC	TGTCTGGGGC	TGTGCACCAT	GGAGACAGTG	120
TCCTGGGCTG	CCTCTAGCCT	GATCTGGTTA	GAATAAGCCC	CTCTCCTTTG	CATGCGTCTC	180
CAACCTGACA	TTTGGAGCAT	CCAAAACAAA	TCATGACATT	CCCAAGTAAA	GATAGAAACC	240
ACCGTCTCCA	CTCCACTCGA	G				261

- (2) INFORMATION FOR SEQ ID NO:657:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 621 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

GAATTCGGCC	TTCATGGCCT	AGATGGTCTC	TGCTGCTCTT	GCCTCTAGTT	CATGGAGATG	60
TGTCTCTGTT	CAGGCCAAGA	TACAGCCAGC	CAGGCCTGTC	GTCTGGGACC	CAGGAGGCCT	120
CTGATGACCA	AGGGCTTTCA	CATCCTAAGT	CATTTGGAAG	GAGGCCTTGA	GAACAAAGTC	180
ACCTTTGTCA	CTCCCAGTGA	ACTGAATGAG	GAACATGCTG	TCTCCTGTCT	TGGCCTCCCC	240
TTTCATGAGA	TACTGGGGAG	AAGAGAACAT	TCCTCCTGGC	TTAGTTGTAG	CAGACCCAGA	300
CCTGTGCCCA	GCTTTGGTCC	CCCTTCCCAA	CTTCTGAAGC	ACGTGCTGCA	GAGCCACCTT	360
GGTCTGAGCA	CCTGAGGACC	AGCCCCTCCT	CCCTCAGTGC	GGGTCATCTC	TTGGGGGATT	420
TTCTTAAAGT	GAAGAAAGGG	GGTGGGGAAC	CATATTGCCC	CTCCCTCCCC	CATCAAACTT	480
CCTTCATTTA	ACTTGCTATA	AAATGAGTCA	TATAAAGAAA	CTCTATATGG	GTGAGGTATA	540
TCCCACTTCT	GTGAAAACAT	TACAAATCAA	ACCGCTTCTC	TCAGTTTATT	TAAGATGCTT	600
TTGTTGCAAG	CGGTACTCGA	G				621

- (2) INFORMATION FOR SEQ ID NO:658:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 567 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

GAAGTCTTGG	AGATTTCTAG	TTTATTCATT	AACAGCAGAA	GGATGGAAGA	AAATTCCTCT	60
GGCAATACCA	TGTCAGCCTC	TTCGATGTTT	AATACAGAAG	AAAGAAAATG	TTTGCAGACT	120
CACAGAGTCA	CGGTGCATGG	GGTCCCAGGG	CCAGAGCCCT	TTACCGTTTT	CACTATTAAT	180
GGAGGCACCA	AGGCAAAGCA	GCTTCTGCAG	CAAATTCTGA	CAAATGAACA	AGACATCAAA	240
CCTGTTACCA	CAGACTATTT	TTTGATGGAA	GAAAAATATT	TTATATCTAA	AGAAAAGAAT	300
GAATGTAGGA	AACAACCATT	CCAGAGAGCC	ATTGGTCCAG	AAGAGGAGAT	CATGCAAATT	360
TTAAGCAGCT	GGTTTCCAGA	AGAGGGATAC	ATGGGCAGGA	TTGTCTTAAA	AACCCAGCAG	420
GAAAACCTAG	AAGAGAAAAA	CATTGTTCAA	GATGACAAAG	AGGTGATCTT	GAGCTCAGAG	480
GAGGAGAGTT	TCTTTGTCCA	AGTGCATGAT	GTTTCTCCAG	AGCAACCTCG	AACAGTCATC	540
AAAGCACCCC	GCGCCAGCAC	ACTCGAG				567

- (2) INFORMATION FOR SEQ ID NO:659:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GAATTCGGCC	TTCATGGCCT	AGGCCCTTTG	GCCCTGGGGT	GGGGGTGCTT	ACTACATCCC	60
TGGAAGGTGC	AGGGAGGCTG	ATGGCCTTGA	TCTCTAACAC	AAACAGGAAC	CAGCTTCCTC	120
CCTCCCCCAC	CCTGGGTTCC	CAGGGCCTCC	GGGTGTGAGA	TCCTCCCCCA	CTGCAGTGCC	180
CCACCCGCTC	CCCACAGAAG	CCCGGAGAGT	GGCTCTGTCA	CCAGAGGTGT	CATTTCCCAG	240
CTGTCTGTGG	GAGGTGAGTG	AGCAGGGAAT	GTGTGTGCTG	GGTGTGGGAA	CTCAGCCCAA	300
TCTAAGAGAA	GATACTCTTG	GCTTCCTCCC	CCTCAGAGGA	GCAGCCGCGT	CCCTGGTCCT	360
TGTGCACTGA	CAGTCCCGGA	GTCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:660:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

GAATTCGGCC	TTCATGGCCT	AGCCAGGAGT	TGAGGTGGAA	GTCACCATTG	CAGATGCTTA	60
AGTCAACTAT	TTTAATAAAT	TGATGACCAG	TTGTTAACTT	CTGTTGGTTT	TTATTCAGAA	120
TACTGGCAGA	TTTTAGGAAT	ATAAAGGTGT	ACTATGAGAC	TTCCACTTTT	CAGGTGGAAT	180
ATATGGGTAT	CTTAGAGTGG	TCTATCCTGT	TTTCGTTGTC	GTTTGAGTCA	TTTGAAAACT	240
GGATTCCGTT	AACTACATAA	TATGTGAGAC	CTGACTGGTT	TTATTGGACA	CTGGCAGTTT	300
			ATTGGTATGG			360
GTTTGTAATG	CACACCCATG	GTTGAGAACC	TAGTGCGCTA	GTAGGCACGT	GTTAAAAAGC	420
TAGTAACTAA	TATTTTTAAA	TTAACCAAGT	TTAACGTCCT	TAAAAAAGGA	TTAAGTGGCA	480
AGGACCTCGA	G					491

- (2) INFORMATION FOR SEQ ID NO:661:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

GAATTCGGCC	TTCATGGCCT	ACCTCAATAT	GCTATCAGAT	TCTGAAAATT	CCCAGCATCT	60
GGAACTTCAT	GAGCCACCAA	AAGCTGTGGA	TAAGGCGAAA	TCCCCAGGGG	TTGATCCTAA	120
GCAGTTGGCA	GCAGAACTCC	AGAAGGTTTC	ACTACAGCAG	TCACCGCTGG	TTCTGTCATC	180
AGTTGTTGAA	AAAGGATCTC	ATGTTCATTC	AGGTCCTACA	TCAGCAGGAT	CCAGTTCCGT	24.0
TCCCAGCCCT	GGGCAACCAG	GGTCCCCCTC	AGTGAGCAAA	AAGAAGCACG	GCAGCAGCAA	300
GCCACTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:662:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 404 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

GAATTCCTAT	GGCCTACTTC	CGGCGCAAGT	GGCTTCTGAT	AATCATGGCG	CCCCTCGGAA	60
CAACTGTATT	GCTGTGGAGC	CTCTTGAGGA	GTTCTCCGGG	CGTGGAACGG	GTCTGTTTCC	120
GGGCTCGAAT	CCAGCCCTGG	CACGGTGGCC	TGCTCCAACC	GCTACCTTGC	TCTTTCGAGA	180
TGGGGCTGCC	ACGCCGCCGG	TTCAGCTCCG	AGGCCGCAGA	ATCTGGTAGC	CCAGAGACCA	240
AGAAACCTAC	ATTTATGGAT	GAGGAAGTTC	AAAGCATACT	CACGAAAATG	ACAGGCTTGA	300
ACTTGCAGAA	GACTTTTAAG	CCAGCTATAC	AAGAACTGAA	GCCACCAACC	TATAAGCTAA	360
TGACTCAGGC	ACAGTTGGAA	GAGGCTACAA	TACAGGCTCT	CGAG		404

- (2) INFORMATION FOR SEQ ID NO:663:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GA.	ATTCGGCC	TTCATGCCTA	ATTTGTGTGA	TGGCCAAAGA	GTTCTTATCA	GAAGTGGCAA	60
AA	ACTACATA	CAGGTTGGCT	TCCAATAACA	TGAGCCAGGT	ATTTTTCAGT	AATATTTTGA	120
AG	TGTCTTTT	CTTTCTAGAC	ATGCACATGA	TGGTGTCCAA	GCCAGAACAG	TGGGTAAAGC	180
CA	ATGGCTGT	AGCAGGAGCC	AATCAGTACA	CCTTTCATCT	CGAG		224

- (2) INFORMATION FOR SEQ ID NO:664:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:664: GAATTCGGCC TTCATGGCCT AGGTCTACCA AAGTGAGGAC ATTACTGCAG ATATTCTTCT CCTTTTCTCC TACATTATCA TTTCTCTTTT ATAACATCAT TTCTGCAGAT ATGTAAAAAT 120 ACATCCCATC TTCAAAAAGA AAAACAAAAA TCTGACTGTA CTTCATATCC CCTTCTAGAC 180 ATTGCCACAT TTCTCTACTT CTGTTTACAA CAAAACTCCT GGAAAGATTT GTCTATACTG GCTTTCTCTA CTTCTTTTAC TTCCATTCCT TTCCTAACCA CTCTAAACAT GCTTGGGTCC 300 CCACCACTGT AACAAATATA ATTTGTGTCC AATAACCAGT GATCTCTGTA TCACCGGTTC 360 CAAGGGTGAG ATCTCAGACT TCACCTTTCT GGATTGATTG ACACATTGGA CTCAGTTGGT 420 TACTCCTCAC TTCTTGAAAC TGTCTTCACT GGGCTTTTTG GACTCCATAT CTCGAG 476 (2) INFORMATION FOR SEQ ID NO:665: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:665: GAATTCGGCC TTCATGGCCT ACTCTCTACT CCTTTGTGCT CAATTTCCAT TGTGGAATTC TGCATATATG ATCTTGTGGC ACATTTCTAC ATTTCCTCAG CCCAGAAGGC CTTCCCTGTT 120 CACTATCTCC TTCTTTTTAC TAACTCTTAC TATATTTCCA GGCACAGTTC AGGCATCAGA 180 TAGCCCTATT TGTTCCAACT TTCACCGTAG GTCAGATTAT AAGCCTTGCA ATCTCGAG 238 (2) INFORMATION FOR SEQ ID NO:666: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 361 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:666: 60 GAATTCGGCC TTCATGGCCT AGACCATTTT CATTGTTTAT AGTTTATTTC TTATAAATAG TGCTTTCTGG AATATCCTTA AATACCTCTA TCTTTTTAAC ATCCTTGTGT ATACATCTTT TCTCACACTT GGCTTCCTCT TGGAATAGAA TCTCCTGGAA ATTAGATAGC TGAGGTAAAA 180 GTCCCTGAAC CTTTTACAAA TTGCTACACA ATAAATACCA AACTGATTTT CAGGAATGTA GTCCCATCAA CAGTGTGCTT GTTTATCCAT ATCGTTGCTG ATCTGAGTTT TGTCAGTCTA TTGATTCCTA CCAATCTGCC AGTATCATAG ATTTTAAAAT ATTTTTTGTG TGCATCTCGA 360 (2) INFORMATION FOR SEQ ID NO:667: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:	
GAATTCGGCC TTCATGGCCT ACTCATACAC AATGAATACA AAAACTGGAA CTCTGCAATT TAATACTGTT TCCAAACTGG ACACTGGAGA ATATTCCTGT GAAGCCCGCA ATTCTGTTGG ATATCGCAGG TGTCCTGGGA AACGAATGCA AGTAGATGAT CTCAACATAA GTGGCATCAT AGCAGCCGTA GTAGTTGTGG CCTTAGTGAT TTCCGTTTGT GGCCTTGGTG TATGCTATGC	60 120 180 240 300 343
(2) INFORMATION FOR SEQ ID NO:668:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 266 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	¥
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:	
GAATTCGGCC TTATCCTACA ACTTTGAATA GACATAAGAG TGCCTGTCTG CATAAACCTT CATCAACATT GGTATTATCT TTCTTTTTCA TCTTTGCTAA TTGGATAAGT TTTAAAAAAGT GTAACACATT TTAGTTTGCA TAGCTTTGAT TATAAGTGAG GTTCGACATT TTTTTTCATT TCTTTACACT TTAAAAAAATC TAACCGTGGC AACGTTTGCA GGTGTGTGT CTTCTTATGT TGCTGAGTGT TATTTACTCC TGGACG	60 120 180 240 266
(2) INFORMATION FOR SEQ ID NO:669:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 452 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:	
GAATTCGGCT TCATGGCCTA CAAAAAAGAA ATTAAGAAGC TCCTAAAGAC GCAAAGAAAT CATCTACTCC TCTGTCTGAA GCAAAAAAAC CAGCTGCTTT AAAACCAAAA GTACCCAAGA AGGAAAGAGTC TGTCAAGAAA GATTCTGTTG CTGCCGGAAA GCCAAAGGAG AAGGGGAAAA TAAAAGTCAT TAAGAAGGAA GGCAAGGCCG CAGAGGCTGT CGCTGCAGCT GTCGGCACTG GAGCCACCAC AGCAGCTGTC ATGGCGGCAG CTGGAATAGC AGCCATTGGC CCTGCCAAAG AACTCGAAGC TGAGAGGTCC CTTATGTCAT CTCCTGAGGA TCTAACCAAG GACTTTGAAG AGGACATCAA GCCTCAGCTG GAGCTAATCG AAGACCGAAGA GAAAACTCG AG	60 120 180 240 300 360 420 452
(2) INFORMATION FOR SEQ ID NO:670:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 284 base pairs(B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

GAATAATTGA CTGAAAGTGT	AGTGTCGAGT	GGTAGAATAA	GTGCTGATCC	TGGGGTCTTA	60
TACCAATGTT GCTAACTGTG	AGCAGCCTTT	GTCAAATCAC	TTGGCTTCAT	TTTCAGTGGC	120
CTAAGAGTAA TAGGTTTAAT	TATTTCCATA	ATTCCTTTAA	GTTTTTACAT	TTTCTGAGTT	180
CATCTTTTGT GTTTTTCCTG	GCATTTTACT	ATTCCTCTTT	CCTGCTTTTG	GCTATTTTCT	240
CAACAGGTCC ACGACTGGAA	TTTGAAAGCA	AGAAACATCT	CGAG		284

- (2) INFORMATION FOR SEQ ID NO:671:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

GAATTCTGGA	AGCAGCCTAT	CATCGCTCCG	TCTGCCCTCC	ATACACAGCG	TTTGTGTGTG	60
TTATGCCAAA	CTGCTTGGTG	TTTTCCAACC	GTGGACCATG	ATATCTCACT	TCCTTAACCT	120
TACCTTCATA	TGCTTTTCCT	TTGTGTCTTC	TTCTGAAATG	CTTCTTCCTT	TTGTCCAGGC	180
TGACTCCTGT	TTGTCTGAGA	CATGTGTCTC	AGGAAGCCTT	TCCGTTCCCC	TCGAG	235

- (2) INFORMATION FOR SEQ ID NO:672:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

GAATTCGGCC	TTCATGGCCT	AGCATTGATG	GCCCATGTAG	AAGACCTGAT	CATTAAGACT	60
ATAATCTCTG	CTGAACTAGC	TATTGCTACT	GCCTGTAAAA	CCTTTGTTCC	TCATCGCAGC	120
AGTTGTTTTG	AACTCTATGG	CTTTGACGTG	CTCATAGATT	CTACTCTGAA	GCCATGGTTG	180
TTGGAAGTGA	ATCTCTCTCC	TTCTTTGGCC	TGTGATGCGC	CTCTGGACCT	AAAGATTAAA	240
GCCAGTATGA	TTTCAGATAT	GTTCACTGTT	GTAGGATTTG	TGTGCCAAGA	TCCTGCCCAG	300
CGGGCATCAA	CTCGGCCAAT	TTATCCCACC	TTTGAGTCTT	CCAGGCGAAA	CCCTTTCCAG	360
AAACCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:673:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi)	SEQUENCE	DESCRIPTION:	SEO	ΤD	NO - 673 -

GAATTCGGCC TTCATGGCCT ACACAGACAT CATCATGCAG AAGATGACCA TTTCCAACAT	60
GGAGGCAGAT ATGAATAGAC TCCTCAAGCA ACGGGAGGAA CTCACAAAAA GACGAGAGAA	120
ACTITICAAAA AGAAGGGAGA AGATAGTICAA GGAGAATGGA GAGGGAGATA AAAATGTGGC	180
TAATATCAAT GAAGAGATGG AGTCACTGAC TGCTAATATC GATTACATCA ATGACAGTAT	240
TTCTGATTGT CAGGCCAACA TAATGCAGAT GGAAGAAGCA AAGGAAGTAC TCGAG	295
(2) INFORMATION FOR SEQ ID NO:674:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 156 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(and) appropriately and an area of	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:	
GAATTCGGCT TCATGGCCTA CCTGCCTCGA GTGATGGGTA TCGGGATGGG TATCGGGATG	60
GCCCACGCCG GGATATGGAT CGATATGGTG GCCGGGATCG CTATGATGAC CGAGGCAGCA	120
GAGACTATGA TAGAGGCTAT GACTCCCAGA CTCGAG	156
(2) INFORMATION FOR SEQ ID NO:675:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 265 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(11) Holdcold IIIE. CMA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:	
-	
GAATTCGGCC TTCATGGCCT AATAATTTGT AAGTTAAAAT AAGTAATACA AATTAAATGC	60
AAATCAAATG CCTGAAGAAG AAGCACGAAT ACCTATTTTG AAATCTGCTG TAGCCGAGAC	120
AGCTTCTAAA TCTCCCACTT GGGTTCTGTT TCTGGAAGGT GTGGGTCCTG TGGTAGCTGG	180
AGTGTTGGTG GCCATCTTGG TGCTGGCGGT CCTCATGCTG ATGTACTACT GCTGCAGACA	240

(2) INFORMATION FOR SEQ ID NO:676:

GAACAACAAA CTTGGCCAAC TCGAG

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

GAATTCTGGA	TCAAAACAGA	GGAAAATGGT	GGGAATTCTT	GTATAGATAC	AGTCTAACAT	60
AGAAACCCAT (GCCCATCAGC	AGTAATTTCC	AGTCCCCCAG	TCCTCCAAGC	CCTGGTACTC	120
GAG						123

265

(2) INFORMATION FOR SEQ ID NO:677:

308	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 373 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(2) INFORMATION FOR SEQ ID NO:680:	
GAATTCTAGA CCTGCCTCGA GTACCTGATC TTTTACTGTC TCTATAGGTT CATCTTTTTC TTCCCTTTGT TAATTCTACT TTTTAGTTTT TTTGCTAGAT TTTTCTTGCA ATTGGATAGG CCCATTTAAC CTATTTTGCC TCCACTCTAA ATTCAGTACT CCAAGAATTG GTTTCACTCT TCCAAATTTT GTATATAAGC CAGAGTTCTG CATAAAGGAA AATACTTAAA TTCTTTCTAA TCTAATGTGG TTTCCTGCAT CTTTCAGGAA ACTTTTCCTC GAG	60 120 180 240 281
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:	
(ii) MOLECULE TYPE: cDNA	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 283 base pairs (B) TYPE: nucleic acid	
(2) INFORMATION FOR SEQ ID NO:679:	
GCGATTGAAT TCTAGACCTG CCTCGAGACC ACCTATGGAA GCCAAGTGTT CCCGGGCCAT GAGACCTGCC CAATCAAGCA GAAACACATT TGGAGAGACA AACAATCACG ACACGCTCGA G	60 120 121
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:	
(ii) MOLECULE TYPE: cDNA	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	-
(A) LENGTH: 121 base pairs (B) TYPE: nucleic acid	
(i) SEQUENCE CHARACTERISTICS:	
CCG (2) INFORMATION FOR SEQ ID NO:678:	243
GAATTCAGAG ATAAAGCTAA AGTTCCATTT GAGCACCAGC CCAAATCCTG GACTTCTTTC TGCTCCTCCT CAGAGGTTCT CTGGTTATAA GTTTTATGTG TATCTTGCCA GAATTTTTCC TATGTTATTA ATACAAATAT ATGTAGCCAC AGAAATTATA GCGTGTCATT CAGCCTTTGG TTTTATTTGC ATTGATAGTA TTATGTCCAT ATCACTCTAC AACTTCTTAG GCCATGAAGG	60 120 180 240
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:	
(ii) MOLECULE TYPE: cDNA	
(A) LENGTH: 243 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(i) SEQUENCE CHARACTERISTICS:	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GAATTCGGCC	TTCATGGCCT	AGGGTTTGTG	GCTAAAAATT	ATGCTTAAGA	ACACATCTAA	60
CAAACCTAAA	GCTGCAAAGA	CATAATGTTA	ATGTAGGTGA	AAATTTCACT	TGTGTTTATT	120
CTGATAGACA	AAATTGTATT	TTAGATGAGA	AGCAACAATT	TTCATGTTGT	ACTGAGATTG	180
TTAGTAATGA	AATACTTCCA	AATATTAGTG	ATGGTAGAAA	TCTAGTGTAG	GGCTCTTTGC	240
TGAGAAGGGA	AAAAAGTCAC	ATAAGAAATC	TACTTTTCAG	TAAACTGCAA	ATATGTGTGC	300
TTCAACCTAT	AACATATTCT	GTCACTTTGA	GCTTGTCATA	TTGACAGAGA	ATGAAAACTT	360
GATAAGACTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:681:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GAATTCGGCC TTCATGGCC	T AGAGCGACTT	CGACACCATG	CCAGACATTG	AGAGTGATAA	60
AAACATCATC CGGACCAAG	A TGTTCCTTTA	CCTGTCAGAT	TTGTCCAGGA	AGGACCGGAG	120
AATTGTCAGC AAAAAATAT	TTTATTTAAA A	TTGGAACATC	ATCACCATTG	CTGTGTTTTA	180
CGCGCTGCCC GTGATCCAG	C TGGTCATTAC	CTATCAGACA	GTAAGTGCTA	AACCTAGCCC	240
CAAACCCCTC GAG					253

- (2) INFORMATION FOR SEQ ID NO:682:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

•						
GAATTCGGCC	TTCATGGCCT	AATCGAGGAG	AATGGAGACC	AAACCTGTGA	TAACCTGTCT	60
CAAAACCCTC	CTCATCATCT	ACTCCTTCGT	CTTCTGGATC	ACTGGGGTGA	TCCTGCTGGC	120
TGTTGGAGTC	TGGGGCAAAC	TTACTCTGGG	CACCTATATC	TCCCTTATTG	CCGAGAACTC	180
CACAAATGCT	CCCTATGTGC	TCATCGGAAC	TGGCACCACT	ATTGTTGTCT	TTGGCCTGTT	240
TGGATGCTTT	GCTACATGTC	GTGGTAGCCC	ATGGATGCTG	AAACTGTATG	CCATGTTTCT	300
GTCCCTGGTG	TTCCTGGCTG	AGCTCGTAGC	TGGCATTTCA	GGGTTTGTGT	TTCGTCATGA	360
GATCAAGGAC	ACCTTCCTGA	GGACTTACAC	GGACGCTATG	CAGACTTACA	ATGGCAATGA	420
TGAGAGAATG	CTCGAG					436

- (2) INFORMATION FOR SEQ ID NO:683:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:683:	
TTTTTTTTA C ATAACATTAA C GTCACCATTC T	TTCATGGCCT AGTCCCCACT TTATCTCTTT AAACGGTTTC TTTTTTCTTT GACCTCTCAG GGATGAAACA TTTTATTTTT TAAACTAGTT TTTTTTTTAA CACATGCTGA ATGCTTAAAT CTTTTTTAGAA TTCAGAAAGG TAAAATGAAA TCATTCTCAT CATCTTACTC CCAGAGATGA TTGTTATTAA TATTTCCAGA GTATATGCAA ACAGCAATAT ATTGTAGCTG CTCGAG	60 120 180 240 286
(2) INFORMAT	FION FOR SEQ ID NO:684:	
(i) S	GEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:684:	
ACTTCTCAGC (ACTCCCATCT TTATGGTATT	TTCATGGCCT ACCCTTACCA GATACTGAAT CTGCCAGTGC CTTATTTTGG CTCCTGGGCT GGGTGAGGTG GTTCACTACC AGCCTTGGCA CCATAGTGAG CTACAAAAAA AAAAAAAAA AAACTTTCTG TTGTTTGTAA GCTACCCAGT TTGTTACAGC AACCCAAACA GTCTGAGACG TTTAGCTTAA CTCCTGTATG AGTCTGCACT TTGACATCAA TCTCGA	60 120 180 240 276
(2) INFORMA	TION FOR SEQ ID NO:685:	
(i) S	SEQUENCE CHARACTERISTICS: (A) LENGTH: 155 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:685:	
CTTATTACAT	TTCATGGCCT ACTAAGAATA GGAAAAAAAA TAACACTATG ATACCACAAC CAAACTGCTT TGGGCTTTAT CCTCTTTAAA GTGTGCTCAG GTGTTCAGCC TGACAGCCCT CATAAGACCT TCGAG	60 120 155
(2) INFORMA	ATION FOR SEQ ID NO:686:	
·(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 301 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: CDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:686:	

60

120

GAATTCGGCC TTCATGGCCT ACTTTGAAGA GTACGATTTC AAAACCAGCA ATTGGTGTGA

ATGCAAAAAC ATTTGTTGGC ACCATTTATT TAAAAAAAAA AAAAGCTGTA TGCAGCAGAA

AGCCTTATAC AAGTTGTTTT TCTTTTTTC CTTTTTCTTT TTTTTGGTAC CTTCATTTCT GTTACTTTTA TATAAAATTC TCTGCAAAGG AAGGCCTCTC TTTGGACTAC AATTTGGAGG CAGCCACTTG TTGTGCCTGC TTCTGTTAAA GAATGTGGAT ATCAAGCCCC CCCGACTCGA G 300)
(2) INFORMATION FOR SEQ ID NO:687:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:	
GAATTCGGCC TTCATGGCCT AATTTTACA GAAATTATTT CCACAATCAG AAGTACTGTA CTGATTGCAT TTCTTTGTCT CAAAAAGTTT TCCTTATGTT TCTCAAAGCA GTATTTACAC TAATTATTCA ATTCTTATCT TTCTTTCAGT TTTCTCCAAT AGACTGTGAG ATCTTTGAGG GCCAGGTTGA CATGCTCTG ATACCTACAC CCTATGCAGC TCCTAGTGCA GGACCTTGCA GTGACAAGCT CGAG 256	0
(2) INFORMATION FOR SEQ ID NO:688:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 261 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:	
GAATTCGGCC TTCATGGCCT AATATTTATT TAGATGCTAT TATTACTGTT TGGACTTTTA 6 TTTTGGCAGG CTTTGTTCCA GACTGTAGGG TTTTCCAATG TGACTAATGA CCACTCCTGC 12 CTCTCCCGTG GTGTATTTTG GGCACCCTCC CACCCGGCTG CATACCCGGC CAGGGCTCCC 18 ACAGAGACAA GGAGGCACA GGTGTCTGCC CCCTCTTTGA AATCGATATA CACACATCCA 24 CGCACATGCG GCCCACTCGA G 26	0
(2) INFORMATION FOR SEQ ID NO:689:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 214 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:	
GAATTCTAGA CCTGCCTCGA GCTTCTGGCT GTTGTCTTTG CTGGGCATCC TTTTTACAAG TGGAAGAACT AGGATGGCTT TCCAAAGTCT TCTAGAAATG AAGTTCTTTC TCTGTGCAGC TTTCCCCCTT GGAGCAGGAG TGAAGATGTT TCATTATCTT GGGCCTGGGA AACCACTTCC CCAGGCTTCT CCCTCCCCCC ACCCCCGACT CGAG 2	9 (9 (

(2) INFORMATION FOR SEQ ID NO:690:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GAATTCGGCC	TTCATGCCTA	CAAACTTAAA	AGTAAATCTT	TGGAAATCAG	ATAGTAGTCT	60
TGAAACTATG	GAAAACACAG	GAGTGATGGA	TAAGGTTCAG	GCAGAGTCTG	ATGGGGACAT	120
GTCTTCAGAT	AATGACTCAT	ACCACTCTGA	TGAATTCCTT	ACAAATTCTA	AGTCTGATGA	180
AGACAGGCAG	CTAGCTAACT	CATTAGAGAG	TGTAGGGCCA	ATAGATTACG	TTCTTCCTAG	240
TTGTGGTATT	ATTGCCTCAG	CGCCTCGATT	GGGCAGTCGG	TCCCAGTCTC	TTAGCAGCAC	300
ACTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:691:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

GAATTCGGCC	TTCATGGCCT	ACTCCATATT	TATTTAGATG	CTATTATTAC	TGTTTGGACT	60
TTTATTTTGG	CAGGCTTTTT	TCCAGACTCT	AGGGTTTTCC	AATGTGACTA	ATGACCACAC	120
CTGCCTCTCC	CGTCGTCTCT	TCTGGGCACC	CTCCCACCCG	GCTGCATACC	CGGCCAGGGC	180
TCCCACAGAG	ACAAGGAGGG	CACAGGTGTC	TGCCCCCTCT	TTAAAATCGA	TCTACACACA	240
TCCACGCACA	TGCGACCCCG	AGGAAACGAA	ACCCACTCTA	GAAAACGCGA	CCTTGGCCGC	300
ACCTAAAGCA	GCCAGCCGTG	AGTGCAGACC	CCTTGGCCAG	CGTGGCGCAG	TGGCCCTGAG	360
CAGTAGTGGC	GTGTGTGTAG	ATCAAGTCGG	ATCTAGTCCA	GCTCGGTTCA	TTAGCGATCC	420
ATGTAATCTG	ACGTCATCTT	GTCTCGAAGT	CTCTTTTTTT	GGCCCAGGCC	TTGAAGAATA	480
CACTGGACTC	GAG					493

- (2) INFORMATION FOR SEQ ID NO:692:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GAATTCTAGA	CCTGCCCCTG	CCTCCTGCAT	CCAGCCCCCA	ACATGGTGCC	AAAGCTTCCA	60
GAAGCCAAAA	AGCTTCTGAT	TTTTAAGGTA	GTGGGCATCT	CTCTCCTAAT	GACGAAGCTG	120
CTCAGCAACT	CCACCTGCCC	GCCGCAGGAA	GGAGCAGTCC	CCTGCTATCC	CTGCAGCCAC	180
TCCCAGCACA	CCCGCACACA	GCCAGCACCA	CCGCCCACTC	TCGAG		225

- (2) INFORMATION FOR SEQ ID NO:693:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) Torobodi. Illiedi	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:	
GAATTCGGCC TTCATGGCCT ACTGGCTCAT ACAATACATC AATAAGTATG CAACTTTTCA	60
TTTGTTATTT CGTTGCTGGA AGTGGGAAAT ACCCCATCTT CCCAGGAGTG AAATGGTTCT	120
ACTITICTCC CGTGGTGCCC TGTATCATTA CTCAGCTCTG CTGCTGCTCT CCGCAGCCCC	180
TAAAAGTAGC ATGGATCGGG GAAGAAGGAA GGACGGCAGG AAGGCAGGCA GAGATCCTCA GGCAGGTCGA G	240 251
(2) INFORMATION FOR SEQ ID NO:694:	
(2) INFORMATION FOR SEQ ID NO. 054.	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 294 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:	
GAATTCGGCC TTCATGGCCT AGTGTGTGT TGCGTGTGTG TGTGTTTACA TATAAAGTTT TTTGGTAACA AATAAATTTT GTTAGAGCTA GTCAGATTTT TGTTTGCTTA ATCTGCTAGT	60 120
TTTGGTAGGT TATATTTTTC AAGGAATTTG TCCATTTCAC CTATGTTGTT GAATTTTGGG	180
TGTAACGTTT TTCATTACTC TTTTCTTTTT AATATCTGTG GGATCTGTAA TGATGCCCCC	240
TCTTTCATTC CTGATATGAG TAATTCTTAT TCTCTTTTTG TCTATCAGCT CGAG	294
(2) INFORMATION FOR SEQ ID NO:695:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 246 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:	
GAATTGGCCT TCATGGCCTA ATTGGGACCA AATAGAGGCT CACAGATATT TGGATTATTT	60
TATGTGCTTA TTATTAAATA AGGAAAGCAT TTTGTGATAT GTGGAAGACG CTATGTGAAG	120
TTTTACCTAT CTTCTCAAAG ACCTTTTCTT TTGTATTTTC TTTTGGTGTT TCTTAAAGCC	180
AAACAAAGAA ATGTTCTTAA GGAGACAGGG TGGGTTTTTC TGTGGGCCTA GGCCATGAAG	240
GTCGAG	246
(2) INFORMATION FOR SEQ ID NO:696:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 349 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

GAATTCGGCC	TTCATGGCCT	ACCCTAATAT	AAAAAGCATT	GTCACCATGT	TGATGCTGAT	60
GCTATTGATG	ATGTTTGCTG	TCCACTGTAC	CTGGGTCACA	AGCAATGCCT	ACTCTAGTCC	120
AAGTGTAGTC	CTGGCCTCAT	ACAATCATGA	TGGCACCAGG	AATATCTTAG	ATGATTTTAG	180
AGAAGCTTAC	TTTTGGCTAA	GGCAAAATAC	AGATGAACAT	GCACGAGTAA	TGTCTTGGTG	240
GGATTATGGC	TATCAGATAG	CTGGAATGGC	TAATAGAACT	ACGTTGGTGG	ATAATAACAC	300
CTGGAATAAC	AGCCACATAG	CACTGGTGGG	AAAAGCTATG	TCTCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:697:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 220 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GAATTAAATA	AGTTACTGAC	TTTGTGACTT	ATTTAATTCA	TATTAATATA	TTAGGCTTCC	60
CAACTGACGG	TGTTGCAGTT	GAGCTAGCTT	CCAGTTTTGG	AGAAACACAT	AGTTGATTAG	120
TTCTGTCAGT	AATTTTCAGG	GATATTAATA	TAACTTTGAT	ATTAGTGAGA	AATTTTCTTT	180
CAGTAGTAAA	ATGTTTTCTA	ACTTAGGAGC	TGTTCTCGAG			220

- (2) INFORMATION FOR SEQ ID NO:698:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

GAATTCGGCC	AAAGAGGCCT	AGCAGAGCTT	TCATATCCAC	GATGCGTTTT	CTGGCCGCCA	60
CGATCCTGCT	GCTGGCGCTG	GTCGCTGCCA	GCCAGGCGGA	GCCCCTGCAC	TTCAAGGACT	120
GCGGCTCTAA	GGTGGGAGTT	ATAAAGGAGG	TGAATGTGAG	CCCATGTCCC	ACCGATCCCT	180
GTCAGCTGCA	CAAAGGCCAG	TCCTACAGTG	TCAACATCAC	CTTTACCAGC	GGCACTCAGT	240
CCCAGAACAG	CACGGCCTTG	GTCCACGGCA	TCCTGGAAGG	GATCCGGGTC	CCCTTCCCTA	300
TTCCTGAGCC	TGACGGTTGT	AAGAGTGGAA	TCAACTGCCC	CAGTACAGTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:699:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GCGATTGAAT	TCTAGACCTG	CCTCGCTTCC	CCACCCTTAC	TAACATTAAC	GAAAATAACC	60
CCACCCTACT	AAACCCCATT	AAACGCCTGG	CAGCCGGAAG	CCTATTCGCA	GGATTTCTCA	120
TTACTAACAA	CATTTCCCCC	GCATCCCCCT	TCCAAACAAC	AATCCCCCTC	TACCTAAAAC	180
TCACAGCCCT	CGCTGTCACT	TTCCTAGGAC	TTCTAACAGC	CCTAGACCTC	AACTACCTAA	240
CCAACAAACT	AAAATAAAA	TCCCCACTAT	GCACATTTTA	TTTCCCCAAC	TCCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:700:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GAATTCGGCC	TTCATGCTTA	GCCTCAGCTC	TTTCTTCTGG	GTTGTTTGTA	TTTTCTTTTC	60
TGTCCCAAAC	AGTTTCCCCC	ACAAAAAGAA	CTTTATGTCT	TTCTCTGTCT	TCCCTCAGTC	120
CTTCCAGTCA	GCAGCCTGTG	ATTGGGCTTT	TCCCCTCAGA	AACGAACAAT	CCAGAACCCA	180
CTGTTTAAAA	CAACTGTATT	TTGCCTTGGG	AAGTCCCATT	GCCTTCCCTG	AAAACATTAA	240
ACATTCCTCC	GATCCCCAGC	CTGAGTCTCT	CTGTCTCTGG	GCCCCATCCT	GCTCCACAGC	300
AGGGCTGGTG	TGTCCAGCAC	AGAGTGACCC	TCCGATGCCC	TTTCCCACCC	GCCGCCCTGC	360
CTCCCTCGAG						370
						370

- (2) INFORMATION FOR SEQ ID NO:701:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GAATTCGGCC	TTCATGGCCT	AGGAAAGATC	TAATTATCAT	GGACCTGCGA	CAGTTTCTTA	60
TGTGCCTGTC	CCTGTGCACA	GCCTTTGCCT	TGAGCAAACC	CACAGAAAAG	AAGGACCGTG	120
				TGCTCAGAGT		180
ACCATGATGC	CTTCTTGGGT	GCTGAAGAAG	CAAAGACCTT	TGATCAGCTG	ACACCAGAAG	240
AGAGCAAGGA	AAGGCTTGGA	AAGATTGTAA	GTAAAATAGA	TGGCGACAAG	GACGGGTTTG	300
TCACTGTGGA	TGAGCTCAAA	GACTGGATTA	AATTTGCACA	AAAGCGCTGG	ATTTACGAGG	360
ATGTAGAGCG	ACAGTGGAAG	GGGCATGACC	TCAATGAGGA	CGGCCTCGTT	TCCTGGGAGG	420
AGTATAAAAA				AGATCCTGAT	GATGGATTTA	480
ACTATAAACA	GATGATGGTT	AGAGACGTTC	TCGAG			515

- (2) INFORMATION FOR SEQ ID NO:702:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

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PCT/US98/06955	
GAATTCGGCC TTCATGGCCT AGGGGACCTG ACGTTCACTG TGGCCCAAAA GATGGCTGAG	60
CCAGAGAAGG CCCCAGCCCT CAGCATCCTG CTGTACGTGC AGGCCTTCCA GGTGGGCATG	120
CCACCCCTG GGTGCTGCAG GGGCCCCCTG CGCCCCAAGA CACTCCTGCT CACCAGCTCC	180
GAGATCTTCC TCCTGGATGA GGACTGTGTC CACTACCCAC TGCCCGAGTT TGCCAAAGAG	240
CCGCCGCAGA GAGACAGGTA CCGGCTGGAC GATGGCCGCC GCGTCCGGGA CCTGGACCGA	300
GTGCTCATGG GCTACCAGAC CTACCCGCAG GCCCTCACCC TCGTCTTCGA TGACGTGCAA	360
GGTCATGACC TCAAGCTCGA G	381
(2) INFORMATION FOR SEQ ID NO:703: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:	
GAATTCGGCC TTCATGGCCT AGCTCCACTT TCTCTGAAAA TTTATTCATA TTGTTAATTA	60
AATTTGTTTT TATTATAGAA ATAATATATT GCATGATTTG TAAAAATGCA GAGGAACAGA	120
ATGGCACAAA ATTATGTAAC CCTTTCTATC TCCCCTTGGT GTACCTCCTT AATCATACTT	180

(2) INFORMATION FOR SEQ ID NO:704:

CAGGCATGCA CCACCACTCA GCTCGAG

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 base pairs

CTCAGAACCA TTGTCAATAA TTTGCTGGGA GTTCTTCTGA TGGTTACCAT CGTGACTGAT

AGATTTATTT CCCAGGTTCA AGCGGTTCCC CTGCCTCAGC CTCCCGAGTA TCTGGGACTA

240

300

327

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

GAATTCGGCC	TTCATGGCCT	TGCCTTTTTT	CTTTCACCAC	TTTACTACAC	ACAATTACTG	60
GATTAATCTC	TTTAATGCCG	AGATCTTTTT	TCCTTAGTGA	CACCTTAATC	ACTCTTAGCT	120
TAACATATAT	GGTCATCCAT	TACTGGGTTG	CCTCTGCCTT	TCCAGGATTG	GCTGCCACTG	180
CTCCTCCACA	TACCCTGTAT	TCTAGCCAAA	TGGAATCACT	GCTGTGTCCC	AAGCAGATTC	240
TTTATTTCTC	TTGGCTGTTG	CTCTCTATTT	CTAATGCTAC	CTGCCCTTCA	AAACTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:705:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GAATTCGGCC TTC	CATGGCCT	ACTTGATTTG	TGGCTTATCT	CAAGTTACCA	TTTTTCAGTC	60
AAGTCTGTTT GT	TTGCTTCT	TCAGAAATGT	TTTTTACAAT	CTCAAGAAAA	AATATGTCCC	120

AGAAATTGAG	TTTACTGTTG	CTTGTATTTG	GACTCATTTG	GGGATTGATG	TTACTGCACT	180
ATACTTTTCA	ACAACCAAGA	CATCAAAGCA	GTGTCAAGTT	ACGTGAGCAA	ATACTAGACT	240
TAAGCAAAAG	ATATGTTAAA	GCTCTAGCAG	AGGAAAATAA	GAACACAGTG	GATGTCGAGA	300
ACGGTGCTTC	TATGGCAGGA	TATGCGGATC	TGAAAAGAAC	AATTGCTGTC	CTTCTGGATG	360
ACATTTTGCA	${\tt ACGATTGGTG}$	AAGCTGGAGA	ACAAAGTTGA	CTATATTGTT	GTGAATGGCT	420
CAGCAGCCAA	CACCACCAAT	GGTACTAGTG	GGAATTTGGT	GCCAGTAACC	ACAAATAAAA	480
GAACTAGTCT						494

- (2) INFORMATION FOR SEQ ID NO:706:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

GAATTCGGCC CTTCATGGCC TA	ACTCCCGAG C	CTCTACTGAC	TCCCAAAAGA	GCGCCCAAGA	60
AGAAAATGGC CATAAGTGGA GT	TCCCTGTGC I	FAGGATTTTT	CATCATAGCT	GTGCTGATGA	120
GCGCTCAGGA ATCATGGGCT AT	TCAAAGAAG A	AACATGTGAT	CATCCAGGCC	GAGTTCTATC	180
TGAATCCTGA CCAATCAGGC GA	AGTTTATGT T	TTGACTTTGA	TGGTGATGAG	ATTTTCCATG	240
TGGATATGGC AAAGAAGGAG AG					300
TTGAGGCTCA AGGTGCATTG GO					360
CAAAGCGCTC CAACTATACT CO	CGATCACCA A	ATGTACCTCC	AGAGGTAACT	GTGCTCACGA	420
ACAGCCCTGT GGAACTGAGA GA	AGCCCAACG T	FCCTCATCTG	TTTCATCGAC	AAGTTCACCC	480
CACCACTCGA G					491

- (2) INFORMATION FOR SEQ ID NO:707:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GAATTCGGCC TTCATGGCCT ACCTTATCTT CTTAAC	
GCTTGGTGCT TCCCATCTAT TGCAATACCC CTTTAG	
CAAATTCATT TTATTTGACA ATGTTTACAA ACAACC	CCAG GACGATAACA ATTACACTCT 180
CAATACTGGC ATCACACCTT CACAATTACA CTAACC	
AG	242

- (2) INFORMATION FOR SEQ ID NO:708:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

GAATTCGGCC TTCATGGCCT AGACAGAATT ACTGGGAACC ATTTTCCAAG TAGCCCACCA CAAAGGTTGT ATTTGTCAA ATTGAAGGAG TCATCTGACT TTCCTTAATC ATAAGCTACA AATATAATAA GCTACATTAA TAGATTTTCT AATATTTATT TAACTTTGAA TTTCTGGAAA AAACCCAACT TGGTAATGAT TTATCATCTG AGCTTTGTTT TTGGCTTTGG TATGCTAATT TTTGGCTTAG GATTTTTATA TCTATTTCAT GAGTGGCACC TCGAG	60 120 180 240 285
(2) INFORMATION FOR SEQ ID NO:709:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 319 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:	
GCACGCCATG GGAGAAAAG AAGAAGCCAA AAAAACAGAA GACAAGTCTT TGGCAAAGCC TGAAACTGAT AAAGAACAGG ACAGTGAAAT GGAGAAGGGT GGAAGAGAAG ATATGGATAT AAGTAAATCT GCAGAGGAGC CACAGGAAAA AGTTGACTTG ACTCTAGATT GGTTAACTGA AACCTCTGAA GAGGCAAAAG GAGGAGCAGC ACCAGAAGGA CCGAATGAAG CTGAGGTCAC TTCTGGGAAG CCAGAACAGG AAGTACCAGA TGCTGAGGAA GAAAAATCAG TTTCTGGAAC TGATGTCCAA GATCTCGAG	60 120 180 240 300 319
(2) INFORMATION FOR SEQ ID NO:710:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 190 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:	
GAATTCGGCC TTCATGGCCT AGACACATAC AAAGATAAGG CTTTGATAAA ATTCAAGAGT TATTTGTATT TTGAGGAAAA AGACTTTGTG GATAAAGCAG AGAAGAGCCT GAAGCAGACT CCCCATAGTG AGATAATATT TTATAAAAAAT GGTGTCAATC AAGGTGTGGC TTACAAAGAC ATTTCTCGAG	60 120 180 190
(2) INFORMATION FOR SEQ ID NO:711:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 199 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:	
GGATTGAATT CTAGACCTGC CTCGAGTAAG ACCCCTTTTT AAAATGACTC CCACTGTCTA	60
TTCCACAGCC GGTGTGCGGC ATGCTGATTC AATCCCCACA ACAGCCCAGG AGGTAGGCGC CGTCCCATCC TCCTTTACAG GAGGGGAAAC TGAGGTTCAG GTGGTCAGAT GGTCAGCTGC	120 180

CTCCAAGACC ACGCTCGAG

180

199

(2) INFORMATION FOR SEQ ID NO:712:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

					TCAGCGTTCT	60
GTGGTTGTCA						120
TGGCCTGAGA	TCTGGGGGAG	AAAATCACCT	CTGGCTTCTT	GAAGGAACCC	CCTCTCTCCA	180
GTCATGTTGG	GCTGCCTGCT	GCCAGGACTC	TGCCTGCCAT	GTCTTTTGGT	GGCTAGAAGG	240
GATGTGCATT	CAGGCAGACT	GCAGCAGGCC	CCAGAGCTGC	CGGGCTTTTA	GAACACTCCT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:713:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

- (2) INFORMATION FOR SEQ ID NO:714:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

GAATTCGGCC TTCATGGCCT ACCGAGATGG AAATAACCT	'A AGAAAAAGAG GGCATCCAGC 60
TCCATCTCCC ATTTGGCGTC ATGCTGCTCT GGGTCTGGT	A ACTCTTTGCC TGATGTTGCT 120
GATTGGGCTG GTGACGTTGG GGATGATGTT TTTGCAGAT	A TCTAATGACA TTAACTCAGA 180
TTCAGAGAAA TTGAGTCAAC TTCAGAAAAC CATCCAACA	
GCAACTGGGC AACTCCAACA ACTTGTCCAT GGAGGAGGA	A TITCTCAAGT CACAGATCTC 300
CAGTCTTAAC CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:715:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

GAATTCGGCC	TTCATGGCCT	AGGCAATATC	AAGGTTTTAA	ATCTCGGAGA	AATGGCTTTC	60
GTTTGCTTGG	CTATCGGATG	CTTATATACC	TTTCTGATAA	GCACAACATT	TGGCTGTACT	120
TCATCTTCAG	ACACCGAGAT	AAAAGTTAAC	CCTCCTCAGG	ATTTTGAGAT	AGTGGATCCC	180
GGATACTTAG	GTTATCTCTA	TTTGCAATGG	CAACCCCCAC	TGTCTCTGGA	TCATTTTAAG	240
CANTGCACAG	TGGAATATGA	ACTAAAATAC	CGAAACATTG	GTAGTGAAAC	ATGGAAGACC	300
ATCATTACTA	AGAATCTACA	TTACAAAGAT	GGGTTTGATC	TTAACAAGGG	CATTGAAGCG	360
	CGCTTTTACC					420
•	CTTATTGGAT					456

- (2) INFORMATION FOR SEQ ID NO:716:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

TGGAGTCAGA CAGTCTCATG AACTTCATTT	TTCATGGCCT ATCTTTTATC CTACTTTCCT GTAACGGAAG	TAAAGGAGAT TTAAAATGAA AATCAAAATT	ATTTTCATCC ATTGCTGTTC AGAGCCCGGG	TTAGATTAAT TTTTTTTAAT TCTCATCCTA	GTCCTCTTCA TGATTTGGCC CGGTATCTCG	60 120 180 240
AACTTCATTT	GTAACGGAAG	AATCAAAATT	AGAGCCCGGG	TCTCATCCTA	COGIMICICO	• • • •
TCCTGAACCT	CTGGTCTCCC	TCAAGAATGA	CTCAGAAGGA	CGGACTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:717:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

GAATTCGGCC	TTCATGGCCT	AAAAAAAA	GCCTTTTAAA	CTTGTAGGAA	TTAAGAAATA	60
AGAATAACCT	ACAAAATGCT	AGCAAAATTT	ATCTCATTTT	TTTTCATTGT	ATTTTCAGGT	120
	TGAATGACAG					180
TCACACCATC	TAAATGGACA	CTGCACAGT	CCAACTTCTC	AGAGTTGCAG	TTCTGGAAAA	240
1CAGACCA16	GTGCCGATGT	TTCAAAACTA	AATCGCTGGG	GTCCTGGAAG	ACCACCAGTT	300
	GIGCCGWIGI	IICAMAGIA	Micacios	0100100110		306
CTCGAG						500

- (2) INFORMATION FOR SEQ ID NO:718:
 - (i) SEQUENCE CHARACTERISTICS:

WO 98/45436 PCT/US98/06955 (A) LENGTH: 294 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:718: GAATTCGGCC TTCATGGCCT AATATTTATT AAATGACTTG GTAGATAGAG CAACTGACTG 60 120 TTTCTCTTTC CCCTTTTATC CAGGGTAGGT CCAGGTAAAG CCAAAGGCCT TATCCTTATC 180 TACACTGCTG GGGGACACAA CACAAGAATT TCAAGTTCAA GTATTATTTC TCATTTTGAG 240 294 TAATTTTGTT CTCATTTTGT TCCAGTTCTC ACTCTCAGAA AAAGATTACT CGAG (2) INFORMATION FOR SEQ ID NO:719: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:719: GAAACAATAG AAACACTGAG AGAAAATTCA GAGAGACAGA TTAAGATACT GGAACAGGAA 60 AATGAACATC TGAATCAAAC AGTGTCTTCC TTAAGGCAGC GGTCCCAGAT AAGTGCAGAA 120 GCAAGAGTGA AAGACATTGA AAAAGAAAAC AAAATTCTTC ATGAATCTAT CAAAGAAACA 180 240 AGTAGCAAGC TAAGCAAGAT TGAATTTGAA AAAAGACAAA TTAAAAAAAGA ATTGGAACAT 263 TATAAAGAAA AAGGAAGCTC GAG (2) INFORMATION FOR SEQ ID NO:720: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 320 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

GAATTCGGCC TTCATGGCCT	ACCTGCCCTT	CTGCGGTCAC	AGCTGCCTGC	TGGGTGGGAG	60
TCCGGGGGAA TGGTATGTGT					120
ATCCTGGCAG AGTCTCGGAT					180
GTGGGGGAAG GAGGCAGGGG					240
ACACATTGAC AGTCTCTATG	TTGGCTTCAC	CAGCGCTTCT	CTGTTTGTCT	CGTCCCTGGA	300
TTTCTAACAG TTGCCTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:721:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

GAATTCGGCC	TTCATGGCCT	AGTCGGGAGT	GTCTTAAGCT	TTTCATTTAA	CCTAAAGTAC	60
AGAGTCTGCT	CTGTAGAAAT	ATGTCATTAA	GAAAATATTT	GAGTCCCAGC	TCCTCCTTGT	120
TGTGTAATGT	CTGATAATTT	CACTCATTAA	ATTACCCAGA	CAGACCATAA	AGTCCTCTCA	180
GTTTGCATCA	CCTGAAAGTC	AGTCAGCCTG	GGCTGTGAGG	ATTGTGAGGT	AGAACTCACT	240
GTGGAAGGAC	GGCATTAGGG	AAGACTTTAG	GAAAATGGAG	CGGAACCTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:722:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

CTCGAGACCT	GTGTGCGCAG	GCAACGGGGA	AACTGGAAAT	GCGTTGACAA	ACTGACGCAA	60
AACTGGGCCC	AACAGCCACA	AGGCACTGGT	CGTTTTCCAC	TGGGCAAAGT	TCAGTCGCAT	120
TTCTTTCTGT	TCTCTTTCTT	TCTTTCTTTT	CTTTTTTCTC	TTTCTTTCTT	TCTTTCTTTC	180
TTTCTTTTTT	CTTTCTCTCT	CTCTTTCTGT	CTGTCTCTCT	CTTTCTTTCC	TTCTTTCCTT	240
CCTTCCTTCT	TTCTTTCCTT	CCTTTCCTTT	CTTTCTTTTT	TTTTTTTTT	AAGAGACGGA	300
GTCTCGCTCT	GTTACCCAGG	CCGGAGTGCA	ATGGCACAAT	CTCGGCTCAC	TAGGCCATGA	360
AGGCCGAATT	С					371

- (2) INFORMATION FOR SEQ ID NO:723:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GAATTCGGCC TTCATGGCCT	AGTTCCTTGG	TGGTTTGAAA	GTTAGAGAGA	TCCTGATAAG	60
CATAATGACC AACATAGAAG	AGATTAAGTA	CCTTTACTCA	TAAATGTGAG	TTCACAGACT	120
TCAGGTCTAA ATTCGTAACA	ATATTTAAGA	TGTATATGGC	TTAAAGTGCT	GGTAGTTTTG	180
ATTAGAATCC ATAGGTTTCT	AGTCACTGCT	CTTTTCATTA	TTTGAGTTTT	TATGTATTTT	240
TTAACTAGAA ATAAGAGGGT	CTCGAG				266

- (2) INFORMATION FOR SEQ ID NO:724:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GAATTCGCCT	TCATGGCCTA	GAAAGTTTTT	CAAAAATTCT	TCAATTGTCT	CTGGTTGATG	50
CAACTTAATT	TTTTGCTGAG	AGAGACCTTA	AATGTAATTA	GTATTGTATA	ATTAGCCTGA	120
TTAATCTGAC	CTGTACATCA	CGAGTCACTT	GTCTTTAGCC	CAAGAGGAAT	GCTTCCTTTC	180
TGATTTGAGG	CAGTGGCCCA	TCATTGCTTC	TAGCAACCTT	CCTACTTACT	AGATGACCTT	240
GAGTCAAGGT	TTCTGTATAT	ATGATTTCAG	ATTTGTCCCC	TAGAACTGAA	AAAGGGTAGG	300
AGAGGCAAAG	ATAGGAAAAA	TATTTTTTAA	AAATTTTTAA	GTATTTTATT	TTTATTGGGA	360
AAATATTTAT	TGTAAGTCTT	CCATTTGTTA	TCCTTCTGCC	ACTAGCATTA	CGTAAAAAGT	420
AAAAAGAGCT	TTACATCAAA	AAGCACAATG	AAACTTTGTA	TCCTTAAGTC	CGTACTCGAG	480

- (2) INFORMATION FOR SEQ ID NO:725:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

GAATTCGGCC	TTCATGGCCT	AGTCGGAGGT	GTAGGAGGG	CCGTGGAGGT	CCAGGTGACT	60
GCTTAGAAAA	CTGCACAGCA	TCTGATGAAA	TTAGCGAATA	AGAACATCAA	CCATGTCTTA	120
CACTCCAGGA	GTTGGTGGTG	ACCCCGCCCA	GTTGGCCCAG	AGGATCTCTT	CTAACATCCA	180
GAAGATCACA	CAGTGTTCTG	TGGAAATACA	AAGAACTCTG	AATCAACTTG	GAACACCTCA	240
AGATTCACCT	GAATTGAGGC	AACAGTTGCA	ACAGAAGCAG	CAGTATACTA	ACCAGCTTGC	300
CAAAGAAACA	GATAAGTACA	TTAAAGAGTT	TGGATCTCTG	CCCACCACCC	CCAGTGAACA	360
GCGTCAAAGG	AAAATACAGA	AGGATCGCTT	AGTGGCAGAG	TTCACAACAT	CACTGACAAA	420
CTTCCGCAAG	GACTCGAG					438

- (2) INFORMATION FOR SEQ ID NO:726:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 416 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

GAATTCGGCC	TTCATGGCCT	AGCTACCTAT	CTACAAAAAC	TCCTGGATCC	TTTATTACGA	60
ATTGTGATCA	CATCCTCTGA	TTGGCAACAT	GTTAGCTTTG	AAGTGGATCC	TACCAGGTTT	120
GTCATCTTTT	CACATAGAAC	CGCTGTTTTT	TGTTTTTTT	TTTTGTTTGT	TTGTTTTACT	180
AACACTGCAT	GAAGCAAGGC	ACCTTCTCCC	CTTGATCATT	AAAATTAGTT	TTTAATTATA	240
AAAGTTATAT	ACAAATACAC	GTTTCTTTAA	TGATATCTGT	AATTTTTTTT	TAAGGTATCC	300
TTTTATTTGC	CTTAGATCCA	GGGACAAACT	AGAGAAAGGT	GTCTTTGACT	TCCACCTCCA	360
GAGACTGTTA	CTAGTTAAGT	CTGTTCCCCT	GTCCTTTTTC	CATGCACCGC	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:727:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

GAATTCGGCC	TTCATGGCCT	AAGGAGGTCC	ATGAGGAAGT	GTCCCAGCCT	GTCAGTGCAT	60
CTCATGAGTT	CGCTGAGTGA	TCAGCAGACA	GTTCCAGGAA	GTGAACAAGT	CCAAGAGGAC	120
TTCTGATTAG	TCCACAGTCT	CCTCTATAGG	CTCAGTAGAT	GAAGGCGTTT	CTGAGGGCTT	180
		CTAGCACTAA				240
		AACTCTACAT				300
AAGTCCAAAT	GGTCCCGACA	GACCTTTTCA	GTGTCCAACC	TGCGGGGTGC	GATTCACCCG	360
TATTCAGAAC	CTAAAGCAGC	ACATGCTCAT	CCACTCAGGA	ATTAAACCAT	TTCAGTGTGA	420
CCGCTGTGGG	TCTCGAG					437

(2) INFORMATION FOR SEQ ID NO:728:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid.
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

GAATTCGGCC	TTCATGGCCT	AGATCACTGC	CCTTTCAATA	ACACTCTTGC	CTCTAGAATC	60
ATATGTTCAA	AGTATGAATA	CACACCTAGC	ACATAGTAGG	TGCTCAAATA	TTAATTTCCT	120
CCTTGCCTTC	CTTATCTACC	CTGTGTCCTC	CATTTCCCCG	TATGATTCCA	ACCCAATATA	180
GCAAATGACA	TTTACATGTT	ATGAAAACAT	CTATTGGGTA	AAATCAGATC	TTGGATAAAG	240
AAATTCTGAC	TTTTATATAA	GCTTTTGGTA	GACAGAAAAA	ACAGAAAGGT	ATTCGTTGGT	300
		AAAGAAAGCT				360
ACTTTGACTG	AAACACGTTT	TTGGTGGATT	TCTTTTCCTC	AAAGAACTCT	CTAAATGCAA	420
CTCCTTGCTG	GATTCCTCAC	CCGATCTCGA	G			451

- (2) INFORMATION FOR SEQ ID NO:729:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

GAATTCAACC	ATTAAAGATA	ATTTATATTA	GTGTTTCTAT	AACTTCTAAA	ACATCTTTTG	60
ATAAGGATAA						120
ATAGCTCTGA	TTAAGAACAA	TTGAACCATT	CAATTTTTTA	TTAGCCTCTA	TTTTCACTAG	180
CCAGGATATT	TTCATGAAAC	TTTTTAGTTT	CAAAGCAAGT	TTTTTCTTTC	CAATAGAAAG	240
TGTTATATTA	GTAAACAATT	TTGTCTTCTG	CCAAGACCAG	CTCAGTCGGG	AAGATCCTAA	300
CCCAGTGGCA	AAACTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:730:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GAATTCGGCC	TTCATGGCCT	AGGGAAGAAT	AAAGAACAAA	ACCCAAAACT	TTGGACCTTA	60
AAAAACCCAG	GCTGGCATTT	TAGTAGCAAT	TGGGTGTGTT	CGGTTTTGAA	TATATTTGTA	120
TATACATGCC	TCCATGTGCT	TTGGCCTTCT	GGTATCTTCA	CCAGATGCTG	CCTTTTTTTT	180
TTTTTTTAAC	AAGTTCCTGT	TTCACTTTTC	CAGCTAGCTG	CTGGGTATCT	CCAACAAAAT	240
ATCTCATAGA	TCTCCCAACT	GTAATGTATT	CAAGCCAAAA	ATCAGCTCTG	CCCATTCTCC	300
ATCCCAAAGC	CCCTCCTCTT	GGTTACCAGA	CAACCTTAAC	CAAACCACTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:731:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C, STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

GAATTCGGCC	TTCATGGCCT	AGAGGAGGAA	GGCCTTCGTA	AAGGTTGCAT	CTCCGTCCCT	60
TCGCTCCCGG	GGACCCGCGG	GAAAAAAAA	AATCCAACAC	CCAGGCCCCG	CGGCTAGCCC	120
CTTCCCACAG	GCTCTCTCCG	CTCGATTTTG	TCACCGTTAT	${\tt GTGGGAAGCG}$	AATCCATGTA	180
TTTGCATGCC	CGAGTCTTTG	AGCCGTGCTA	TACCAGTTTG	TCCAGATTGT	TTATACTAGC	240
AATGCAGTTT	ACGGTGAAGA	CCTGCCTTCC	CTCTGGGAAT	CTGGAGCTTC	AGTAACAGGA	300
GATGTTTCAC	AAAGCAGAAG	AATTATTTTC	TAAAACAACA	AACAATGAAG	TGGATGACAT	360
GGACACGTCA	GATACCCAGC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:732:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

GAATTCGGCC	TTCATCCCCT	ACTOCOTOTO	CAAAAAAAAA	********	CTTCACCAAC	60
GAM11CGGCC	TICATOGCCI	ACTOCGICIO	CAAAAAAAA	WWWWW I WO I	GIICAGCAAG	60
GTTGAAGCAT	AAAAGGTTAA	TAGCCAGAAT	CATTTATCAA	TTGTATTTCT	ATACATCTAC	120
AAGACACAAT	CTGAAAATGA	AATTAGAGAA	ACAATTTCAC	TGGGCAACAA	GAGCAAAACT	180
TCATCTCAAA	ATAATAATAA	TAATAATAAT	AATCATCATC	ATCATCATCA	TCTACAATGT	240
CATTTCCCAT	CCAAGTCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:733:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

GAATTCGGCC	TTCATGGCCT	AGACCTGCCT	CGAGCTCCTG	GCCTCGGGCA	CTCTACCCGC	60
TTCAGCCTCC	CAAAGTGCTG	CGACTGATTA	CAAGTATGAG	CCACTACGCC	TGACCATAAC	120
ATGTAAAATT	ATGGCAAATG	GTAATTCACA	GCTCAATTCT	AAAATGTGAT	GAAATTTAAA	180
TCAGAAAGGC	CAAATGAGTC	ACTTTTTCTT	AACACTAAGA	ATTATAAACC	TTTAAATTTC	240
TTTTGTACTG	TAATTTTTTA	TGTGACATGT	ATATGCTTTT	TAATATGTGT	GATAGGATGA	300
GGGGCAGGAG	AGGGGGCTCT	AGACATGAGG	GTGCCTGGGG	CCTCTGTAGA	CCTTCAGATG	360
$\tt GCCCTGGGTG$	TTATAGCAAG	AGCTGGTCTA	CATCTAATAC	TACTGCAGGT	GCTGTCATGA	420
ATTCTTTGTA	TAATTCTTTG	TATATTAAAT	GACATTATTC	TATGTATAAT	GTCATTTAAT	480
ACTTATAACC	TACTTTCCTC	GAG				503

(2) INFORMATION FOR SEQ ID NO:734:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

GAATTCGGCC	TTCATGGCNT	AATGGATTCA	TTTTTTTCA	GCAGCATGGC	ATAGTGGATT	60
ATGAAATCAA	AATTAACTAC	ATGTGGAGTC	NTACATTGAA	ATCCCCCTTC	AACAAAATAG	120
TATACTATGA	GTATTTTTAA	ATTATTTAAC	CCCTCCGAAC	ACCAATTTGT	ACACGAATAA	. 180
AACTTGACAC	AACAGGATTT	TGTGGGGCGT	GAGTAACACA	ACATATACAA	AAGCACCTTA	240
TAAAGTGTTC	TATATAGCAA	CTTCTCTCTC	AGTTTGAACG	GGTCTCAGGA	TAAATTAGCA	300
AATATGAATT	CTAACCTTTG	TACTTACATT	TTAATTCTGC	TAAGTGTGTG	AACCCCAATT	360
TAGCAATTAA	AATATTTATT	TCCAGAATGT	TTTGACCCTG	AGCATATTTT	TAAAAAGCAC	420
AGTAGCTCGA	G					431

- (2) INFORMATION FOR SEQ ID NO:735:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

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ACTAAATCCA GTGAAATATG ACTTCTCTAA CTGAGCTTGA CATATCCTGG TTATATCTCA	120
TGGCAGCTGA AAACTAGAAA TGACTTATTT TTACCTTGTA GCCACAGCAC ACTTGAGGTT	180
ATTCTTAGGT TTTTGTTAGA GACAAAGCTG GTTAGTGACT CCTGGATTAA GAATTATGAG	240
TGATCCCATA ACCCTCGAG	259

- (2) INFORMATION FOR SEQ ID NO:736:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

GAATTCGGCC	TTCATGGCCT	AAAGGATATT	GGCATGTTCC	TCTTCTCATC	AATATCCTAA	60
AAGACATTTA	TTTTTTACAC	ACTCCTTGGG	AAAAATTAAC	TTTTTTTCAC	TGAAAATATT	120
TCCTTTTTTG	GTTATCTTGA	TCTCAGATTA	TTTTGTGAAA	GAATTTTACT	GTACTTAGTT	180
CAAAAGAGTA	GAAAGAATGA	TTTACTATTG	CAGACATATG	TAGGGTAAAA	TCATAATTTA	240
TTTAAACTGA	CTGTACAACA	CCATTTAGAG	TTGATATTGA	CATAAATGTT	ATTAGCCTAC	300
TAATTTGGAA	CTGCATTTCT	CAACAATGCT	GGCAAGCATC	TTCCGTACTT	AGCATACCAA	360
GTTGTAGGGG	AGAGACTGTG	TATATATTT	TTAAAAGCAA	TCCAATGGAT	TTGTTTTTGT	420
TCATATTTTG	GAAACAACTC	GAG				443

- (2) INFORMATION FOR SEQ ID NO:737:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

GAATTCGGCT	TCATGGCCTA	CAAAAGATGG	CCCTAAGCCT	GGCCTCTAGC	TTTCACTCGT	60
GGTGAATATT	TCAGACCTAA	AGATCCAGAT	AGTATCTCTG	TTCATATGTG	AATAAGTTGA	120
AGATTGTGGG	GCTACTTTTT	CTCATAGCAC	TTTATTTTGA	ATGTTGTTAG	TTTGTGCTGA	180
GAATGGTCGT	CCGTATTTGA	ACCAATTATT	TATTTTAAAA	TATATTTAAG	CTACATTTTT	240
GTTTTGAAAA	ATTGCCATAA	ATTTGGTGCC	ACTTTCTTTT	ATTTATTTGA	CTGAGTTAAT	300
ATTATTGTAT	TAACATTTTA	AGTATATGGT	GTTTACATTC	TTATTTCTTT	TGACATTTTG	360
GAAATAATCA	TAACTTGTCT	TTCCAAAATA	ACCATTTTCT	TGATGGAACT	CTTCCTAGAG	420
TTTTTACCAA	ATAGCTAACT	TTAGTAGTAA	AACCTCATTG	TGTATCCATT	CCCCCACTCG	480
AG						482

- (2) INFORMATION FOR SEQ ID NO:738:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

GAATTCGGCC TTC	ATGGCCT AGATTGTCAC	TTTATCTTAG	ATGATGAGGA	AGCAGTACCA	60
AGAAAACACT TGG	GGGTTGA TACAACAGG	ACATGAGCCC	TTAAAACTCC	TTCCTGTTTT	120
TTTTCTTTTT TTT	TTCTCTT AGGTAGATT	GTGCATTTAA	AGCCTGAAGT	TAATTTGACC	180
TAAAATTTTT ATA	AGTCTTT GCAGAAAGTT	CACTTGTTTC	CTGAAATCAT	CTCCTTGATA	240
ATTITTTATG TAA	CAGTTGT TCATATTGT	GGAATGATAT	ATATGTCATC	CTGTTACACG	300
TGTCAGGCAC TTC	CAAAAAGA CTCCAAGAGA	ACATGCCTGA	GAAAGATAAC	TCCCAATTAA	360
AAATGATTCA GTC	CCTCACT TGCAATATT	AGGATAAATG	TGTGGAAACA	TTAGGCTACC	420
AGATAAATAA AAG	GTAGTTA TTTCCTAGG	TGACTCAGCA	AGATATTTCT	CGAG	474

- (2) INFORMATION FOR SEQ ID NO:739:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

GAATTCGGCC TTCATGGCCT AGCCTTTGAG ATCAATACCT GTG	GAAAAGTA GGGAAAGAAA 60
GCAGATGAGG CATAGGGAAA AGGTGGACTG CCACAGGCAA CCC	CAGCGAAC CTCACCAGCA 120
GCTCTGGAGC TAAAATAGCT CTTCAGAATT GTCCAGAGTT GGG	GCTGAGGA GGCCAGAATT 180
TTATTTGTGT TCCCACGATG ACGACTTCGA G	211

- (2) INFORMATION FOR SEQ ID NO:740:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

GAATTCGGCC TTCATGG	CCT AAATACCTTA ATG	GTGGTAG AGCCTTTACC	TGTAGCTTGA 6	0
AAGGGGAAAG ATTGGAG	GTA AGAGAGAAAA TGA	AAGAACA CCTCTGGGTC	CTTCTGTCCA 12	0
GTTTTCAGCA CTAGTCT	TAC TCAGCTATCC ATT	TATAGTTT TGCCCTTAAG	AAGTCATGAT 18	0
TAACTTATGA AAAAATT	ATT TGGGGACAGG AGT	TGTGATAC CTTCCTTGGT	TTTTTTTGC 24	0
AGCCCTCAAA TCCTATC	TTC CTGCCCCACA ATC	TGAGCAG CTACCCCTGA	TACTCCTTTT 30	0
CTTTAATGAT TTAACTA	TCA ACTTGATAAA TAA	ACTTATAG GTGATAGTGA		_
TTCCAAGAAT GCTCGAG	;		37	7

- (2) INFORMATION FOR SEQ ID NO:741:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

CATGGCCT AAGGCGTTTG	GGGTTTCCTA	GTTGTGCTGC	TGCTCTTGCC	60
CTTGCTT TGGCCTCTTT	CCTTGGGGCA	AGAGTGAGGG	GGACAGGGAG	120
CCTCCATG TTGAAGTTTG	GTAGAAGCTC	TGCCCACACC	TTGGACTGGA	180
CAATCCCC ATGATCACCA	ATCCGAACCC	CTTGAAGTAG	AATTTTCATA	240
ACCACCTT CTTAGCCAGG	CCATAGCCAT	TCAGCAGTGC	CTCCTTCCTC	300
CAGCCTTG AACAGAAAGG	TGGAACACTC	GAG		343
	TCTTGCTT TGGCCTCTTT CCTCCATG TTGAAGTTTG CAATCCCC ATGATCACCA ACCACCTT CTTAGCCAGG	CCTTGCTT TGGCCTCTTT CCTTGGGGCA CCTCCATG TTGAAGTTTG GTAGAAGCTC CAATCCCC ATGATCACCA ATCCGAACCC ACCACCTT CTTAGCCAGG CCATAGCCAT	TCTTGCTT TGGCCTCTTT CCTTGGGGCA AGAGTGAGGG CCTCCATG TTGAAGTTTG GTAGAAGCTC TGCCCACACC CAATCCCC ATGATCACCA ATCCGAACCC CTTGAAGTAG	CATGGCCT AAGGCGTTTG GGGTTTCCTA GTTGTGCTGC TGCTCTTGCC CCTTGCTT TGGCCTCTTT CCTTGGGGCA AGAGTGAGGG GGACAGGGAG CCTCCATG TTGAAGTTTG GTAGAAGCTC TGCCCACACC TTGGACTGGA CCACCCC ATGATCACCA ATCCGAACCC CTTGAAGTAG AATTTTCATA ACCACCTT CTTAGCCAGG CCATAGCCAT TCAGCAGTGC CTCCTTCCTC CAGCCTTG AACAGAAAGG TGGAACACTC GAG

- (2) INFORMATION FOR SEQ ID NO:742:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GAATTCGGCC	TTCTGGCCTA	GAGTCCTTGT	TGTCCTTTGC	AAAGGTTGCT	CATCACCTCT	60
CCCCTCCCTC	${\tt TGGCTCTTTT}$	CCGTGGTGAT	GCATAGTTCA	ATGCGCCCAG	GAAGCTTCAT	120
GATGAGGCCG	TCACCCAAAC	TAGCAGCCCT	CCTTTCCTTC	TTTCTTTGCC	AAGTGTCCTG	180
GACATCAGCT	CTTCCTCAGT	CTTTGACTCT	AAATAAAGAA	CTTGAATTTC	ACCATTCAAC	240
TGAAATCCCT	CTAACCTCG					259

- (2) INFORMATION FOR SEQ ID NO:743:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GAATTCGGCC TTCATGGCC	T ACACCGTCGC	CATTGCCAGA	AAGAGCGATT	TATGGCTTTG	60
TTCTTTTCTT AAGCTCCC	A TTTGGCTTCA	TACTTTACCT	CGTGTGGGCC	TTTATTCCTG	120
AATCTTGGCT AAACTCTTT	A GGTTTAACCT	ATTGGCCTCA	AAAATATTGG	GCAGTTGCAT	180
TACCTGTCTA CCTCCTTA	T GCTATAGTAA	TTGGCTACGT	GCTCTTGTTT	GGGATTAACA	240
TGATGAGTAC CTCTCCACT	C GACTCCATCC	ATACAATCAC	AGATAACTAT	GCAAAAAATC	300
AACAGCAGAA GAAATACCA	A GAGGAGGCCA	TTCCAGCCTT	AAGAGATATT	TCTATTAGTG	360
AAGTAAACCA AATGTTCT	T CTTGCAGCCA	AAGAACTTTA	CACCAAAAAC	TGAACTGTGT	420
GTAACCATAG TAACACCA	G CACACTCGAG				450

- (2) INFORMATION FOR SEQ ID NO:744:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

GAATTCGGCC	TTCATGGCCT	AAATCTTCAG	GGTCTTAACT	TAGTTTTTGA	TCCCTAAAAT	60
TAGTGCTGCA	TATGTAGACT	CAGAAACCTC	ACGTAAAAAT	TTAAATTGGC	CTCAGGTTGG	120
CAATGTTCCA	AGGCAATGGT	TAGAAGCAAA	TTCAGATTCT	CCAAGGCCTC	AAATAATTCC	180
TACAGATAAA	ATCCCAAGGA	AATTCAGCAG	TGCCTAGTCA	AAAATCCACA	AATCAGGCTC	240
GAG						243

- (2) INFORMATION FOR SEQ ID NO:745:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

PC1/0598/06955	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:	
AAGCGAGGCC CTGGGGGACA ACGTGAAACA ATACTGGGCT AACCTAAAGC TGTGGTTCAA GCAGAAGATC AGCAAAGAGG AGTTTGACCT TGAAGCTCAT AGACTTCTCA CACAGGATAA TGTCCATTCT CACAATGATT TCCTCCTGGC CATTCTCACG CGTTGTCAGA TTTTGGTTTC TACACCAGAT GGTGCTGGAT CTTTGCCTTG GCCAGGGGGT TCCGCAGCTT CTCGAG	60 120 180 236
(2) INFORMATION FOR SEQ ID NO:746:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 215 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:	
GAATTCTAGA CCTGCCTCGA GCCTGCAGAC ATCTCCTCCT TCTTTGTGGT TCTGGGAGCC ATTCTGTGCC TCTAAGGTCC TCTTTCTTTT TTCTCACCAA TACACATATT TTCTGTCCTT CGCAATTCTA TTAAACCTCA CATTTGATGG TTGTTTTCTT AAAATTCCTT TACTTGGTTC CTGCATTCCT CATTCCTTCC CAGCACAATC TCGAG (2) INFORMATION FOR SEQ ID NO:747:	60 120 180 215
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:	
GAATTCGGCC TTCATGGCCT AGAAGAAAAC CCATCAGATA TTATAATAAG ACAATAACTC AATTTCAGAC TTGTAAACAA AGGTGACATT AATCTATTGA AATGTGGGAA AATAGTCAAC CTGTATCCTT CTCATACCAT AAATCAGCAT GTTTGATCAC TGGAAGCTTC ATTTTGATGA TTAGCAGTCA TGTATTGAGG CTAAATGATA TGTTTGTCGC ACAGCATCTC GAG (2) INFORMATION FOR SEQ ID NO:748:	60 120 180 233
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 270 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:	
-	

120

180

GAATTCGCCT TCATGGCCTA CACAGGAGAA AAACCCTATG AATGTAGTGA ATGTGGGAAA ACTTTTGTTC AGAAGTCCAC CCTCAGAGAT CATCACAGAA TTCACACAGG GGAGAAATCC

TTTCAATGCA ATCAATGTGG AAAAACATTT GGCCAGAAGT CAAACCTCAG AATACATCAG

AGAACTCACA CTGGGGAGAA AACTTACCAG TGTAATGAAT GTGAAAAATC CTTCTGGCGA AAAGATCATC TCATTCAACA TCAACTCGAG	240 270
(2) INFORMATION FOR SEQ ID NO:749:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 309 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:	
GAATTCTAGT TTAATTACAT ATACCTCTCT GTTGGCTTAG TAGTAATAAA AATATTTTCT GTAGGTGTAG AATATCCTTA CAGTCCAAAA GGAGAGTACA TGTTCACAAT TAAAGTTTGA AATTTGTGCT TTGATAACAG CATGTTTTAT TCATTCATTT TTATAATAAT ATTACTGAGC CTGTATCATA TAGTGATGAA CTTTTCAGCT GTTTTGAGGG TTTGTGTTAG CCACATTCAC ATTTGTATAA CCTGTGTTTC TTTTTTATTT TCATTTATTT TCATTTTAGA TTCAGGGGGT CGGCTCGAG	60 120 180 240 300 309
(2) INFORMATION FOR SEQ ID NO:750:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 328 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:	
GAATTCGGCC TTCATGGCCT AAGCTCTTT AGTGAAGGAT TGTTTTAAAT AAGAGCTCTC AGTTCAAGAC AACTACTGTT AGGAGCTTAA ATCGGAACCA CAATCAGCAT ATAAAGGTCC TAATCCTGAC CTTAATCCCT TTGGAATATT GGTTTTATAA ATCATCAATC AACAGTGTTC CACTATGAAA GCATATTCTG TCTTCTTCTT TTCATGTATT CCTTCACTGC TGGTGCTTAA TGTCTTTCCT TCCTCTTCTG CCATTTCTCT TTCCATGAAT TATAATTGCC TTTTGAATTC AGAAATTAAA ACCACTCCAC AGCTCGAG	60 120 180 240 300 328
(2) INFORMATION FOR SEQ ID NO:751:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 239 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:	
GAATTCGGCC TTCATGGCCT AATAAGGAAG AAATTGTCTC ACTTTATTGA ATAGTTGATT TAAATTTTCT GGTATTTAGA GGTAATATAG TATAAGTTTT TTGTATATTT ATCTAAGATT TTCCTTTTGA AAATTTTCTT CCCTTTTCAT ATTATTTTCA TTAAACGATT TTCCTTTAAA ATTTGTTACT AACAAGAACT ATCTAATATG CAATGAGATT TTTGCAGGGC ATTCTCGAG	
(2) INFORMATION FOR SEQ ID NO:752:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGIH: 231 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(11) Hobbedd III Com	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:	
GAATTCGGCC TTCATGGCCT AAGGAAAGTA CTTTAGACAA AAAAAAAAAA	60
TTAATTCCTG GGGCAATGAA AGGAAATGTC ATTGGCAGTT TTACCTTTAT TCTGCTAATG	
ACTION CONTROLLE	120
GCTATTGTGT GTCTGTTTAC CTGGAGGCAC TTGGAACTTG TGGCACAGAA TGCTGTATGT	180
ACAGGATATC ATCTACATGG GAATAATTGT TGTAAACACC CCAAACTCGA G	231
(2) INFORMATION FOR SEQ ID NO:753:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 308 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(II) MODECULE TIPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:	
·	
GAATTCGGCC TTCATGGCCT ACAATAGAGC TCTTAAACTT ATTTAACTGA AATTTTGTAT	C 0
CTTTTCACCA ACATTTCCCC AACTCCCCTT TACCCCAACT ACTCCAGCCA CTGATAACCA	60
CONTRACTA ACAITICCC AACICCCCII IACCCCAACI ACICCAGCCA CTGATAACCA	120
CCATTCTGTT CTCTATTTCT TTTTCTTTTT TTTTTTTTT TTTTTAAGAG ATGGCGTCTT	180
GCTGTGTCGC CCAGGCTGAA GGGCAGTGGC ATGATCTCGG CTTACTGCAA CCTCTGCCTC	240
CCCGGTTTAA GCAATTCTCT ACCTCAGCCT CCCGAGTAGC TGGGATTACA AGCACCCATC	300
CACTCGAG	308
	300
(2) INFORMATION FOR SEC ID NO 354	
(2) INFORMATION FOR SEQ ID NO:754:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 124 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
•	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:754:	
the content of the co	
GAATTCTAGA CCTGCCTCGA GCCCTTTGTG GTTTTTAAGA AAAAAATTCT GTGCAGATCT	60
GTTCCTCCTC CTGCTCCTTC CCTTTTCTCT ACATACAGTG CTCATTGGAG GCTCCCCACT	120
CGAG	124
(2) INFORMATION FOR SEQ ID NO:755:	
To, and state and tell and tel	
(i) CEOUGNICE OUNDACTION CO	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 369 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(11) NOUBCODE TIPE: CDNA	
332	
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

GAATTCGGCC	TTCATGGCCT	AATCGGTGTC	TTTGGTAAAA	ATTCTATGAG	GATGACATAT	60
TCCATCATGT	TATTCGTTTC	ACATTTCCTT	TTGCTCAGTC	TCCAATGCAA	GCACAGCTTG	120
TGGTATAACC	TATTGTTTTC	CCATTCTAAT	AACTTCTCAA	TCGATCTTCG	TGTTCTTTTA	180
CTGAGGCAAA	TAACTGGCCA	CATACTGCAA	CCTAATGTGC	AGCAGCAACA	AAGGCAGCCA	240
CAAAGTAGCC	AACGTACATT	AACAGGAAGG	TTCTTCTTAA	GACAACTGTT	AACTCTGTTG	300
ATGCTGGCTT	TAAATTCTTC	AGGAGCTACT	TTTTCAGTTA	ATGAAGAAGG	GAATTCAGAT	360
TCAAATTTG						369

- (2) INFORMATION FOR SEQ ID NO:756:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

GAATTCGGCC TTCA	TGGCCT ACCGGCGAGG	AATAGGAATC	ATGGCGGCTG	CGCTGTTCGT	60
GCTGCTGGGA TTCG	CGCTGC TGGGCACCCA	CGGAGCCTCC	GGGGCTGCCG	GCACAGTCTT	120
CACTACCGTA GAAG	ACCTTG GCTCCAAGAT	ACTCCTCACC	TGCTCCTTGA	ATGACAGCGC	180
CACAGAGGTC ACAG	GGCACC GCTGGCTGAA	GGGGGGCGTG	GTGCTGAAGG	AGGATGCGCT	240
GCCCGGCCAG AAAA	CGGAGT TCAAGGTGGA	CTCGGACGAC	CAGTGGGGAG	AGTACTCCTG	300
CGTCTTCCTC CCCG.	AGCCCA TGGGCACGGC	CAACATCCAG	CTCCACGGGC	CTCCCAGAGT	360
GAAGGCTGTG AAGT	CGTCAG AACGCATCCT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:757:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

GAATTCGGCC TTCATGGCC	ACTGATGTTG	AAGACGACAC	CACGGCTTTG	ATGGAATATC	60
AGATATTGAA AATGTCTCTC	TGCCTGTTCA	TCCTTCTGTT	TCTCACACCT	GGTATTTTAT	120
GCATTTGTCC TCTCCAATG	T ATATGCACAG	AGAGGCACAG	GCATGTGGAC	TGTTCAGGCA	180
GAAACTTGTC TACATTACC	A TCTGGACTGC	AAGAGAATAT	TATACATTTA	AACCTGTCTT	240
ATAACCACTT TACTGATCTC	CATAACCAGT	TAACCCAATA	TACCAATCTG	AGGACCCTGG	300
ACATTTCAAA CAACAGGCT	GAAAGCCTGC	CTGCTCACTT	ACCTCGGTCT	CTGTGGAACA	360
TGTCTGCTGC TAACAACAA	ATTAAACTTC	TTGACAAATC	TGATACTGCT	TATCAGTGGA	420
ATCTTAAATA TCTGGATGT	TCTAAGAACA	TGCTGGAAAA	GGTTGTCCTC	ATTAAAAATTA	480
CACTAAGAAG TCTCGAG					497

- (2) INFORMATION FOR SEQ ID NO:758:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

GAATTCGGCC	TTCATGGCCT	AACCAAATCA	ACAACAACCT	ATTTAGCTGT	TCCCCAACCT	60
TTTCCTCCGA	CCCCCTAACA	ACCCCCCTCC	ТААТАСТААС	TACCTGACTC	CTACCCCTCA	120
		CACTTATCCA			•	
	· · ·					180
TCTCTATACT	AATCTCCCTA	CAAATCTCCT	TAATTATAAC	ATTCACAGCC	ACAAAACTCG	240
AG						242

- (2) INFORMATION FOR SEQ ID NO:759:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 221 base pairs
 - (B) TYPE: nucleic acid
 - (^) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

GAATTCGGCC TTCATAGCCT ACCTAAA	TTA ATAATAATGT	ATAGTTCAGA	ATTGCTAAGA	60
GTACTTTTT TTTTTTTTT TNGAGAC	AGG TTCTCGCTCT	GCCCTCCAGC	CTGGTGACAG	120
AGCAAGATTC CATCTCAAAA AAGAAAA	AAA ACACACAGCT	AATAGAATTG	CCATTGTTTT	180
TCATAATAGA ATCTAGCTGC TTACTCC	AAC CTCACCTCGA	G		221

- (2) INFORMATION FOR SEQ ID NO:760:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

(GAATTCGGCC	TTCATGGCCT	AAAATCAAAG	ACTTTGCCAA	TACCATTCCT	GGCCATGGAG	60
(GCATCATGGA	TCGCTTTGAC	TGCCAGTATC	TGATGGCCAC	CTTTGTCAAT	GTATACATCG	120
	CCAGTTTTAT	CAGAGGCCCT	AACCCAAGCA	AACTGATTCA	GCAGTTCCTG	ACTTTACGGC	180
•	CAGATCAGCA	GCTCCACATC	TTCAACACGC	TGCGGTCTCA	TCTGATCGAC	AAAGGGATGC	240
•	TGACATCCAC	CACAGAGGAC	GAGTAGGGC	CACCCAGGGC	CAGGAGAACA	GGAACAGAAC	300
٠	TGAGCAGGGG	CAGGTCTCCA	AGGCAAGCCC	AGCTGGTGTG	ACTTAGACAA	TGACGAGGCT	360
٠	TCAACTCACT	GTCTTTTTTT	TTTTTTTTTG	GAGGGTATTT	TTTATTTGTG	GGTTCAAAAA	420
	ATCTGTATAT	ACAGTCTATG	TGTTTAGAAT	TTGTGTTGTA	AGTAAACTAC	AGCTTTGAGT	480
	TGGAAAGAAG	TCACGGGTTG	TAAAACCATT	TGGATTTTTT	TAAAACAAAA	GTATTAATAA	540
	TCTGGAAGAC	TCGAG					555

- (2) INFORMATION FOR SEQ ID NO:761:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

GGCCGATCAG	GTTATTTTTT	GAAAGTTTTA	CTTACAGAGC	ATATAAATTA	CCCTTGGTTA	60
TTCTCAGCTG	TGATTGAGTT	CTGTGAAAGC	ATAGTACCCT	AGTACCCTGG	GATATCTCTA	120
CATGTGAAAT	TATTCAAATG	TCTCCCTTAC	TTTTTTTTT	TTTTTTTTTG	AGACAGGCTC	180
TGTTGCCCAT	GCTGCAGTGC	AGTGGCACAA	CTATGGCTCA	TCTCAGCCTC	GACCTCCTGG	240
GCTCAAGCGA	TCCTCCCACC	TCAGCCCCCC	AGGCAGCTGG	GACCACAGGC	ACACACCACC	300
ATGTCCAGCC	AATTCCTGTA	TTTT				324

- (2) INFORMATION FOR SEQ ID NO:762:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

GAATTCGGCC	TTCATGGCCT	AGTGCCGGGG	AGAAAGGGCT	TCCTCCCCCA	CACATCAGAC	60
AGGGCACCAA	TGAGTGGGGC	ACTCAAAAAA	GAGAGCAGGC	CCTGGAGAGG	AAACCAAAGC	120
AAAGGTTAGT	TTTATAATCT	GATCCCTCAA	TTACCTGTAA	TTCATATTTT	CTAAATGCAT	180
TAGCTCTAAT	TCATTGTACT	GCCCCAAAA	CAGAATAATA	CTTTGAAACA	TTAAATACAA	240
ACTACAACTA	AAAAAAAA	ATTAGGCCTG	GCGTGGTGGC	TCATGCCTGT	AATCCCAGCA	300
CTTTGGAAGG	CCGAGGCGGG	TGGATCACTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:763:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

GAATTCGGCC	TTCATGGCCT	AATTTGAATC	AACACAACCA	CCCACAGCCT	AATTATTAGC	60
ATCATCCCTC	TACTATTTTT	TAACCAAATC	AACAACAACC	TATTTAGCTG	TTCCCCAACC	120
TTTTCCTCCG	ACCCCCTAAC	AACCCCCCTC	CTAATACTAA	CTACCTGACT	CCTACCCCTC	180
ACAATCATGG	CAAGCCAACG	CCACTTATCC	AGTGAACCAC	TATCACGAAA	AAAACTCTAC	240
CTCTCTATAC	TAATCTCCCT	ACAAATCTCC	TTAATTATAA	CATTCACAAC	CACAGAACTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:764:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

GAATTCGGCC	TTCATGGCCT	AGGGATTTAA	AGAGTTTTTC	TTGGGTGTTT	GTCAAACTTT	60
TATTCCCTGT	CTGTGTGCAG	AGGGGATTCA	ACTTCAATTT	TTCTGCAGTG	GCTCTGGGTC	120
CAGCCCCTTA	CTTAAAGATC	TGGAAAGCAT	GAAGACTGGG	CITTITITCC	TATGTCTCTT	180
GGGAACTGCA	GCTGCAATCC	CGACAAATGC	AAGATTATTA	TCTGATCATT	CCAAACCAAC	240
TGCTGAAACG	GTAGCACCTC	TCGAG				265

- (2) INFORMATION FOR SEQ ID NO:765:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

GAATTCGGCC	TTCATGGCCT	ACCAACAGCA	AGCTCCAATA	TCACACATCC	AGACTCCTAT	60
GCTTTCCCAA	GAACAGGCAC	AACCCCCGCA	GCAGGGTTTA	TTTCAGCCTC	AGGTGGCCCT	120
GGGCTCCCTT	CCACCTAATC	CAATGCCTCA	AAGCCAACAA	GGAACCATGT	TCCAGTCACA	180
GCACTCAATA	GTTGCCATGC	AGAGTAACTC	TCCATCCCAG	GAACAGCAGC	AGCAGCAGCA	240
ACAGCAGCAG	CAACAGCAGC	AGCAACAACA	ACAGAGCATT	TTATTCAGTA	ATCAGAATAC	300
CATGGCTACA	ATGGCGTCTC	CAAAGCAACC	ACCACCAAAC	ATGATATTCA	ACCCAAATCA	360
AAATCCAATG	GCTAATCAGG	AGCAACAGAA	CCAGTCAATT	TTTCACCAAC	AAAGTAACAG	420
TCTCGAG		•				427

- (2) INFORMATION FOR SEQ ID NO:766:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

CGATTGAATT	CTTGTCTGTT	CTGCCTCACT	CCCGAGCTCT	ACTGACTCCC	AACAGAGCGC	60
CCAAGAAGAA	AATGGCCATA	AGTGGAGTCC	CTGTGCTAGG	ATTTTTCATC	ATAGCTGTGC	120
TGATGAGCGC	TCAGGAATCA	TGGGCTATCA	AAGAAGAACA	TGTGATCATC	CAGGCCGAGT	180
TCTATCTGAA	TCCTGACCAA	TCAGGCGAGT	TTATGTTTGA	CTTTGATGGT	GATGAGATTT	240
TCCATGTGGA	TATGGCAAAG	AAGGAGGGTC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:767:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

GAATTCGGCC TTCATGGCCT ACGTAATTCT GGAAAAGTGA ATACTTGTGA AGAGTCGTCT 60
TGAATGATTT GTAAAAAATC CTGTTCTTAT ATTCAACGAG TTTCGAATCT TTGTCAGAGG 120

PC1/U898/00955	
AGTATTACCA TTAGATTGAA AAAAAGGAAA ATAAATAATA AACACTTTTA AAAAAACTCC CCATTCTCTT ATTCTCACTT TTAGGAAAAG AGACTGACTA ATACCTTCTCTC CCACAAATAC CGATGTTCTT AAAAATATTT ATGGGÁCTGC TTTTGGCAAC CAGCCCTATT TTGTTTTCAT ATCCCTTTTT GCTCCCATCT TTCCAAACTC ATAAACTCGA G	180 240 300 341
(2) INFORMATION FOR SEQ ID NO:768:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 281 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:	
GAATTCGCC TTCATGCCT ACAGAAAGAG TTTGAGACCT GAATAGCTCC CAGATTCAG TCTTTTCCTG TTTTTGTTAA CTTTGGGTTA AAAAAAAAAA	60 120 180 240 281
(A) LENGTH: 352 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:	
GAATTCGGCC TTCATGGCCT ACTAACGAGG AAAGGGATTT AAAGAGTTTT TCTTGGGTGT TTGTCAAACT TTTATTCCCT GTCTGTGC AGAGGGGATT CAACTTCAAT TTTTCTGCAG TGGCTCTGGG TCCAGCCCCT TACTTAAAGA TCTGGAAAGC ATGAAGACTG GGCTTTTTTT CCTATGTCTC TTGGGAACTG CAGCTGCAAT CCCGACAAAT GCAAGATTAT TATCTGATCA TTCCAAACCA ACTGCTGAAA CGGTAGCACC TGACAACACT GCAATCCCCA GTTTAAGGGC TGAAGCTGAA GAAAATGAAA AAGAAACAGC AGTATCCACA GAGAGACTCG AG	60 120 180 240 300 352
(2) INFORMATION FOR SEQ ID NO:770:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 316 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:	
GAGCGTGGTG GATATAAAAC AGGTAAGAGA CTTTCATGGT ATACCTTTAT ATTGTTGGAT	60

316

CCAGGCTGGT CTCGAG

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 473 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:	
GAATTCGGCC TTCATGGCCT ACTTTGATGG AATATCAGAT ATTGAAAATG TCTCTCTGCC	60
TGTTCATCCT TCTGTTTCTC ACACCTGGTA TTTTATGCAT TTGTCCTCTC CAATGTATAT GCACAGAGAG GCACAGGCAT GTGGACTGTT CAGGCAGAAA CTTGTCTACA TTACCATCTG	120
GACTGCAAGA GAATATTATA CATTTAAACC TGTCTTATAA CCACTTTACT GATCTGCATA	180 240
ACCAGTTAAC CCAATATACC AATCTGAGGA CCCTGGACAT TTCAAACAAC AGGCTTGAAA	300
GCCTGCCTGC TCACTTACCT CGGTCTCTGT GGAACATGTC TGCTGCTAAC AACAACATTA	360
AACTTCTTGA CAAATCTGAT ACTGCTTATC AGTGGAATCT TAAATATCTG GATGTTTCTA	420
AGAACATGCT GGAAAAGGTT GTCCTCATTA AAAATACACT AAGAAGTCTC GAG	473
(2) INFORMATION FOR SEQ ID NO:772:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 253 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:	
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THIS CLARES OF A SAME OF THE S	
ATACAGTAAT CAAAGTAAGT AATATTTCAA TCCAATATTT TTAAAAATCA GAATTAATGC	60
AAAAAAACC ATGATGAACA AAATATTAAA ATTTAAAATA AAGACAGGAT TAGTATTACT GAGTTTTCCT TTTGTCCCAG GCTCTAATAT GGCTTGGCAT GGGGCAGAAC ATTACAACAT	120
ACCAGTCGTG TCATGGTGCC CAAGGCTCCA CAGACCTCAG TGGCTCCCTG CTGCCTGCCA	180 240
CAGCAATCTC GAG	253
(2) INFORMATION FOR SEQ ID NO:773:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 286 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(D) TOPOLOGY: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:	
GAATTCGGCC TTCATGGCCT AGTGAGAATT GACTGTTGCT TTTGTTTGCC TGCTTACTGT	60
TTTCTTTAT TTATTTGTTT TTGGACCTGT GGCACAAAGG ATCTGTTTAC TGACCATCCT TATTGTGAGG CACACAGTCA CCATGGCACC CTGCGCGTTA CTCCTGTTCC ACTTGTTTAT	120
TCTCTGTATC CCCATACTAG TTATTATCGA AACCATCAGC CTACTCATTC AACCAATAGC	180
CCTGGCCGTA CGCCTAACCG CTAACATTAC TACAGGCCAC CTCGAG	·240 286
	200

- (2) INFORMATION FOR SEQ ID NO:774:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

GAGGCTGACA	AAATACTCAC	CTTTACCTTT	ATTTTTGCAT	TTTATACTCA	CAACCATATT	60
TTTTTTGGCC	CCCTTCCCTT	TATTTTAACT	CATAACTGAT	ACTTAAAGGT	GCTCTGCCTT	120
ATTAAATCAG	CTCCTAGGCT	${\tt GCAAGTGCAT}$	AAATTTAAA	AATTTGCAAC	TTTGACTTTT	180
TAAAAATCTG	GTCTTGGTAT	GGAGCAACTT	TGCCTTTTTT	TTTTTTTTTT	TTGAGACAGA	240
GTCTCGCTTT	NTCGCCCAGG	CTGGAGTGCA	GTGGTCCCAT	CTCAGCTCAC	TGCAACCTCC	300
TCCTCCCGGG	TTCAAGAGAT	TCTCCTGCCT	CAGCCTCCCG	AGTAGCTGGG	ATTACAGGTG	360
CCTGCCCCAA	CACCCTCGAG					380

- (2) INFORMATION FOR SEQ ID NO:775:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

GGCCTGGTAG	GATAAGAATA	TAAACTTCAG	GGTGACCGAA	AAATCAGAAT	AGGTGTTGGT	60
ATAGAATGGG	GTCTCCTCCT	CCGGCGGGGT	CGAAGAAGGT	GGTGTTGAGG	TTGCGGTCTG	120
TTAGTAGTAT	AGTGATGCCA	GCAGCTAGGA	CTGGGAGAGA	TAGGAGAAGT	AGGACTGCTG	180
TGATTAGGAC	GGATCAGACG	AAGAGGGGCG	TTTGGTATTG	GGTTATGGCA	GGGGGTTTTA	240
TATTGATAAT	TGTTGTGATG	AAATTGATGG	CCCCTAAGAT	AGAGGAGACA	CCTGCTAGGT	300
GTAAGGAGAA	GATGGTTAGG	TCTACGGAGG	CTCCAGGGAA	GCTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:776:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

GAATTCGGCC	TTCATGGCCT	AAGAGGATAA	GGGAAGAAAA	AGAAGAAAGT	ATTCCATTCC	60
CACATCCCTT	TAGGTTGGCT	TCTTATTTTA	TGTTTTTGTT	GGTGTGTTTA	TTTTGCTTTG	120
TTAACATTTT	CAACTAGCTA	TAGAAACGTT	TGCAATTCTT	ATTACTGATT	AGCATTCCAA	180
AACTTTGTAA	TGAACATTTT	TCTCTCTTTC	TTTTTTTTT	TTTTTTTNGAG	ACAGGGTCTC	240
GCTCTGTCAC	CAAGCTGGAG	TGCAGTGAGC	CAAGATCCTA	CTGCTGTCCA	TTCCAGCCTG	300
GGTGACAGAA	CAAGACCTTG	TCCGCCCACC	TTCCACCCCC	CCCTCGAG		348

(2) INFORMATION FOR SEQ ID NO:777:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid (D) TOPOLOGY: linear
 - (C) STRANDEDNESS: double
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

GAATTCGGCC	TTCATGGCCT	ACATGTTTAT	TGAGCATTTA	CTGTTTACCC	ATCAGTATTC	60
TTGATGCTAA	GGATATAGCA	GTGAACAAAA	CAATCCTTGT	GGACTTACAT	CATAGTAGGG	120
AAAATAGACA	TAAATAAAT	GTATGATAAG	TCAGTTGATA	${\bf ATAAGTGCTA}$	CGAAGTAAAA	180
CAAAGCAGGA	ATAAAGTTGG	GGAGAAAAGT	${\tt GGAGGGTGAT}$	TGCTATTTCA	GTTGAGATCA	240
TTGGGATGGT	CTTTTCTGAG	GAGGGGACAT	TTGCATAGAG	AAGCAAGGAT	GTGAGTTATG	300
TGTCTGCTGT	GTGTAGAACA	TTCTGGGAAA	GGGCAGAGAA	GGGAACAAGA	CTATTCCAGA	360
AAAAGAGGGC	ACTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:778:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

GAATTCGGCC	TTCATGGCCT	AGCACAGCTA	GACGGTTCCA	GCTCAGGGTC	TCTCATGAAG	60
TTGCAATCAA	AATATTGGCA	GGAGAGAAAA	ACATATTTTC	AGAAGCTGCA	GGCATAGGAA	120
GACTTGGCTG	GGGTTGAAGG	ATCCACTTCC	AAGATGGCGC	ACTCAGTGGC	TCTTGGCTGG	180
AGGCCTCAGT	TCCCTGCTGC	GTGGAGCTCT	CCCTCCAGCT	GCTTGAGTGG	ACTCATGACA	240
TGCAGCTGGC	CTCCCCTGGA	GCAGTCGATC	CAACAATGAG	CATGGCCATG	AACTAGAGCT	300
CGAG					•	304

- (2) INFORMATION FOR SEQ ID NO:779:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

GAATTCGGCC	TTCATGGCCT	AGCCAAAACC	ACAGAATATA	TAATATAGAT	CTTGGGGATA	60
CAGCAGAGAA	AAAAGACAAA	AATCCCTGTT	ACAATCCGTT	CTAGAATTGA	TGTTCCTTTG	120
TTGGTTAATT	CAAGTTTTGA	TTTCAGAAAT	CTTACCTCTT	GGTGACTGCC	TAGAGTGGCA	180
TTGGGCTGGA	GGGGAGGAAC	TGTTCATGTT	GGAAATGGGG	AATGGGCCAA	AAATGCAATT	240
GAGTAGGTTG	ATTAACTTGT	CTGCTGTCAG	AGTGGAAGCA	GGGGTAGTTT	CCCTTTCCGA	300
CCAGAGGCAT	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:780:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:	
GAATTCGGCC TTCATGGCCT ACAGAAGATT TGGACAATTC CATTGATAAA ACAGAAGCTG GAATTAAGGA GCTTCAGAAG AGTATGGAGC GCTGGAAAAA TATGGAAAAA GAACATATGG ATGCTATAAA TCATGATACT AAAGAACTGG AAAAGATGAC AAATCGGCAA GGCATGCTAT TNAAGAAGAA AGAAGAGTGT ATGAAGAAAA TTCGAGAACT TGGATCACTT CCCCAGGAAG CATTTGAAAA GCACCAGGCT CGAG	60 120 180 240 264
(2) INFORMATION FOR SEQ ID NO:781:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 580 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:	
GAATTCGGCC AAAGAGGCCT AGCGATTGGG TCTTTGATAT CTGTAAGCCG TTGAATTAGC	60
CCTGCCCTCT GTTCTTAGTT TAGGAGACCA TAGATGTGCC CTTATTATTG AAACTGATTT TATTCAGTTA CTGAAGTTAT CTTACCTGAT ACATAATTTT ACCCATAGAA AATAATATGA	120 180
AAATAGCAAA ATCACTCAGG TAAGATAGAT GAGTGCCTGC TGTGTTCAAG AGACTGTTAA	240
TATGAGGCTC TGGGGCTGCA AAAAATCAAG TTGCTAAGAA ATATGAGGTC AGAGCAGCAG AAGTTCTGAG TAACCACTGA TTACTGGACT TGGGGTGATC AGAAGTGACT GTGTGGGAGA	300 360
GGTGAAATTG AGCAGACTCT GAAGGAACCT CTGGGTTTTG GTAAATAGGG AGCTGGGGAT	420
GAGGATGCCC CAGGTTTTAG AAAGAACACA GGCTGTTGAA TCACACCTGG GTTCAAACCC	480
TGGCTTGCTA CTCCCTAGTT TGTGACCTTG TCAAATTCCT TGATTTCTTT TTTCTTTTTC TTTTTTTAAT TTTGGAGACA ACAGTCTCGC TCTGTCACCC	540 580
(2) INFORMATION FOR SEQ ID NO:782:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 131 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:	
GAATTCGGCC AAAGAGGCCT AGAATGGTAG AGTAAAAAGA ACCCTCTGCT GAGTAACCAA GCCTTTAATT TCCTGTTCCT GCTGTAGGGC TTTCACAAAT GCATTTTTCA GCCGGTTGGT GTGTCCTCGA G	60 120 131
(2) INFORMATION FOR SEQ ID NO:783:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 121 base pairs	
(B) TYPE: nucleic acid	

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WO 98/45436
                                                               PCT/US98/06955
                          (C) STRANDEDNESS: double
                           (D) TOPOLOGY: linear
                    (ii) MOLECULE TYPE: cDNA
                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:
             GAATTCGGCC AAAGAGGCCT AGATTGAGGT TGTGGTAGAT TAGGCGTAGG TAGAAGTAGA
                                                                                 60
             GGTTAAGGAG GGTGATGGTG GCTATGATGG TGCGGCTCGA GGCAGGTCTA GAATTCAATC
                                                                                 120
                                                                                 121
              (2) INFORMATION FOR SEQ ID NO:784:
                    (i) SEQUENCE CHARACTERISTICS:
                           (A) LENGTH: 405 base pairs
                           (B) TYPE: nucleic acid
                           (C) STRANDEDNESS: double
                           (D) TOPOLOGY: linear
                    (ii) MOLECULE TYPE: cDNA
                    (xi) SEQUENCE DESCRIPTION: SEO ID NO:784:
              GAATTCGGCC AAAGAGGCCT AAGCAAGATG AAGCCCAACA TCATCTTTGT ACTTTCCCTG
              CTCCTCATCT TGGAGAAGCA AGCAGCTGTG ATGGGACAAA AAGGTGGATC AAAAGGCCGA
                                                                                 120
              TTACCAAGTG AATTTTCCCA ATTTCCACAC GGACAAAAGG GCCAGCACTA TTCTGGACAA
                                                                                 180
              AAAGGCAAGC AACAAACTGA ATCCAAAGGC AGTTTTTCTA TTCAATACAC ATATCATGTA
                                                                                 240
              GATGCCAATG ATCATGACCA GACCCGAAAA AGTCAGCAAT ATGATTTGAA TGCCCTACAT
                                                                                 300
              AAGACGACAA AATCACAACG ACATCTAGGT GGAAGTCAAC AACTGCTCCA TAATAAACAA
                                                                                 360
              GAAGGCAGAG ACCATGATAA ATCAAAAGGT CATTTTCACA GGGTA
                                                                                 405
              (2) INFORMATION FOR SEQ ID NO:785:
                     (i) SEQUENCE CHARACTERISTICS:
                           (A) LENGTH: 642 base pairs
                           (B) TYPE: nucleic acid
                           (C) STRANDEDNESS: double
                           (D) TOPOLOGY: linear
                     (ii) MOLECULE TYPE: cDNA
                     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:
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GAATTCGGCC	AAAGAGGCCT	ACTACTCACC	TCTTGCTCTC	TCCCAACCAT	AGAAACAGCC	60
ACGACTCCTA	CCACAAACTT	GGGAAACACC	ACCACTGAGA	CCACCTCCCA	CAGTACTCCC	120
AGCTTCACTT	CTTCAGCCAT	CTACTCCACC	GTCAACATAT	CCACAACTAC	CATCTCCTCA	180
TTTCCCCCTT	CCTCAGGTAC	CATGGTGACA	TTCACAACCA	TGAACCCATC	CTCTCTGAGT	240
ACAGACATAT	CTACCACCAC	ACTGAAAAAT	ATCACCCAGC	CTTCTGTGGG	CTCTACTGGT	300
TTCCTGACTG	CAGCTACAGA	CCTCACCTCA	ACATTCACTG	TTTCCACTTC	CTCAGCAATG	360
TCCACAAGTG	TCACTCCATC	TGCCCCCAGC	ATCCAGAATA	AAGAAATCTC	AACACTTGTG	420
AGTACAACCA	CTACCACCAG	TCCCACTGAG	AGAATGACTC	TCACAAGTAC	AGAGAATACC	480
CCGACAAGTT	ACATCCTGAC	CACCAGTCCA	GTGACATATT	CATTTTCCCC	TTCCATGTCT	540
GCCAGCAGTG	ACTGGACCAC	TGACACAGAG	AGCATCTCCT	CAGCTCCAGC	CATCACCAGT	600
ACACTCCACA	CAACAGCTGA	ATCCACCCTG	GCAGGTCTAG	AA		642

- (2) INFORMATION FOR SEQ ID NO:786:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GAATTCGGCC A	AAGAGGCCT	ATGGCCTTGG	AAGGGATGAG	CAAACGGAAG	AGAAAG AG AA	60
GTGTCCAGGA G	GGAGAGAAT	CCTGACGACG	GCGTTCGCGG	GAGTCCGCCG	GAAGACTACA	120
GGCTTGGACA G	GTCGCCAGT	AGCTTATTTC	GCGGCGAACA	CCATTCCAGA	GGTGGCACCG	180
GTCGGCTGGC G	TCCCTCTTC	AGTTCTCTGG	AGCCCCAGAT	TCAACCCGTG	TACGTGCCTG	240
TGCCTAAACA A	ACCATCAAA	AAAACGAAAC	GGAATGAGGA	GGAAGAAAGT	ACATCCCAGA	300
TTGAAAGACC A	CTTTCGCAA	GAACCTGCCA	AAAAAGTGAA	AGCGAAGAAG	AAACACACTA	360
ACGCAGAAAA A	AAGTTGGCA	GACAGGGAAA	GCGCTCTAGC	GAGTGCTGAT	TTAGAAGAAG	420
AAATTCACCA G	AAACAAGGG	CTTAGCTCGA	GCAGGTCTAG	AATTCAATG		469

- (2) INFORMATION FOR SEQ ID NO:787:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

GAATTCGGCC	AAAGAGGCCT	AAGAAAAGAT	ATAAATCAGA	GAAAAAGCAT	GAAGCGTATC	60
ATATTGATTT	TAACAGTATT	GCTTGCCATG	TTAGGGCAGG	TTGCCTATGC	GCAGAAAACG	120
TGTGTCATCG	CATCGGCAGA	AAATCATGTG	CCTATTCGTG	AAGCACTTAT	TCATACCAAT	180
AACAATCATT	GGGCAAGAAC	AGATTATCGG	GGCTATTGGA	CGATGCGCTA	TCAGTTTGAT	240
TCAGCAACCG	TATCGAAACC	TGGTTTTATG	AAGGCAACTA	TCCGGTACAA	GGAACTGCCG	300
GATACTCTGT	TTCTCTTGCC	GGATGCCAAA	CAGTTAGGCG	AAGTGACAGT	TTGGGGCAAG	360
AATCAGGAAG	GCATCAAAAA	TATGGAAGAG	GATATTCAGG	AGAAGATAAA	CTCTTTGCCA	420
ACTTCATCTG	CTGGCATTGG	TTTTGATGCT	TTCGGATGGA	TGGATAAACA	GGGAAAACGT	480
GATAAGAAGC	ATCTGCAACA	G				501

- (2) INFORMATION FOR SEQ ID NO:788:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

TGATGATCGA	TATCCAGAAA	GACACTGCGG	TGGAAGGTGA	GGAGATTGAA	GTCAACTGCA	60
CTGCTATGGC	CAGCAAGCCA	GCCACGACTA	TCAGGTGGTT	CAAAGGGAAC	GCAGAACTCG	120
AG						122

- (2) INFORMATION FOR SEQ ID NO:789:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs

- PCT/US98/06955 WO 98/45436 (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:789: GGTGAGCTGA GATCGCACCA CTGCACTGCA AGACCCTGTC TCAAAACAAA CAAACAAACA 60 ACAACAACAA CAACAAACCA AACCAAACAA AAAACCTGCA TAGCCAACTA GACCAGCATA 120 GAGGGCGAAA ACCATGCTTT TTGTCAAATG GTACTGTTTA TTCTGTTTTG CTGTCAGCTG 180 GTTTGCCGCT TCTGATAAAG CTAGCCCTTG CTGTGTGCAT GCAGGTTATA GTGCCCAGGC 240 274 TCATATTTCC TCTTCTTGCT GCACCTCACT CGAG (2) INFORMATION FOR SEQ ID NO:790: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 209 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:790: GAATTCGGCC TTCATGGCCT AGGGAAAGGA GGCGGCAGCC AGGCTGTGTC CCCTGACCGT TGGAGCGTCT GCGACCCCCG CATCCCCGCA CCCTCAAGGC ACCTCCAAAG ATGATGATGG 120 GTTGTGGGGA GTCAGAGCTG AAGTCGGCGG ACGGGGAAGA AGCCGCGGCG GTCCCGGGGC 180 209 CACCCCGGA GCCCCAAGTC CCGCAACCG (2) INFORMATION FOR SEQ ID NO:791: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 389 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:791: GAGAGAATTA AAGAGAACCA CNAAGCTGAA CCTCAAAAAG TTAGCCTGGC GAGGGGAGGA 60 TGATGAGATT TCCCCTGTTG TCACATAAAC AAGGAAGTAA AGGGGGCCCC TTGTGCTCTC 120
 - (2) INFORMATION FOR SEQ ID NO:792:

AGAACACAGA GATAACCCCG GAACTCGAG

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs

AGAACTCCAA GCATGAAACG ATAGCAAAGG GAAAAACAGC TAAGTGTTTC CTGGCTGAAT

TTTATTTTGC TTTCAGTTTC TGCCATTTCA GTTCCTGTTA TCGTGCTTTG AGGTGCACTG
AACTGCAGCA AACCCAGGGG ATCCAAGGCT ACGTTGAAAA GCCTTTGACC ACAGTGCAGG

GAGCAGAAGA CATTAATGAC GTGATGTCGA CACAGCCCGC ACTCAGGATC CTCCAGGAAA

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

180

240

300

360 389

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

GTGCTTTGGA	TTTTGCATCC	AGCTTTTTCT	CAACACCCCC	GCTGGAACTC	AGCGGCTCCA	60
TCTCTTCGCC	TTCGGAAGCA	CCTGCGTCTC	TGTCTCTGAT	${\tt GCCGAGTGAC}$	TTGTCCCCCT	120
TCACATCTCA	GTCTTTTTCT	CCCTTGGTTG	AGACATTTAC	ATTGTTTGAC	TCTAGTGATC	180
					CAGCTCCAGC	240
CAAGTTCCGA	GCTGCCTTTA	AACACCATCA	TGTTGCTACC	TANCCGTTCT	GAGGTGTCAC	300
CATGGTCAAG	CTTCCCTTCT	GATTCTCTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:793:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

GAATTCGGCC TTCATGGCCT	ACTGGAATTT	CTTTCTTGCC	CTTTCATATT	TTAAGATGGC	60
TGGAATAGCA CAGGGAGTAT	ATAGCAGATA	TCTTCTGGGA	AATAATTCAT	CTGAGGATAG	120
CTTTTTATTT GCCAATATTG	TGCAACCTCT	GGCAGAAACT	GGACTACAAC	TCTCCAAACG	180
AACTTTCAGT ACTGTACTAC	CACAGATTGA	TACTACTGGA	CAGTTGTTTG	TACAGACTCG	240
GAAAGGTCAG GAAGTTCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:794:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GAATTCGGCC TT	CATGGCCT ACTATGCCG	T CATGATAGAG	AAGATGATCC	TGAGAGACCT	60
	GTTTGTCT ACGTCGTCT				120
GCTGATTGAA GA	CGGGAAGA ATGACTCCC	T GCCGTCTGAG	TCCACGTCGC	ACAGGTGGCG	180
GGGGCCTGCC TG	CAGGCCCC CCGATAGCT	C CTACAACAGC	CTGTACTCCA	CCTGCCTGGA	240
GCTGTTCAAG TT	CACCATCG GCATGGGCG	A CCTGGAGTTC	ACTGAGAACC	ATGAACTTCT	300
CGAG					304

- (2) INFORMATION FOR SEQ ID NO:795:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GCGATTGAAT TCTAGACCTG CCTCCAAGCA GCTGCAGTAT CTCGGAAGAA AAAACGAAGA ATGGGAACCT ATAGCCTGGT TCCTAAGAAA AAGACCAAAG TATTAAAACA GAGGACGGTG ATTGAGATGT TTAAGAGCAT AACTCATTCC ACTGTGGGTT CCAAGGGGGA GAAGGACCTG GGCGCCAGCA GCCTGCACGT GAATGGGGAG AGCCTGGAGA TGGACTCAGA TGAGGACGAC TCAGAGGAGC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:796:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:	
CTAGTCTTCC AACCCTTCTG GACTTTCTTT GCTCTTGTCT TGTTTTGGGT GTACTGGATC ATGACACTTC TTTTTCTTGG CACTACCGGC AGTCCTGTTC AGAATGAGCA AGGCTTTGTG GAGTTCAAAA TTTCTGGGCC TCTGCAGTAC ATGTGGTGGT ACCATGTGGT GGGCCTGATT TGGATCAGTG AATTTATTCT AGCATGTCAG CAGATGACAG TGGCAGGAGC TGTGGTAACA TACTATTTTA CTAGGGAAGT ACTCGAG	60 120 180 240 267
(2) INFORMATION FOR SEQ ID NO:797:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 185 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:	
GAATTCGGCC TTCATGGCCT AGGGGGAGTT TAGCTGAAAC AAGTTTTACA GAAGCAGAGC TGGCAAATAG TTAAAATATT AATTGGTTAC AATAGCAGTT ACAAAACAAA	60 120 180 185
(2) INFORMATION FOR SEQ ID NO:798:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 434 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:	
GGGCGTGTGA CGACTGCTGG GAGAGGAAAG CGAGACATCA TTCCAACCCT CCAGAAGCTA AAGATCCTGG AACTCAAGGG GAAAACTAAC GTAAGTGCGA AAGCGAACAA GCAAACATGT CCTCAACGGG GCAGGCAGGC TGTCGGGGTA CAGAGCTGGA ATCTGGGAAG GAACAGAGAG GGCCGCTCAG GGAGAGGAAG CACAGTGCCA CCGGAGGCAC GACTCAGCA GGCACTCGCA GGCTGGGCAG ACGTGAGAAA GCACCCCTTTAG	60 120 180 240

AGCCGGGCAG GAGAGCTGGT GTGGGACCTG GGAGGAGGAC AGGAGCCTTC AAAGCAGCAC CGCCTGATTG CAGCCAGGAG GGTAGCATCA AGGAAGATGG AACTGCGGCC AGGCCACATC CAGGGGTGCT CGAG	360 420 434
(2) INFORMATION FOR SEQ ID NO:799:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 424 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:	
GAAAAGTCGG ATGCTGGCCT CTGGAAATCA GCCAGATCAA GATATTACAC ATTTCTTCCA ACAGATCCAG GAGCTCAATT TGGAAATGGA AGACCAACAG GAGAACCTAG ATACTCTTGA GCACCTGGTC ACTGAACTGA GCTCTTGTGG CTTTGCGCTG GACTTGTGCC AGCATCAGGA CAGGGTACAG AATCTAAGAA AAGACTTCAC AGAGCTACAG AAGACAGTTA AAGAGAGAGA GAAAAGATGCA TCATCTTGCC AGGAACAGTT GGATGAATTC CGGAAACTT CCAGAAATGG TTGAAAGAAA CTGAAGGGAG TATTCCACCT ACGGAAACTT CTATGAGTGC TAAAGAGTTA GAAAAGCAGA TTGAACACCT GAAGAGTCTA CTAGATGACT GGGCAAGTCT CGAG	60 120 180 240 300 360 420 424
(2) INFORMATION FOR SEQ ID NO:800:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 300 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:	
GAATTCGGCC TTCATGGCCT AGGGGTGCTG TGTGTTTTTC AGGGCGCCCT GCGTCCGGCA GAGGAGGCGA GCATCCCGCT CAGGTGATGA GGAACCCCTC GCGCACCCAG CGCAGAAGGC TGCTGCCGCC GGACGCCTCC ATTGTTTGAC CACAACAAGG GCCGGATTCT CACCCAGCAG GATCCTAAGG CCTTTGTAGT CCTTCAGCCA CTGTGGGCCC TGCCTCTGCC TGTTCTTCTG GAATGTCTTG GGGGTTTTGA TCCTGTCACT GTGACCTGCA AATCCAAGAG ACAACTCGAG (2) INFORMATION FOR SEQ ID NO:801:	60 120 180 240 300
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 306 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:	
GAGAAATCAG TGAAGGATTT GCAACGCTGC ACCGTTTCTC TAACTAGATA TCGCGTCATG ATTAAGGAAG AAGTGGATAG TTCCGTGAAG AAGATCAAAG CTGCCTTTGC TGAATTACAC AACTGCATCA TTGACAAAGA AGTTTCATTA ATGGCAGAAA TGGATAAAGT TAAAGAAGAA GCCATGGAAA TCCTGACTGC TCGTCAGAAG AAAGCAGAAG AACTAAAGAG ACTCACTGAC	60 120 180 240

CTTGCCAGTC AGATGGCAGA GATGCAGCTG GCCGAACTCA GGGCAGAAAT TAAGCACGGT CTCGAG	300 306
(2) INFORMATION FOR SEQ ID NO:802:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 263 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:	
GCTCGCGGCC GTTCAGAATT ATAAGGCTGT CTGCAGAGAT TTGAAAAATG GCAACAAATG AAAGTGTCAG CATCTTTAGT TCAGCATCCT TGGCTGTGGA ATATGTAGAT TCACTTTTAC CTGAGAATCC TCTGCAAGAA CCATTTAAAA ATGCTTGGAA CTATATGTTG AATAATTATA CAAAGTTCCA GATTGCAACA TGGGGATCCC TTATAGTTCA TGAAGCCCTT TATTTCTTAT TCTGTTTACC TGGATGTCTC GAG	60 120 180 240 263
(2) INFORMATION FOR SEQ ID NO:803:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:	
GAATTCGGCC TTCATGGCCT AAATAGTTAG TCACCTTCTG ACCTTCTCCT CTTTCTCAAA GCCTTCTGTC CCTGGTTTTT GCAAGTGCTG CATTTCCGCC GAGAATCCGC GTTGCCTACT GCTGCCACCT CCTGTTCATT TAGAACTATG CAAAGACTCC GCTTCCGTTT TCCTGAGCTC CTCGGGCCCC AGAGTCTCTG TTTGATTATT TATTTATTTA TTTATTTATT TGCCAAAAAT TCTCCTCTTC AACTTATAGA ATGCACCCAA CTCGAG	60 120 180 240 276
(2) INFORMATION FOR SEQ ID NO:804:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 580 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:	
GAATTCGGCC TTCATGCCTA CAGCCATATT AAAACTAAGT AAACTCGTCC CTGGGAACTA	60
CACTTTCAGC TTGACTGTAG TAGACTCTGA TGGAGCTACC AACTCTACTA CTGCAAACCT	120
GACAGTGAAC AAAGCTGTGG ATTACCCCCC TGTGGCCAAC GCAGGCCCCA ACCAAGTGAT	180
CACCCTGCCC CAAAACTCCA TCACCCTCTT TGGGAACCAG AGCACTGATG ATCATGGCAT	240
CACCAGCTAT GAGTGGTCAC TCAGCCCAAG CAGCAAAGGG AAAGTGGTGG AGATGCAGGG	300
TGTTAGAACA CCAACCTTAC AGCTCTCTGC GATGCAAGAA GGAGACTACA CTTACCAGCT CACAGTGACT GACACAATAG GACAGCAGGC CACTGCTCAA GTGACTGTTA TTGTGCAACC	360 420
TGAAAACAAT AAGCCTCCTC AGGCAGATGC AGGCCCAGAT AAAGAGCTGA CCCTTCCTGT	480

-:

GGATAGCACA ACCCTGGATG GCAGCAAGAG CTCAGATGAT CAGAAAATTA TCTCATATCT CTGGGAAAAA ACACAGGGAC CTGATGGGGT GCAGCTCGAG	540 580
(2) INFORMATION FOR SEQ ID NO:805:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:	
CAAATTGATT TCGGCACAGT TCTGGGAGCT GGGACATTCA AGGTCACCAC GTTGCCACCT GTGAAGGCCT TCTGCTGCAT CCTCATGTTG GGGAAGATCA GAAGTGAGAA CACATGCTGG CCAGTCCTTT CACAGCAGCA TCAATCCGTG CATGGGGCAG GGCCCTCGGC CTGAGCGCCT CCCCCAGGCC CTAACTCCCA GCACTGCCCT GCTGGGGATG GAATTTCCAA CATGAATCTG GGGGATGCTT TCGGACCACA GCCGGGGAGC CTGCCCTGGC TTCCAGCTGC TGGTGGCCCA GGGGCTCCCT GGCTTGCCTC GAG	60 120 180 240 300 323
(2) INFORMATION FOR SEQ ID NO:806:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:	
GCGATTGAAT TCTAGACCTG CCATTCTCGC TCTGCCGACG TTGACTCTCT CTCTGAATCC AGTCCCAACT CCAGCCCTGG CCCCTGTCCT GAGAAGGCCC CACCACCCCA GAAGCCCAGC CATCTCCCAG GGGGCCCTCA TCGCCATCGT CTGCAACGGT CTCGTGGGCT TCTTGCTGCT GCTGCTCTGG GTCATCCTCT GCTGGGCCTG CCATTCTCGC TCTGCCGACG TTGACTCTCT CTCTGAATCC AGTCCCAACT CCAGCCCTGG CCCCTGTCCT GAGAAGGCCC CACCACCACT CGAG	60 120 180 240 300
(2) INFORMATION FOR SEQ ID NO:807:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 556 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:	
GAATTCGGCC TTCATGGCCT AGATATGAGA AATGAGTGTT GGACGTCGAA GAATAAAGTT GTTGGGTATC CTGATGATGG CAAATGTCTT CATTTATTTT ATTATGGAAG TCTCCAAAAG CAGTAGCCAA GAAAAAAATG GAAAAGGGA AGTAATAATA CCCAAAGAGA AGTTCTGGAA GATATCTACC CCTCCCGAGG CATACTGGAA CCGAGAGCAA GAGAAGCTGA ACCGGCAGTA CAACCCCATC CTGAGCATGC TGACCAACCA GACGGGGGAG GCGGCAGGC TCTCCAATAT	60 120 180 240 300
AAGCCATCTG AACTACTGCG AACCTGACCT GAGGGTCACG TCGGTGGTTA CGGGTTTTTAA	

CCTCACTCCA CATTTTGCCA GAAGGCAAGC AATCCGGGAA TCCTGGGGCC AAGAAAGCAA	420 480 540 556
(2) INFORMATION FOR SEQ ID NO:808:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 359 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:	
GGAAACTTCT AAACTATTTT GCTCGCAACT TTTACAACAT GAGAATGTTA GCCTTATTTG TCGCATTTGC TATCAATTTC ATCTTGCTCT TTTATAAGGT CTCCACTTCT TCTGTGGTTG AAGGAAAGGA GCTCCCCACG AGAAGTTCAA GTGAAAATGC CAAAGTGACA AGCCTGGACA GCAGCTCCCA TAGAATCATC GCAGTTCACT ATGTACTAGA GGAGAGCAGC GGCTACATGG AGCCCACGTT GCGTATCTTA GCTATTCTGC ACACGGTCAT TTCTTTCTTC TGCATCATTG GATACTACTG CTTGAAAGTC CCATTGGTTA TTTTTAAGCG AGAAAAGGAA GTGCTCGAG	60 120 180 240 300 359
(2) INFORMATION FOR SEQ ID NO:809:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 299 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:	
GAGANACGAC AATGTCCAGG AAACAGAACC AGAAGGATTC ATCAGGATTC ATTTTTGATT TGCAGTCCAA TACCGTACTG GCCCAGGGAG GAGCTTTTGA GAACATGAAA GAGAAGATAA ATGCGGTACG TGCAATAGTT CCTAATAAGA GCAACAATGA AATTATCCTG GTTTTGCAGC ACTTTGATAA CTGTGTGGAC AAAACAGTAC AAGCATTCAT GGAAGGTAGT GCCAGTGAAG TACTCAAAGA ATGGACAGTA ACAGNCAAGA AAAAGAACAA AAAGAAGAAG AAACTCGAG (2) INFORMATION FOR SEQ ID NO:810:	60 120 180 240 299
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 413 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:	
GAATTCGGCC TTCATGGCCT AGTAGCTGTT CCAGTACAAT TCAATGTTAT CCAGGTTGGG TGCATGTGTA ATGATATTTC TGTACTTTTG TATCAACTCA GAATTTCCAG AGAGCTCTTC CTGGCTGAAA AGATGTCCAA GGATCATCTC CGGAATGGAA GAGGTGAGGC CTGTTAGCTT GTGGGCTGCC CAATCCATCC AACCCTTGGC ATTGGGATCA ATGTTGATGA GGACAAGACC TTCAACAGTG TCCGGGTGGT TAAGAGCATA TCTCGCCAGG ATGTAGGCTC CAGCTCCAAC	60 120 180 240 300

ACCAACTCCA ATTATTGTAG AGAAATTTAG GTACTGCAGG ACGCAAGGGA TCATGTCTGC AAGCTGGTCC AGAGATGGGT ACTGATATCC CAAAGGGAAC ACAGGGGCTC GAG

360 413

(2) INFORMATION FOR SEQ ID NO:811:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 324 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:	
TTGGTATTGT CTCTGTACTA GTCTTTCCAA ATTCTGCTGT GAGCTTTTTG CTTAGACTGT AAGCCTTAGA GTCACTCATC ACAGTAATCC TAAAGACAGA TJTTTCTGTT CTATTTGATA AGGCCTTTTT GTGGGTTGTG CCGACTGTCA GTTTCATGTT TGTTTGTTTG TTTTGGAACT GCAGTTACAT CCAGGAGACC TGTGGTGAGC ATAATGGGCT GTAGTTTGTG CAGTTGTCAG TATAGCTTGT TAGGGAGCTC TTCCTGGGCA GAGTCTTGCA CAGCAGAGCC CAGTGCTGAG CTGAGTTCTT GGCACCATCT CGAG	60 120 180 240 300 324
(2) INFORMATION FOR SEQ ID NO:812:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 352 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:	
ACATTTCTTT GTAAGTTNNN AAAAGCCTAT GAGGGTTTTT TCCACGATTC CGTTCCCAGT TTGGCTTTTG TTGTTGTT GGCTGTTCTT GGCCCCCTG GGCCCTGCAG TGGAGTGGGG GGCTGCACCT GGGAGCCTCG AGCTGAGGCC CAGCCCCTCC TGCCCTGCAT TTTCCTGCCA AGCAGCACCT GAGACTCTGA AGCCGATGCC TATACAGGCA GAAACCTGCC AATTCCAGCT TGAACGACTG GAGGGTCCTG AGGATGGGGG TCCCTGGGGT GCCATCATGG GCAGGTGCA TCTGTTTGGG TATGCTGCCC CCCAGCTGGC GGGGCACCGG GGACAGCTCG AG	60 120 180 240 300 352
(2) INFORMATION FOR SEQ ID NO:813:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:	
GAATTCGGCC TTCATGGCCT AGGGAAAGGG AANGTGGGGA GGGTCCGAGG GGAAGGGGAC CCCAGCTTCC CTGTGCCCGC TCACCCCACT CCACCAGTCC CCGGTCGCCA GCCGGAGTCT CCTCTCTACC GCCACTGTCA CACCGTAGCC CANATGGATA NCACNGTTGT CAGACAAGAT TCCTTCAGAT TCCGAGTTGC CTACCGGTTG TTTTCGTTGT TGTTGTTGTT GTNTTTNTTT TTNTTTTNNN TNCGGAAGAC AGCAATAACC ACAGTACATA TTACTGTAGT TCTCNATAGT TNCACATACA TTNATACCAT AACCTCGAG	60 120 180 240 300 329

(2) INFORMATION FOR SEQ ID NO:814:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GAATTCGGCC	TTCATGGCCT	ATCCATTTCC	AAATCCACCA	AGGTCCAGTC	GACAGACATT	60
TCCAAAAAGA	ATCCTGTTCT	AGGACCACTT	GCGCTGAGAG	CACACCCGGG	GGTCAAAGGG	120
CAGCCACCGG	${\tt GGGTCAAAGG}$	${\tt GCAGCCATCA}$	${\tt GGTACTCCCC}$	AGGGAAGGGC	TTGCGGCCAC	180
CAGTCACTGC	AACCCCGCCT	CACCTCCGAT	GCCTGCTGTG	CCCAGGGTGG	TCCCGCTCAT	240
AGCGACGGCC	TGNGCGTNCA	TANGACCTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:815:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 584 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GATTGAATTC AATGTTAAGC ACCAATGCTG GATTTGGTGG TGGACTGAAC ACCAGTGCTG	60
GCTTTGGTGG TGGCCTAGGC ACCAGTGCTG GCTTCAGTGG TGGCCTAAGC ACAAGTTCTG	120
GCTTTGATGG TGGGCTAGGT ACCAGCGCTG GCTTCGGTGG AGGACCAGGC ACCAGCACTG	180
GTTTTGGTGG TGGACTGGGC ACCAGTGCTG GCTTCAGTGG CGGACTGGGC ACCAGTGCTG	240
GCTTTGGTGG TGGACTGGTC ACTAGTGATG GCTTTGGTGG TGGACTGGGC ACCAATGCTA	300
GTTTCGGCAG CACACTTGGC ACCAGTGCTG GCTTTAGTGG TGGCCTCAGC ACCAGCGATG	360
GCTTTGGCAG TAGGCCTAAT GCCAGCTTCG ACAGAGGACT GAGTACCATC ATTGGCTTTG	420
GCAGTGGTTC CAACACCAGC ACTGGCTTTA CTGGCGAACC CAGCACCAGC ACGGGCTTCA	480
GTAGTGGACC CAGTTCTATT GTTGGCTTCA GCGGTGGACC AAGCACTGGT GTTGGCTTCT	540
GCAGTGGACC AAGCACCAGT GGCTTCAGCG GCGGACCGCT CGAG	584

- (2) INFORMATION FOR SEQ ID NO:816:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GAGAATGTCC	AGCAAGGAAG	TGAAGACTGC	TCTAAAAAGT	GCTAGAGATG	CAATCAGAAA	60
CAAAGAATAC	AAAGAAGCTT	TGAAACACTG	TAAGACAGTG	TTAAAGCAAG	AGAAAAATAA	120
CTATAATGCC	TGGGTTTTTA	TTGGCGTTGC	TGCAGCTGAA	CTAGAACAAC	CTGATCAGGC	180
CCAGAGTGCC	TATAAAAAAG	CTGCTGAATT	AGAGCCAGAC	CAATTACTAG	CTTGGCAGGG	240
GTTAGCAAAC	TTGTATGAGA	AATATAATCA	CATAAATGCT	AAGGATGACT	TGCCTGGTGT	300
TTACCAAAAG	CTCCTGGATC	TTTATGAGAG	TGTTGACAAG	CAGAAGTGGT	GTGATGTCTG	360

CAAGAAACTT GTGGATCTAT ATTACCAAGA AAAGAAACAC CTAGAGGTGG CTCGAACATG

GCACAAGTTG ATAAAAACAC GGCAGGAACA AGGTGCAGAA AATGAAGAGC TTCATCTCGA

420

480 481

(2) INFORMATION FOR SEQ ID NO:817:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 209 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:	
GAATTCGGCC TTCATGGCCT AGGGGGAGTG GTGGGTATTG CTAAGTTATC AGTTATTTAA CCTTATGGAG TTTTATTTAA CCGTTTTTGT TTGACATGTT TTATATATAT GTAATTTTAT TTATTCTTCA CAAAATCCCT GTGAGGGGGG TGGTACTATT GTCCCCATTT AAAGATGAGA ACACTGAGGC ATGTCTAGAA TTCATCGAG	60 120 180 209
(2) INFORMATION FOR SEQ ID NO:818:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 220 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:	
GGCTCTGTGG AATTCCATGG CATCTTCCCC GCCCCCCCA ACCCCCCCT TTCCCCCTTC TTTTTTTTT TTTCTTTTCT TTTCTCCCCT CCCCCCCTTT CACCATTTCC CCTCGGAGGC GCTTTCCCCG GGCAGGGGCA GAGCCGGTCT CACCCCCCGC CTCTCCCCGG CCCCCGCCGC CCTATGGCGA GAGGGAGCCC CCTCCCAACC CGGGCTCGAG (2) INFORMATION FOR SEQ ID NO:819:	60 120 180 220
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 346 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:	
GAATTCGGCC TTCATGGCCT ACACATTCTT TTAGTCAGAA ACATTAAAAT AGTAGAGTAA GTTGGCTTGA AGTGAATTTT TGTGTGAAAT CTTTTCTCTG CCCTAGCCTA GTTTGTCCAT GCACATTTGC ACACAGGAAG AACATTTTTA GACCTGCCAG AATATGCAAT GACAGGGTAA AAAATGCCGG AGGTTGACTG TGTTCATAGA CATTGTGCTA AACACTCAAC ACTCCTGATC ACACTGAATG CTTTTGACAG TCCTGTGAAT TGAGGGCTAT TATTATCCCC ATTTTATATA TGAGCGAGCA GAGGCCCAGA CAGATTAACA AAGGTGCTCC CTCGAG (2) INFORMATION FOR SEQ ID NO:820:	60 120 180 240 300 346

(i) SEQUENCE CHARACTERISTICS:

(1) BEQUEECE CHECKIOTICS.	
(A) LENGTH: 355 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:	
SCTTATACAG TGTCCGATAG ACACCAGGAA GCNACTAGCA GAGAATTTGG TAGTCATAGG	60
TGGCACTTCT ATGTTGCCAG GATTTCTCCA CAGATTGCTT GCAGAAATAA GGTATTTGGT	120
AGAAAAACCA AAATATAAAA AAGCACTTGG CACTAAGACA TTTCGAATTC ATACTCCACC	180
GCAAAAGCT AATTGTGTGG CCTGGTTGGG AGGGGCTATT TTTGGAGCAT TACAAGATAT	240
ACTTGGGAGC CGTTCTGTTT CAAAGGAATA TTATAATCAG ACGGGCCGTA TACCTGATTG	300
STGTTCTCTC AATAACCCAC CTTTGGAAAT GATGTTTGAT GTCGGGGAAC TCGAG	355
(2) INFORMATION FOR SEQ ID NO:821:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 273 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:	
GCTCGAGGGC GAAGGGGAGC AATGGCATTT GCGTTGGCCA TCCGTGACAC GGCATCCTAT	60
GCTCGCCAGA TGATGTTCAC GACCACCCTT CTCATTGTGT TCTTCACTGT CTGGATCATT	120
GGAGGAGGCA CGACACCCAT GTTGTCATGG CTTAACATCA GAGTTGGCGT CGAGGAGCCC	180
TCCGAAGAGG ACCAGAATGA ACACCACTGG CAGTACTTCA GAGTTGGTGT TGACCCCGAT	240
CAAGACCCAC CACCCAACAA CGACAGACTC GAG	273
(2) INFORMATION FOR SEQ ID NO:822:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 286 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:	
GAGATAAACA AAATTGATTG CCCCATTCTC TCACTTCCCC ATCTTGTCTT CCTAGACCCC	60
ACAGAGTTAA AACTTGGGAT TCCCCTGGCC CCCCCAGAAC ACTTGTATAT TGTTTGTTTG	120
AGGTTCGTGC CGCAGTAACA GACACAGTAT TTAATTGCAC ATACAGATGT TTGCTGGGTA	180
TATTCACTGT AAATTTTATT TAATCTGTTT TTTTGTTTGT TTGGGGGTTA TTTGGGGGGA	240
GGTTGGTTTT GTTTTTAAAT ATAAAAAAA AAATCTGTCA CTCGAG	286
(2) INFORMATION FOR SEQ ID NO:823:	
(A) CHOMPAGE CHARACTERISTS	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 297 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
254	

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GGTCTGGAGG	AGGCCCGGAG	GGGCTGTGGG	TGGACCACTG	CAGTAATCTG	GGTGAAAGAT	60
GATGATAGGC	TAGACTAATA	TGGTACCAGA	GACAAAGAAG	AGGGACTTGA	GAGTTATTTA	120
GGAGGAAAAA	AACAAAACAA	AACAAAAATC	AACCAGACTT	ACGTTTTGAA	ATAGGACAAG	180
TGAGGAAAAG	GAGGGTTTCG	AGAATAGCTT	ATAGTTTTCG	AGAAGATGAG	GTTGGACAAG	240
ATGCCACTGC	TTTTCTTAGC	ACTCTTCCCT	CCCCTAAACC	ATCCCGTAGT	GCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:824:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

GAATTCGGCC	TTCATGGCCT	ACCCTCATTA	CCCCAAGTGC	CTCCTAATGG	ATCTGTCCTT	60
ATTCTTCCTT	GTTCTGTCTC	CCTCATGCCC	TGGAGCTCCT	CTCTTTGGGA	CCTTCCTCTC	120
CCAAGTCACC	ACCCTCTCTC	CCCTTCTACC	ACTCAGCCAT	TCCCCAGTTT	CCACAGTTCC	180
TCAAACATTA	CCCCACTCCC	CACTCCCCAG	TTTCCTCCCC	CTCCCCATTT	GTCCCCCTCA	240
CCTGGGGGTC	CCCGAAGTAG	ATCTGCAG				268

- (2) INFORMATION FOR SEQ ID NO:825:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

GAATTCGGCC	AAAGAGGCCT	AGATGTGAGC	TGGGGAAGGG	AGGGTGGCCA	GTAATGGGTT	60
TGTTATCAAG	CAGGTTTGTT	ATCACTGTGG	GTGACAAGCC	CCTTCCCATT	TGGGGCCTCT	120
GGGATCCAGT	GCAGAACATA	TCCCTCGCAG	GAGATGAGGA	ACTGGGGTGT	TCACAGAGTA	180
ATTCCCTCCC	TCACTAGTTG	AGGGCTGCCT	CTGGGGGTGG	CTGAACTACC	TCATGCAGCC	240
AGAGAAAGTC	CTCAGGCAAT	GAAATACAGA	CACTGGCCAG	CCAGCACTGA	GGTGGCGAGA	300
CCTTACTGGC	TGGTCCCCAG	AGTGTCTGCA	GCATTGTGTG	AGATCTTAAA	CTGGCTAGAA	360
GGACGGTAAC	AGCAGCACCT	GTTTCATAGG	ACGTGAAGAT	AGACGAGACA	G	411

- (2) INFORMATION FOR SEQ ID NO:826:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GAATTCGGCC	AAAGAGGCCT	ACTAAAACCA	TAATTGCTTG	TTTTTGCCTG	TATCTGTCTT	60
TTCACGAACA	TTTTGAGTTT	AGCTCTGTCT	TACATTCCCA	TCCCTAAAGA	TCATCAGGAC	120
TTTTGTTTTC	GTGACAATGC	TGGGACCAGA	TTGGCCTTCA	TCATCTCATA	ACACCCTTAT	180
TTCCTATGGA	AAAGTAAAAT	TGAATTATTC	CAGATATGAT	GACTTTAGGA	TATCCTTTTC	240
CCTCTTGTAC	ATCCTTCATT	GTATTTGTGT	TTTCCCTTTG	GTCTCCAACG	TCCCCACCAC	300
CCCCAATCCC	TCCACGACTT	TTAAGCCCTT	GGAAGCCAAC	TTGATTAGTC	AGG	353

- (2) INFORMATION FOR SEQ ID NO:827:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

GAATTCGGCC	AAAGAGGCCT	ACCGTGAGTT	CCCAGGGTGG	CCGGGAGGGG	GAGCTGCGGG	60
GTTCACAGCG	GCTCCTCTCA	ACGTTCCTGG	CTCCGCTCCC	GACTTCTCAG	CCCTGCCTGG	120
AGGGGCTCAG	CCACTGCTTT	TAGCTGTCTG	CTGGCTTTCC	ACCCTTCCAG	CCTGAACCCT	180
GACTTCCCCA	TGAGGCCTTC	CTGTGGCGGG	GACACTCCAG	GTCGCTGCAC	CCCTTCTCTC	240
CTGAATTTCT	GTAACGACAT	CTAACTTTTA	TTTAATTAAT	TTATTTATTT	AGAGATGGAG	300
TTTCTCTCTT	GTTGCCCCGG	CTGGAGTGCA	ATGGCACCAT	CTTGGCTCAC	TGCAACCTCC	360
GCCTCCCAGG	TTCAAGTGAT	TCTCCTGCCT	CGGTCTCCTG	AGTGGCTGGG	ATTGCAGGCA	420
CCCATCTG						428

- (2) INFORMATION FOR SEQ ID NO:828:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

GAATTCGGCC	AAAGAGGCCT	AAGCGGTATT	TCAGCCACAG	AGTTGGTGTT	GGGTTTACTT	60
					TGGGAAATGC	120
TGTACCAAAA	AATGTTATCT	TGCT				144

- (2) INFORMATION FOR SEQ ID NO:829:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GAATTCGGCC AAAGAGGCCT AGCGGACTAG GAGTCAATAA AGTGATTGGC TTAGTGGGCG AAATGTTATG CTTTGTTT TGGATATATC TGGAG	60 95
(2) INFORMATION FOR SEQ ID NO:830:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 610 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:	
GAATTCGGCC AAAGAGGCCT AGTGGCTACC TAAATTGAGT ATCTGGCAAG AGTAAGATTA AGCAGTAATT TGTTCCAAAG AAGAATCTTC TACCAAGGAG CAACTTTAAA GAATGAAATT AACTTTCTTC TTGGGCCTGT TGGCTCTTAT TTCATGTTTC ACACCCAGTG AGAGTCAAAG ATTCTCCAGA AGACCATATC TACCTGGCCA GCTGCACCA CCTCCACTCT ACAGGCCAAG ATGGGTTCCA CCAAGTCCCC CACCTCCCTA TGACTCAAGA CTTAATTCAC CACTTTCTCT TCCCTTTGTC CCAGGGCGAG TTCCACCATC TTCTTTCTCT CGATTTAGCC AAGCAGTCAT TCTATCTCAA CTCTTTCCAT TGGAATCTAT TAGACAACCT CGACTCTTTC CGGGTTATCC AAACCTACAT TTCCCACTAA GACCTTACTA TGTAGGACCT ATTAGGATAT TAAAACCCCC ATTTCCTCCT ATTCCTTTTT TTCTTGCTAT TTACCTTCCT ATCTCTAACC CTGAGCCCCA AATAAACATC ACCACCAGG ATACAACAAT CACCACAAAT CCCCCCACCA CTGCAACAGC (2) INFORMATION FOR SEO ID NO:831:	60 120 180 240 300 360 420 480 540 600
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 564 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:	
GAATTCGGCC AAAGAGGCCT AGGAAGAAC AAGAACAAGA AAAAAGATTA TATTGATTTT AAAATCATGC AAAAACTGCA ACTCTGTGTT TATATTTACC TGTTTATGCT GATTGTTGCT GGTCCAGTGG ATCTAAATGA GAACAGTGAG CAAAAAGAAA ATGTGGAAAA AGAGGGGCTG TGTAATGCAT GTACTTGGAG ACAAAACACT AAATCTTCAA GAATAGAAGC CATTAAGATA CAAATCCTCA GTAAACTTCG TCTGGAAACA GCTCCTAACA TCAGCAAAGA TGTTATAAGA CAACTTTTAC CCAAAGCTCC TCCACTCCGG GAACTGATTG ATCAGTATGA TGTCCAGAGG GATGACAGCA GCGATGGCTC TTTGGAAGAT GACGATTATC ACGCTACAAC GGAAACAATC ATTACCATGC CTACAGAGTC TGATTTTCTA ATGCAAGTGG ATGGAAAACC CAAATGTTGC TTCTTTAAAT TTAGCTCTAA AATACAATAC AATAAAGTAG TAAAGGCCCA ACTATGGATA TATTTGAGAC CCGCCGAGCT CGAG	60 120 180 240 300 360 420 480 540
(2) INFORMATION FOR SEQ ID NO:832:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 424 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

GAATTCGGCC AAAGAGGCCT	ANTCTGTTGA	GATTTCCCCC	TTTAGTTTCC	AACCTTCTCC	60
CCACCTACTC ATTTATCCAT	CCCTCCCACC	AACTCATTTA	TCCATCCCAC	CCACTCATTT	120
ATCCATCCAT CCCACCCACT	CATTTATCTG	TCCATCCCAT	CCACTCATTT	ATCCATCTAT	180
CCCACCCACT CATTTATCTG	TCCAACCCAT	CCACTCACCC	ACCTACTCAT	TTATCCATCC	240
CATTCGCTTA CCCATCCATC	TATCCCACCT	AACAATACAT	CCAACCATTC	CCTCACCTAT	300
GCATCTGTCT GTTCAGCTGT	TCATCCATTC	ATTGATCTTT	CCATCCATTC	ATCCACTCAT	360
TCACACACCT ACCTACCTAC	CCACCCGCTC	ATTTATTCAC	CCACCTACCC	TCTCATCCAT	420
CCAG					424

(2) INFORMATION FOR SEQ ID NO:833:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

GAATTCGCCA	AAGAGGNCTA	GTCTACATCA	GCTAACTTTC	CTACAAGATT	ATCAAATTTT	60
ACACAGTATT	TTTCTGTATT	TAATGACTGC	CATGGTCTGC	AAAATTATGT	GATTAGACAA	120
TGAATGACGC	TTAAAGAATG	ATGACCTATT	TTCTAAAGTA	CACTCAAAAT	ATTAAACTTT	180
AGAGACAAAG	CAAAATCTAT	CATAAAGTTG	GCTTCTGTTG	ATAGAAACAG	AGAGGTAGGT	240
TAATAATCAC	TGTCCTAAGA	TAAGCNAGAA	TGCTTAGAAA	TAAAAGTTGA	GACCCTGCTT	300
CAAAAAAGAG	AAGTTGAACC	TTCCAGCCCT	GAGTTTCTAA	TATTACATGA	AAATTATGAA	360
AATGAGCATT	AAGCCAGTCG	CAG				383

(2) INFORMATION FOR SEQ ID NO:834:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

GAATTCGGCC	AAAGAGGCCT	ACTACGTAGT	TGGAGCTNTT	TCTTCCCCCA	GCAAAGCCAG	60
AGAGCTTTGT	CCCCGGCCTC	CTGGACACAT	AGGCCATTAT	CCTGTATTCC	TTTGGCTTGG	120
CATCTTTTAG	CTCAGGAAGG	TAGAAGAGAT	CTGTGCCCAT	GGGTCTCCTT	GCTTCAATCC	180
CTTCTTGTTT	CAGTGACATA	TGTATTGTTT	ATCTGGGTTA	GGGATGGGGG	ACAGATAATA	240
GAACGAGCAA	AGTAACCTAT	ACAGGCCAGC	ATGGAACAGC	ATCTCCCCTG	GGCTTGCTCC	300
TGGCTTGTGA	CGCTATAAGA	CAGAGCAGGC	CACATGTGGC	CATCTGCTCC	CCATTCTTGA	360
AAGCTGCTGG	GGCCTCCTTG	CAGGCTTCTG	GATCTCTGGT	CAGAGTGAAC	TCTTGCTTCC	420
TGTATTCAGG	CAGCTCAGAG	CAGAAAGTAA	GGGGCTTACT	CGAG		464

(2) INFORMATION FOR SEQ ID NO:835:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GAATTCGGCC	AAAGAGGCCT	ACTGGGAGTT	CGGAGTGATT	GTTTCCTGTT	ACAGGCCAAA	60
AAATTTGTTT	GGTTACTTAG	TGGTAGCATT	TTGAGAGGAA	AGTTTACAGA	AAACTAGGGT	120
TATTTTGTGA	TTATGCTTGA	ATTGTCTTTA	TTGTTTCCAA	${\tt GGCATCTTTT}$	TTTTTTCCTT	180
CTAGTTATCA	AGATGTTAGG	TTCTGTGCCC	TTGTGGGCCT	TCCCTCTGCC	CAAAAAAAGC	240
ATGGATGAGC	AGAGTAATAT	CATTAAAATG	GCAGTCTTTG	TTAGTTTTTC	TAGAAAAGAT	300
GGTCTCGAG						309

- (2) INFORMATION FOR SEQ ID NO:836:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

GAATTCGGCC	AAAGAGGCCT	AAGGCAGGTT	TTTTTTTCTA	TGCTTATTGA	TTTAGCCTAT	60
CTATTTATAA	CAGTATAATT	CAGAATATAA	ATATGGAACA	AGTTTCATAA	GGAAGTTTAT	120
CTTTAACTCA	GACATTATAT	CATTAATACT	TCAAATCTCA	TTATACCATT	ATGACCTGAA	180
TGCTACATTT	TTCTTCCTGT	ATGGAGAGCT	TAGGGAAAAA	TTGTGGCCTG	ATGTCTTCAT	240
CCATTCACTT	ATCATAGAGT	ACATAATGAT	CTCAAATATC	CAAAAATGGT	TATATTCAGC	300
TGCATATTTC	TAAGAAAACA	GGCAGGACTC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:837:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 706 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

GAATTCGGCC	AAAGAGGCCT	AATTGATTTC	CCATGAGTCT	TGTAATCTTT	GCTCTGCTGA	60
TTGCGTTTGC	CGTCTCTAGA	CCATCTCGCT	TCGAACAAAT	CGCAAAAGAG	GTGAATTCCA	120
GAAGAACGAC	CTGGATTGCA	GAAGAATCGG	CTCCGTTCCG	TGACTATGCT	CGTTTGATCG	180
GTACCCTTCC	AAATACGGTC	CCTCTTCCGA	GTAAGACTGT	CGATGTCGTG	AAGAACCTTC	240
CTGAGAGTTT	TAACGCATTG	GAAAAGTGGC	CGGAATGCAA	GTCCATCACG	GAAATCCGTG	300
ATCAAGGAGA	ATGTGCTTCA	TGTTGGGCAC	TGGGGAGTGG	CGGAGGTGGC	CACGGATCGT	360
CTTTGCATTT	CTTCCAACGG	AAAGGATCAA	TCCCGTCTCT	CTGCCGAGGA	TCTGTTGGGA	420
TGCTGTGACT	CTTGTGGAAT	GAAATGCAAG	GGAGGGTACA	CGGGGAATGG	CCTGGGAGTA	480
TGTACGTCAG	GTGGGAATTG	TGACGGGTGG	AGCGAATGGA	AACAAGGAAT	GGTGTAATGA	540
GTACGCGTTC	CCGAAGTGCA	GTCACGGTAT	TCAGGGCTCC	TATCCTGAAT	GCTCTTCCAT	600
CCCCCTGAA	GATCCGGAGT	GTTCAACGAC	TTGCATAAAG	GGGTATCCCA	TCCCATATGA	660
TCAGGACCGT	CACAAAATGA	AGTCAGCCTT	CCAGCTGGCA	CTCGAG		706

- (2) INFORMATION FOR SEQ ID NO:838:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GAATTCGGCC	AAAGAGGCCT	ATAAAAGTCT	TATTTTTTAC	TTTGTCCACT	GGAATACATC	60
ATCGTTGGCC	TATCATTCCA	AACTCCCTAC	AGTGTGGCTT	CAGCTTATCT	CTCTCTGTTT	120
TTTACAGGAA	TCCTAAACTC	TAACCCAGGG	ACCCTCAACA	TCTGTGCTGG	GTGGACTGTG	180
GCCACATTTT	CAGCTGGCCA	${\tt GTGTAAGGGT}$	TTTAGAGGCC	CTTACATGAG	AAGAAATACA	240
ATTTTTAAGT	CTCTGAGATG	ATGTGCTTCT	TACATTTTTG	GAATTAAAAT	GCCTCTTTAC	300
TTATAAAATG	CTGGTAGTAA	TAGATGGTCA	TTATCTCACT	GTCATTTGTG	AAAGAAAAA	360
CGATTGTAAT	${\bf AGAATTCTTG}$	CTATTTTTT	TCTCTAAGGG	AGGTAAGTTT	TCTCCCTAAG	420
CAAACTTTAT	GGAATGCACA	ATGCTTGGCT	TTCACCTTCT	TTTATTCTCA	CTACCACCGG	480

- (2) INFORMATION FOR SEQ ID NO:839:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 589 base pairs
 - (B) TYPE: nucleic acid ·
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

GAATTCGGCC AAAGAGGCCT AGAATTAAGG TGTATTATGA GCAGTTGAAG ATATATAGGA	60
AATTITTTCC CAAACCACTA TCTCTGCTCG TTCTATTCAT TCAGTCTGTT TATGTTATTC 12	20
CTTCATTCAT TCATTTTATA GAACAGTGGA GTGCCTACTG TATGCATCTA TTGTTCTGGG 10	80
TCCTGGGGAA AGAAAACAAA GTTCCTGCTT TCATGGAACT TACATTATAT TGGCGGAGAC 24	40
AGTAACAGAC AAACAAATGT AGCCTGTGTA CATGTGTTAC ATGAAAAGCA GGGTAGGGGG 3	00
CTGGGAGAGA GTAGTAGGGA GTGCTATTTT CGAGGTGGTT GTCAGGAAAG GCCTCACTGA	60
GGAGGTGGCA TTTTGAGTAG ACCTGAGCGC AGCGGGGGCG TAAGCCCAGG CAGCATGTGG 4	20
AGGAAGAGTG TTCTTGGTGA AAGGAACAAG GATAGAGGCC CGAAGCTAGA GAGCTCAGCA 4	80
TGATCAAGGA ACAGCAAGCC CCGTGTGGCT GGAATGGAGT GAGCAAAGGA ATGAGCAGTA 5	40
GAAGGTGAGT GAGTTGGGAG GTCACCAGAG ACCATGGCAA AGACTCGAG 5	89

- (2) INFORMATION FOR SEQ ID NO:840:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

GAATTCGGCC	AAAGAGGCCT	AGGGACTAAC	TGCAACGGAG	AGACTCAAGA	TGATTCCCTT	60
TTTACCCATG	TTTTCTCTAC	TATTGCTGCT	TATTGTTAAC	CCTATAAACG	CCAACAATCA	120
TTATGACAAG	ATCTTGGCTC	ATAGTCGTAT	CAGGGGTCGG	GACCAAGGCC	CAAATGTCTG	180
TGCCCTTCAA	CAGATTTTGG	GCACCAAAAA	GAAATACTTC	AGCACTTGTA	AGAACTGGTA	240
TAAAAAGTCC	ATCTGTGGAC	AGAAAACGAC	TGTGTTATAT	GAATGTTGCC	CTGGTTATAT	300
GAGAATGGAA	GGAATGAAAG	GCTGCCCAGC	AGTTTTGCCC	ATTGACCATG	TTTATGGCAC	360
TCTGGGCATC	GTGGGAGCCA	CCACAACGCA	GCGCTATTCT	GACGCCTCAA	AACTGAGGGA	420

430

GGAGATCGAG

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:	
GAATTTTTAC TTGTCTATAG TCTAGTATTG TTATACCATG TGGTCTTGTT ATAATCATGG	60 101
(2) INFORMATION FOR SEQ ID NO:842:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 479 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:	
GAATTCGGCC AAAGAGGCCT AAATGGCGTC GTGGCATTGA GGGGCATCCC TCCTAGAACC TCCAGGAAAA GCTCGCGGAA GACGAGGTTC TGCGGAGAGA GAGGCTCCAA GCAGTCTGGG AAGTGTAGTC CAGTTGGCTT AGCAGTAGTT TCGTTGGGGG GGAGCCGAGG TTCCGGGAAG GGGCTAGGCC GGCTTGAAAA GAGATTATGA CTGTACCTTT TAACTTTGTA GCTGGAACAC AAGAAGTGTT TGTTTAATGA ATGACGTACA CATTTAAGAT CTGTTTGGAC GCGGAGGATA ATCCTGTGAA TTGCTAATAG TTCACTGGGT TTGGCCCTTA GTGTTGACTT CAGTATGCTG AGACGGAAAC CAACACGCCT AGAGCTAAAG CTTGATGACA TTGAAGAGTT TGAGAACATT CGAAAGGACC TGGAGACCCG TAAGAAACAG AAGGAAGATG TGGAAGTTGT AGGAGGCAG (2) INFORMATION FOR SEQ ID NO:843: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 270 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	60 120 180 240 300 420 479
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:	
TGGAAGAGCT AACTCGTCTG GCCTTTGAGC TCTTTGCTGA AGAGCAAGCA GAGGGTCCCA ACCGCCTGCT GTACAAAGAC GGCTTCAGCA CCATCCTGCA CCTGCTGCTG GGTTCACCCC ACCCTGCTGC CACAGCTTTG CATGCTGAGC TGTGCCAGGC AGGATCCAGC CAAGGCCTCT CCCTCTGTCA GTTCCAGAAC TTCTCCCTCC ATGACCCACT CTATGGGAAA CTCTTCAGCA CCTACCTGCG CCCCCCACAC GCATCTCGAG (2) INFORMATION FOR SEQ ID NO:844:	60 120 180 240 270
(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 413 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:	
GAATTCGGCC TTCATGGCCT ACACAGCCAG TATCAGAACC TCAAGAAAAC GAGGACACTG GGGACAGGGA CCAAAATTCA GACCACTTTT TTCTCTTGCC TTTCAATAGG ATATTCTGTT AATTGAATTC ATCTGAAAAT CAAGGTCATT GCAGAGAAGT CAGCATTCTA GAGCACAGAA CAGGGCAAAA CAGGACGAAA GATGGATTTG GAGACCAAAAT GGAGAAGGAA GAACAGAGAT ACGTGTGCTC CAAATATGAC ACCCAACTTC TTTACTCAGA GCAGTTACAT GTCAGATTAT ATTTTAGTTT TTCATTTCTC CTATAGGCAT ACATACTACA AGTCTATAAT AGAAAACTAG GGGCTGGGCG CGGTGGCTCA CGCCTTTAAT CCCAGCACTT TATGGCGCTC GAG (2) INFORMATION FOR SEQ ID NO:845:	60 120 180 240 300 360 413
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 126 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:	
GAATTCGGCC TTCATGGCCT AGGCTCTGTC TACCAAAAAA AAAAAAAAAA	60 120 126
(2) INFORMATION FOR SEQ ID NO:846:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 269 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:	
GCTTCATGGC CTAGTTGAAT AGTCAGTTAG AAATGGAAAG AATGAAAGTT GAACAAGAAA GACAAAGACCT TAGAACAAAA GACACAGCCC TAGAACAGAA GGACAAGGCC CTGGAACCAA AAGACAAAGA CTTAGAAGAA AAAGACAAGG CCCTGGAACA GAAGGATAAG ATTCCAGAAG AGAAAAAGAC AAAAAGGGCA GAACATTAGA GCAAAAAAGAC ACAGCCCTAG AACAGAAGGA CAAGGCCCTA GAACTCGAG	60 120 180 240 269
(2) INFORMATION FOR SEQ ID NO:847:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 264 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GCGATTGAAT	TCTAGACCCA	CCTTCAGACC	ATCTCGGAAG	ATCTAAAAAG	CCTGACCATG	60
GACCCTCACA	AACTGCCCTC	CTCAAGTGAA	CAGGTGATTC	TGGACTTGAA	AGGTTCTGAT	120
TACAGCTGGT	${\tt CGTATCAGAC}$	GCCACCCTCT	TCCCCCAGCA	CCACCATGTC	CAGAAAGTCC	180
AGTGTCTGCA	GCAGCCTGAA	CAGTGTCAAC	AGCAGTGACT	CCCGGTCCAG	CGGCTCCCAC	240
TCGCATTCCC	CCAGCATTCT	CGAG				264

- (2) INFORMATION FOR SEQ ID NO:848:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

GAATTCGGCC	TTCATGGCCT	AGAACATTCC	AAATTTTCTT	GGTTTCAATA	CCCTTTTTTT	60
TCTTTTGAGG	GGAAAAGAGG	GGAGAAAAAC	AGGAGTGATG	TCATTTCTTT	TTCATGTATT	120
CCAATTAAAG	AAACAAGGGC	AGGTCGTATA	ATGGCATATT	AATACATTAG	ACTTAATCTA	180
GAACCCCTGT	${\bf AGCTTTTTGA}$	TGTGTTTTAT	TTCTTATCTC	TTTGAATTCC	TGTTTGGTTA	240
CTTGGCTTCC	AATGGAGGTG	AACTTAACAA	CCATACTTGA	ATATTCCGTC	TTGACTTTGT	300
AAACTGTGGC	TACTTGAAAT	GAAGTTTATC	TGGGGTCTCG	AG		342

- (2) INFORMATION FOR SEQ ID NO:849:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

GAATTCGCCT	TCATGGCCTA	GGTTATTCTA	TTATTTGTAG	CTGAAATAAT	TCCTGGCACA	60
AATGACTTTG	AAATTTATCT	CTGAACATCC	CAAATTCATT	ATTAGCAAAT	ATCAGAAACT	120
TCACATCACT	CCAGTCTGTT	ATTTCACATG	${\tt GTTTTCTTAG}$	GGCCTGGAAA	GTTTTTACAG	180
CTGGCTTTTA	TTGACTGTGG	TGGCTGATAT	GCTGAAGAAT	GGAGCTCATT	GGTTTGAGGC	240
TTCTGCCAG						249

- (2) INFORMATION FOR SEQ ID NO:850:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

GAATTCGCCC	TTCATGGCCT	AGACATGAAT	TCTTTGACTT	GTGCTCATTC	TTTCTGAACT	60
TATTGAGGCT	TATATATATC	AAATAAGGTT	AATTTACACA	TTTATTAATA	TTAATAATTA	120
ATAAACTCAT	TCATGTAGTA	TATTTTAAAA	CATTATTTCC	TCTCATTTTT	CCTTCTCTTT	180
TTTCTTCCTA	TATATTTTA	AGGTTTCAAG	AGAAAACGGG	CTTCAGTTTT	TAAAAAAATG	240
TAGACTTGCA	TTTTTACTGT	GCTTATTTAA	AATAATGGAT	ATAATTTAATA	TTAAGGTCCA	300
ATTTTTAA	TTCACAGGAT	AATCATGGTC	TCTGATAAAA	GATGCCCACA	TTTCTGTGTA	360
$\mathtt{CTCACAGTTG}$	TTGTATATTT	TTCAATTTCA	ATTTTGAAAG	TAAACTCAAC	ACTCGAG	417

- (2) INFORMATION FOR SEQ ID NO:851:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

GAATTCGGCC	TTCATGGCCT	AGCTAGCTAT	TGTAAATACA	AATAATAAAG	TCTGCATTTC	60
CTGTCTTCTT	TAAGCCTTCA	TTGCCTATTA	AATCATTACA	TTTTAGATTA	GATATTATAT	120
TTTGATCATT	TGAGGAACCA	AATTAAAAAT	ATGGAATAAG	TATGGCATTG	AATTATACAT	180
GCCTATTGCT	AATATATTCA	TATTTTATAG	GATTTAATGA	AACAGTCTCC	CAGCTCGAG	239

- (2) INFORMATION FOR SEQ ID NO:852:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

GAATTCGGCC	TTCCCTAGGA	AAGTTCTTCA	CATCAGGAAA	CATTAGATCA	TATACAGAAA	60
CAAACTAAAT	TTGATAAAGT	AGTTATGGAG	TTTTTGCATG	AGTGTATGGT	GAATAAATTC	120
AAGAAAACAT	CTATTCGTAA	GCAACAGACA	AATAATCAAA	CAGAAGTAGT	TAAAATAATT	180
GAAAAAGATG	TTATGGAAGG	TGTTACTGTA	GATGATCACA	TGATGAAGGT	AGAGACAGTT	240
CATTGCAGCG	CTTGCAGTGT	GTATATCCCT	GCTTTACATA	GTTCAGTTCA	GCAGCACTTA	300
AAATCTCCTG	ATCATATCAA	AGGGAAGCAG	GCTTATAAGG	AACAAATAAA	AAGAGAGAGT	360
GTCTTGACTG	CTACAAGCAT	TTAAATAAT	CCAATAGTGA	AGGCGCGATA	TGAACGTTTT	420
GTTAAGGGTG	AGAATCCTTT	TGAAATTCAA	GACCATTCTC	AGGATCAGCA	AATAAAAGGC	480
AGACTCGAG						489

- (2) INFORMATION FOR SEQ ID NO:853:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

GAATTCGGCC TTCATGGCCT ACTTCACTAA CCTTTTTTGT TTTAAAATGA ACCTGCTACT TAAAAAAAAAT ACACATCACA CCCATTTAAA AGTGATCTTG AGAACCTTTT CAAACCAGAT GGAGCATTGC TTGCAAATTT TTTTTCTCTA TGTTTGCATG CGCTCGTGTG TGTGTGTCCA GGCAAGAACA CATTTTATAA AAATAAGAAC ACTTGGGCTG GGCATGGTGG CTCATGCCTG TGATCGCAGC TCTCTCGAG	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:854:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 217 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:	
GAATTCGGCC TTCATGGCCT ACACAGCTGC AGTCAACATC CACAACTACC GGGACCACAG CCCCTACTGC TGGCTGGTGT GGCGTCCAAG CCTTGGCGCC TTCTACATCC CTGTGGCTTT GATTCTGCTC ATCACCTGGA TCTATTTCCT GTCGCCGGGC TACGCTTACG GGGTCCTCTG GCACAGAACC CCAAGGCGGG CAACAGCAGG GCTCGAG	60 120 180 217
(2) INFORMATION FOR SEQ ID NO:855:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 246 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:	
GAATTCGGCC TTCATGGCCT AGACCTGCCT CGAAAATAAA TAAATAACCC ACAGAGCTGA GCACAGGCTT CTTCATGCTT TTCCTTTGGA AGGTGTCCTA GATATATGAT GATTTCTTTT TTCTTTCACC TCCTCTTGAT TGTCACAAGT AGCTTGCTTG GCTCAGGAAC AACAGAAGAG AATAAAGAAA ATGACCTCAG ACCTTCCTTA CCTCAGTCTT ATGCAGCGAC CGCAGCCAGA CTCGAG	60 120 180 240 246
(2) INFORMATION FOR SEQ ID NO:856:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 334 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:	
GAATTCGGCC TTCATGGCCT ACTGTCTCAA AAAACAAACA AACAAAAGA AAGAAAGAAA AAGGAAAGGT AGACTTATAT AAAATAGACA GTAAAGCATA GGGCAGCAGA AAGGAAAACC TACTCCGCAA AAGTCACTTG TTTTAACCTC ATCCAGGAGC TTCCTCTAAG TTCACCTTTTA TTTTTCACAC GTCCTGGGTC CAAATCCCAC CATGCTCTGC CGTATTCTTG CCCTTTGCTC TGTTGTTGAA AGAGTCATGA GCGAGGCCTC TCTATGGATG GTTCCAATGA GCCACATGAA CAAAGCCATC GTCAGTAAGC AGCCACTTCT CGAC	60 120 180 240 300

(2) INFORMATION FOR SEQ ID NO:857:

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 129 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:	•
TCCCACCCTC TTTTCCAAGC TGTTTCGCTT TGCAATATAT TACTGGTAAT GAGTTGCAGG	60 120 129
(2) INFORMATION FOR SEQ ID NO:858:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:	
GAATTCAAGC ACCATAATTT GGCCACTCAG CTGTCATCAG GAACTAAGCC AACATTCCTT TTCAGAAAAA GACTTTGGAG AGGGGCAAAC ACTTCTGACA GTCATACTGT GTACTTATTT TAGAAAATAA GCTGCTCTCA GGCTTCAGTA TCCAGTCAAA TATAATATAG AACTCTAGTC TGTTTTGAGT CCTACTACAA TAATATTTTC ACAATAGACT ACCAGTTATG AAGTTCTCAC ATTTTTCCCG CATGCTCGAG	60 120 180 240 260
(2) INFORMATION FOR SEQ ID NO:859:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 217 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:	
GAATTCCTGT CCCACCTGCT GAATGAGTGC GTGCCAGCTG AACATCAGCG TGGCTTCGTT CTTCAACACA TTTACAAAAG AAGTAAAAAT AAACAGTTTT TTCTTCTCAA TTCTCCTCC TGCTTTTTTC CTTTGGAACC ACAATCATGC CCCAGTAAGT GCTTTCCTAG GTGAGAGGTG TGTGTCCCAG GTTGAAGGCA AGGCCAGTGG TCTCGAG	60 120 180 217
(2) INFORMATION FOR SEQ ID NO:860:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 107 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

(ii) MOLECULE TYPE: cDNA

GAATTCGGCC TTCATGGCCT AGAATATTTT TATCATCCCA AAGCTAAAAC ATTAAAAAAT TTAAAGTTTA TTCTTAGAGA TTGATGCAAC TTGCATATCT AATCGAG	60 107
(2) INFORMATION FOR SEQ ID NO:861;	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 279 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:	
GAATTCTAGA CCTGCCTCGA GGGCATCCTT TACTTTTTT TTTAATTCAG CACAAACCAA ACAAAATTTT AAAATTTGAT GAGATTTGAA GTTGGACAAA AGTGTTATGC AGTTTTAAAA ATTTTTTTTT TTTTTTTTGA GACCAGATCT CACTCTGTTG CCCAGGCTAG AGTGCAGTGG CATGATCTCA GCCCAAACCT CTACCTCTTA GGCTCAAGCG ATCCTCCCAT TTCAGCCTCC CAGGTAGCTG GGAGGCTGAA ATGGGAGGAT CAACTCGAG	60 120 180 240 279
(2) INFORMATION FOR SEQ ID NO:862:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 266 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:	
TGTATTTTA CGTGACCTGT TTTCCAGAAT TTATGATATT TCTATGGTTG GTATTCTCAA TTTTGCAAAT GTGTCTTGGT GTGGAACTTT TTCATTTGTT TTGCTGGGGA ATTGATGGAT CCTTTGCATC AAGATGCTTA TATTTATTCT TCAGTTCTGG GAAACTTCCC TGTATTATTT GTTTGATAAT TGCTTTCTCT CTGCTTTCTC TTTTCCGTTT TTTGGAATTG CTTGTTTGTG TGTTGCATTA CTGCAGAGAA CTCGAG	60 120 180 240 266
(2) INFORMATION FOR SEQ ID NO:863:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 355 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:	
GAATTCGGCC TTCATGGCCT AGTGCTGTGG TAGTTTGTGC CTTTAGAGGG ATTTGTGTAT CTCATATAAT TTAATTTTTT GACATTCACT TTTTCACAAT ATTCTGTTAG AATTCTTTTA ATTTCTGTAA GGTGATATCT ATACTTTCAT TTATGTCTAG TAACTTGAAT CTTCTCTCTT	6: 12: 18
367	

CTTTCAAGTT	TCGGTCAAAC TAATAATACG TCAATTTTAC TGATATATCA GAAGAACCAA TATTAATTTT CTCTATTGTT TTTATTTTCA CTACTTATCT CCATGCTAAT TCTTCCTTCT GTTTACTTTG GGTTAAGTCT GCTCTTTCAC TCGAG	240 300 355
(2) INFORMA	TION FOR SEQ ID NO:864:	
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 205 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:864:	
AGTTTTTTT TGCCTTTAAG	TTCATGGCCT AGCTTACTTT ACAATTCTGC TGTTTGTCAA GTGTTCCTAT AAAGGTATGT TAACTATTTT TCCCTTTTGG TTTATATTTG TAGGAATCTT TGTGCCCGTG CAGAAGAATT ATTTAACATG TTGCAAGAGA TTATGCAAAA AATGTGGAGC TCGAG	60 120 180 205
(2) INFORMA	ATION FOR SEQ ID NO:865:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 368 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:865:	
CTTTTTGTTT AGTTAGCTTA CATATTAGGA GGTTCAGAGA	TTCATGGCCT AGTCACTTGT TCTGTAGAAT ATGTTCAAAT CTGATTTTGT TCTTGTGTTA TTACCTTGTT CCTCTATCCC CTGTTTTTTC TGAAAATGAA GAAGTTTCAT TCCATTCTGG TTCAAAATGC TTAAGTGCTT TATGTCGTGT AACACAGTAT CTAGTGGTCC CAATTTTAGT GATTCAAAAA TCAGTCTCTA TTAATCAGTA GATTCAGAGA TCTCTCCATT GTAAATTTCT TAATTAACCT AATGTTCTGT TCACTGATCG TTGTGGCCCA AATTATTTAT TTCACTAGGG	60 120 180 240 300 360 368
(2) INFORM	ATION FOR SEQ ID NO:866:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 144 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NC:866:	
CTTATAATGG	TTCATGGCCT AAGGAGCAGC AGGAACATGG TACATAAAAT CATCCTGCTT CAGGAATCAG TGGGATATGG TATTTGTGCA GCATGCTGGG GCATCCACTA AAGGAAGACT CGAG	60 120 144
(2) INFORM	ATION FOR SEQ ID NO:867:	

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 268 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:	
GAATTCGGCC TTCATGCGAT TGAATTCTAG ACCTGCCTTG AGCCCCTCCA CCCCCAAATC CTTCCTCTCC TCCCAGTCCC ACCCCTTGCC CCACGGAGTC CTGGGGACGC AGTGCCCCAG CTGGGAAGAG GGCGGGATCG GGCACTGGTT CCTCCTTGTC CCCGCTTTCT TGGGGGCTTG CTACTTTTTG TCTTCTATTG TGTGGCTTTC TGAGTATTTG AACCCCAGTC CTGTGTCACC ITCCTTTTTC CTTCGCTGTC CCCTCGAG	60 120 180 240 268
(2) INFORMATION FOR SEQ ID NO:868:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 384 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:	
GAATTCGGCC TTCATGGCCT ACAGAACTAT AATTTATCTT AGTTTAAGCC ACTGGTAAGT GTAATTGTAA TTGTAATTTG TTACATCTGC TATAGTGAAA CTAATACTGA AATTTAGAAA AGATGGGTAA CTTATTATGT GGTGAAGTTT AAAAAAGATA AGTAACTCGT TGAAGATCAC ATAATTAGAA AAGAAAGCAG TAGAGCTTGG CCTTGAACTC AACCAGTGTG ACTCCAGAGC TTGTAGAACA GAATAACCAC CTCCAAGGCC AGCTGAATCT GACCACAGTC TGGTGGAATT CTAGTACATC TCGTTGAGAA GTGGGATTGC CGGAGGGGAG TTGGTTATTC ATGAAGGTGA TGATGTTTGT CCAATGTCCT CGAG	60 120 180 240 300 360 384
(2) INFORMATION FOR SEQ ID NO:869:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:	
GAATTCGGCC TCATGGCCTA CTTGGAGAGT TTTGTAAGGA GAGTGGCAAA CATAGCACGG ACTAATGCCA CGAACAACAT GAATCTAAGC CGAAGCAGCA GTGATAACAA CACTAATACT TTGGGGAGGA ATGTGATGAG CACAGCAACT TCTCCTCTTA TGGGTGCTCA GAGTTTCCCT AATTTGACCA CACCTGGTAC TACATCAACA GTGACTATGT CAACATCCAG TGTTACTAGC AGCAGCAATG TAGCTACAGC AACAACACTC GAG	60 120 180 240 271
(2) INFORMATION FOR SEQ ID NO:870:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 278 base pairs (B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

GAATTCGGCC TTCATGGCCT	AGGTCAGGAG	CCTTCTTGGA	GTCCCAATTC	TGCATCCCCA	60
AATGATAAAG ATGGGGTGAA	GGAACTGAGA	GCCATGAGTT	GGAGAGTCCT	CTTGCTTGAG	120
GTCCCTGAGA ATGTGGTCCC	GGAGTATCCG	GATCACTGGA	AGCCAGGACT	TCAACGCATT	180
GGGTAGTGAG GGATGGAGGG	AGGGGCTGGA	CGCAGAAGCA	GGATGAAGTC	TGCTGGGTGT	240
GAGCCTCCAA GGAGGTAGAA	CAAAGAGGGC	AACTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:871:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

GAATTCGGCC	TTCATGGCCT	ACCAGACTCC	CATAATAATA	AACCCTGGTA	ATAAACAAAG	60
GAACTCCTTC	CAGTTTCAGT	GTATCAACCA	CCACGTACCA	GATAAAATCT	TATTTCACCT	120
TTCACAATTT	ACCAGTGTTG	GGCTGTGAAT	TAATATTTT	ATTTTTCTGT	GCATTCATAA	180
ATTAAGATTA	TTTTATTGTA	TTGTAACTGT	AATTTTGAGA	CTAAAGTCTA	AAAACAAGAC	240
ATCATGAAAT	GGAGCTGGAG	GATACTCGAG				270

- (2) INFORMATION FOR SEQ ID NO:872:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

GGTTTAGAAA	GGGCACAAAC	AGTGCAAACC	TGTTCATGAA	CCTTTACATG	TCATGAACAG	60
GGCAGAATGC	TTCAGGAAAG	AATTGTCGAA	AGTAAAAAAG	CAAATAATGG	ATGCAGCTTA	120
TTCTAGTTAT	TGAAGAATCC	AACGGGATGG	AAGCTAAATG	TAGCACATGG	CATGGGCGAT	180
GTCTCAACAG	TGAGTGGGAT	AACAAGTCGT	TTTAATGGTT	CAGGGCCAAT	AACCGGGGAG	240
GGTGAGGAAC	GGCATCTCTG	TTTTGAGTAA	ACAAGAGTGA	TTTCCTTCCC	TGACACTGAA	300
AAATGAAACC	TTTGGGGAGA	TAGAGGAAGC	GATCTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:873:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

GAATTCGGCC TTCATGGCCT AACCTTTAAA CCCTAAAATC CAGGAAAAGA AAATAAATAC ATTATCATGG ACCTGAGGGA TTTTTACCTG TTGGCTGCTC TGATTGCCTG TTTAAGGCTG GATTCCGCAA TAGCTCAAGA ACTTATTTAC ACTATTAGAG AGGAATTGCC TGAAAATGTG CCCATAGGAA ACATACCAAA GGATCTGAAC ATTTCTCACA TCAATGCTGC CACAGGGCCA CCTCG	60 120 180 240 245
(2) INFORMATION FOR SEQ ID NO:874:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 233 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:	
GAATTCGGCC TTCATGGCCT AGTTTCTTC ACTGGCATTC ACAAATTTAA GCCATTGCTG CCTCATTAGC CTTGTATTTT GTGTGCATAT CATATATCCA GACCTGTATG TTCACTTTAA GCATTCTTAT ATCACACTGT CTCCTCATCT ACCATATGGT AAATGTTAAA ACTCCACATT TGTCTGCATC AGGGAAAATG CATGGGCACA CATCCTCCCC CCCTTCCCTC GAG	60 120 180 233
(2) INFORMATION FOR SEQ ID NO:875:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 278 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:	
GGACAGGAAG TCAACTTCAA GCAGATTGAC TTGAAACGGG ATCTCATTTA GGAAGCATAA GTGTCCAATC AAAAACTGTG TATTTTTTTA AATTTGAAA ATACTCAAGT TCCAGTTGCT TATCATTCTC CTTCACTTTC TGAAAACCTG GCAATCCCAT GTGGACTTCT GGTAGAATGA GCAATGCAAA GAACTGGCTT GGACTTGGCA TGTCCTTGTA CTTCTGGGGG CTGATGGACC TTACGACCAC CGTTCTCTG GACACCCCAC ACCTCGAG	60 120 180 240 278
(2) INFORMATION FOR SEQ ID NO:876:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 290 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:	
GAATTCGGCC TTCATGGCCT AGTCCTCAAA TTAGTTATTG CATTATTTTC AAGTATTGTA	60

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GCAAATTTGT CAACTAAATT TAATTTAAAA GTAGAGGTCC AAAGCTCGAG

ACTTGTTAAT CAAGCTTTCA GTGAAACAGT TTATCAAACC ATTTTTTTTA TTTTGATTCA

240

(2) INFORMATION FOR SEQ ID NO:877:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 260 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:	
GAATTCGGCC TTCATGGCCT ACTCAAATTG GAAAGAAAGA TTCCTTGAGA CTTACTTTTA AAATCTAAAG TGTGAGGNNA ACANCAGAGT AAAGNCCAGA CTCATTNNAC CTTCGATGTC TGCATAGATC CAGNAGTTGT ACATTTTACC TAACAACATC ACTTTTGTTG AACATTCCAA CTCCAGAATG ATCCCCAATC ACCCTAATCT CAGAATGCTG GAATGATGTC TGTTGGCAAA CCCAGGACTC CACACTCGAG	60 120 180 240 260
(2) INFORMATION FOR SEQ ID NO:878:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 180 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:	
GAAGCGACCA TTCGTCCAAC AGGTATGGCT GGTTTTTGTG CAATGAGAGA ATGTCCACTC GCAATGATGA GCCTGAGAAG GCAAGTCGTC CGTTTGATGT GGATCGCGAT GGTTTTGTTA TGGGTGAAGG TGCCGGGATT CTTATTCTGG AATCACTCGA ACATGCTGAG AAACGTGGAG	60 120 180
(2) INFORMATION FOR SEQ ID NO:879:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 497 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:	
GAATTCGGCC AAAGAGGACT ACACAGAGCC CCTGTTTGGG AATTTGAGAT TCTGTGTCAT GCTGGTTTTC CTTTCAGAAT TGCTTGAAAT CGAGTTCTCT TAGCCACTGG ACACCTAGTT TTCAGGAGAA TGTCCCAAGA TTGTTTATAT ATACAAAATG GCAAAAGTAC TGTTTTTCGA ATTGATAATT CAAGCAAAGG CTTCTCTTTA CTGTCACTGA TTTTTTTTTT	60 120 180 240 300 360 420 480 497
272	

- (2) INFORMATION FOR SEQ ID NO:880:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

GAATTCGGCC AAAGAGGCC	T AGCAAAATCA	AATTCAACCC	ATGAGTCACA	GTGCTTTCTT	60
CAACAAGAAA ACATTGAAC	A CAGAAAGCAA	TTGTGAATAT	AAGGACCCTG	GGAAAATGAT	120
TCGCACGAGG CCCCACCTI	G CTTCTTCACA	GAAACAACCT	CAGAAATGTT	GCTTATTTAC	180
AGAAAGTTTG AAGCTGAAC	C TAGAAGTGAA	CGGTCAGAAT	GAAAGCAATG	ACACAGAACA	240
GCTTGATGAC GTTGTTGGG	T CTGGTCAGCT	ATTCAGCCAT	AGCTCTTCTG	ATGCCTGCAG	300
CAAGAATATT CATACAGGA	G AG				322

- (2) INFORMATION FOR SEQ ID NO:881:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

GGCCCACCTG	TGTCCTGGTT	GAGGGTCTCC	AGGGTTCTTT	GGGGCCCGAG	GCCAATGGTG	60
GCAGAGTCTA	CATAGAACTA	TGCTTCGTGG	TGTTCTGGGG	AAAACCTTTC	GACTTGTTGG	120
CTATACTATT	CAATATGGCT	GTATAGCTCA	TTGTGCTTTT	GAATACGTTG	GTGGTGTTGT	180
CATGTGTTCT	GGACCATCAA	TGGAGCCTAC	AATTCAAAAT	TCAGATATTG	TCTTTGCAGA	240
AAATCTTAGT	CGACATTTTT	ATGGTATCCA	AAGAGGTGAC	ATTGTGATTG	CAAAAAGCCC	300
AAGTGATCCA	AAATCAAATA	TTTGTAAAAG	AGTAATTGGT	TTGGAAGGAG	ACAAAATCCT	360
CACCACTAGT	CCATCAGATT	TCTTTAAAAG	CCATAGTTAT	GTGCCAATGG	GTCATGTTTG	420
GTTAGAAGGT	GACAATCTAC	AGAATTCTAC	AGATTCCAGG	TGCTAGGCCT	CTTTGGCCGA	480
A						481

- (2) INFORMATION FOR SEQ ID NO:882:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GAATTCGGCC	AAAGAGGCCT	AGGGAAGAGT	GGAACAAAAG	TCAGTCGTAC	ATTCAGCTAC	60
ATCAAGAATA	AAATGTCTAG	CAGCAAGAAG	AGCAAAGAAA	AGGAAAAAGA	AAAAGATAAG	120
ATTAAGGAGA	AGGAGAAAGA	TTCTAAAGAC	AAGGAGAAAG	ATAAGAAGAC	TGTCAACGGG	180
CACACTTTCA	GTTCCATTCC	TGTTGTGGGT	CCCATCAGCT	GTAGCCAGTG	TATGAAGCCC	240
TTCACCAACA	AAGATGCCTA	TACTTGTGCA	AATTGCAGTG	CTTTTGTCCA	CAAAGGCTGC	300
CGAGAAAGTC	TAGCCTCCTG	TGCAAAGGTC	AAAATGAAGC	AGCCCAAAGG	GAGCCTTCAG	360

387

GCACATGACA CATCATCACT GCCCACG

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 443 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:	
GAATTCGGCC AAAGAGGCCT AACGCAGCCA TGGCTCGTGG TCCCAAGAAG CATCTGAAGC GGGTGGCAGC TCCAAAGCAT TGGATGCTGG ATAAATTGAC CGGTGTGTT GCTCCTCGTC CATCCACCGG TCCCCACAAG TTGAGAGAGT GTCTCCCCCT CATCATTTTC CTGAGGAACA GACTTAAGTA TGCCCTGACA GGAGATGAAG TAAAGAAGAT TTGCATGCAG CGGTTCATTA AAATCGATGG CAAGGTCCGA ACTGATATAA CCTACCCTGC TGGATTCATG GATGTCATCA GCATTGACAA GACGGGAGAG AATTTCCGTC TGATCTATGA CACCAAGGGT CGCTTTGCTG TACATCGTAT TACACCTGAG GCGGCATAA CACAGCAAGA CGAGAAGACC CTATGGAGCT TTAATTTATT AATGCAAACA GTA	60 120 180 240 300 360 420 443
(2) INFORMATION FOR SEQ ID NO:884: (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 353 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:	
GAATTCGGCC AAAGAGGCCT AAACATCATT TGTACTCTAA TCCAATCAAA GAAGAAATGA CTGAGTCTAA GTTCTCTAAG TACTCTGAAA TGAGTGAGGA AAAACGAGCC AAACTTCGTG AAATTGAGCT CAAAGTTATG AAGTTTCAGG ATGAATTGGA ATCTGGGAAA AGACCTAAAA AACCAGGCCA GAGTTTTCAG GAGCAAGTAG AACACTACAG AGATAAACTT CTTCAACGAG AGAAAAGAGAAA AGAGAAAAAG AAGGAAAAAG ATGAGTGTAC TCCGACAAGG AAG	60 120 180 240 300 353
(2) INFORMATION FOR SEQ ID NO:885:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 475 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:	
GAATTCGGCC AAAGAGGCCT ACAATTTTT GCCTTTTTAC CCTTCTGTCC TTTAATGCCA TCTCTTTCTC AATTATTTC TCTCATTTT TTTCTGAGCA GACTTATACA AAAAGGAACA TAAATTAAAT TTGCCAAATA TCAAAAGAGA GGAACTTTTT ATTTTTATT TTTTTGGAAC GGAGTCTCAA TCTGTCTCCC AGGCTGAGT GCAGTGACGC AATCTCAGCT CACTGCAACC TCCGCCTCCC AGTTCAAGAG ATTCTCTGCC TCAGCCTCCC GAGTAGCTG GATTACAGGT	60 120 180 240 300
374	

ACCCTCTACC ATACTCAGCT AATTTTTGTA TTTTTAGTAG AGACTGGTTC ACCATGTGGG CCAGGCTGGT CTCGAACTCC TGACTTCAGG TGTTCTGCCT GCTTTGGCCT TCCAAAGTGC TGGGATTATA GGCGTGAGCC ACCACTCTCC ACTGAACTTT TTAATCTTAG AGCAG	360 420 475
(2) INFORMATION FOR SEQ ID NO:886:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:	
GAATTCGGCC AAAGAGGCCT AGGGGTGTTA ATTAGCTCAG CTGTAGCAAT CATTTCATAA TGTATATCAA AACATCCCAC TGTATACTTT ATACTTTTT ATAAAAATAA ATATTCTTAC AAAAGGACAG GCGCTGTGC TGTCTGGCTC ACCATTGTAC CCAATACCCA ACAGGGTGCC AAGTACCCAA TACCCAACAG GGTGCCAAGG AACACAAAAG GCACTCAAAA TATGTTTGTT GATTGGAGTT TACAAGGAAG AAAGGTATTT TCTTATCCCT CTCTTCCCTT CCCACCCAAA CATAGCTTCT TCTAAGAAAA GAAACTGAGG CTGGGCAAGG TTAAAAAGCTA GCTCCTGGTA CTTTTGCATC CACACTCAGT TTACCTGTGC CTTAAACCAG ACTTCATCAA ACTTCAGTCT TCACAAAGTCA CTTCACCATT TTTGCTCTAC CTACTTACTG CCTGTGTAGG CCTCTTTGGC CGAG	60 120 180 240 300 360 420 480 484
(2) INFORMATION FOR SEQ ID NO:887:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 184 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:	
GAATTCGGCC AAAGAGGCCT AGTGGGACAT AAGGCTGGAA GGTAGCACAC ACAGCACCAT ATTCTTTTTT ACTTGCATGC GAGTTACTTT GAGTGCTTTT CTCTTTACCA AATATATGAG TTCTATTACT ACATTCCTTT TCTTTGTTTG TTTTAGTGAG ACAGGGTCTC GTTCTGCCTC CCAG	60 120 180 184
(2) INFORMATION FOR SEQ ID NO:888:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 78 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:	
GAATTCGCCC AAAGAGGCCT AGTTTGCGAC TTACTTTTAA TTTCAAATCA GCTGCAGATG TTTGGGAGCC TTCTCGAG	60 78
(2) INFORMATION FOR SEO ID NO:889:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

GAATTCGGCC AAA	AGAGGCCT AATGGAAGAT	ATGCTGAAAG	ACTTTCTCCT	TGGAGAACAC	60
TTATTATTGG TTC	GCAACCA GGGTGTAGG	AAAAACAAGA	TTGTTGACAC	ATTCCTTCAC	120
CTGCTCAACA GAG	CCCCGAGA ATATATTCAC	CTACACAGGG	ATACCACAGT	ACAAACTCTT	180
ACGCTTCAGC CTT	CCGGTTAA AGACGGACTT	ATTGTATATG	AAGACTCACC	TTTGGTTAAA	240
GCAGTAAAGT TGC	GGTCATAT TCTGGTAGT	GATGAGGCTG	ACAAAGCTCC	AACAAATGTC	300
ACGTGTATTT TAX	AAAACTCT AGTAGAAAA1	GGAGAAATGA	TTCTAGCAGA	TGGAAGACGC	360
ATTGTTGCAA ATT	rctgctaa tgtgaatgg	AGAGAAAATG	TTGTAGTGAT	TCATCCTGAT	420
TTTAGGATGA TTC	GTTCTGGC AAATAGACCT	GGATTTCCTT	TCCTAGGCAA	TGATTTCTTC	480
GGTACCTTAG GTC	GATATTTT TAGCTGCCAT	GCAGTTGATA	ACCCCAAACC	CCACTCGGAG	540
CTCGAG					546

- (2) INFORMATION FOR SEQ ID NO:890:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

GAATTCGGCC	AAAGGGCCTA	GAGATTTCAT	GTATTTCTCT	TCACTTCCAA	GAGAGTGGAT	60
AGAATGGAGA	AATCTAGATT	GATCTTTACA	GCTCCAGATA	AAGGGACTAA	AAATATTGGT	120
TTAAAATATT	AAAGGTTAAA	GAAAGAGACT	GTTGGTTTCT	TTCAAAGTGA	TTTAAATTTA	180
AACTAGGTTT	TTATTACTAA	GTTTTGGAAA	TGGGGTAACC	ATTTTTTTCT	CATATCAAGG	240
ATATGTACAT	ATTTCCCATT	TCCCCATAAT	TAAAAACAAA	CAACTCCCAT	CCACTTCTTA	300
TAAATAGTTC	TTAACTTGGG	CTTAGTAACA	ATGTATATTG	TGCCAGTAAT	ACAGAAAAGG	360
TGGGAGTATA	AAGACCATCC	TGTCCTGTTA	GAATCCTATA	GAACCAAGGT	GCTGGATTAT	420
GGTGGTT						427

- (2) INFORMATION FOR SEQ ID NO:891:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GAATTCGGCC	AAAGAGGCCT	AATTTTATTG	AAACTGCTTA	TGTATGTCAA	AGGAGCCCAC	60
AACTTCAGCT	ACACAACTTT	TTGTATTGAA	AGAACTCATA	CTTTTTGTAG	CTTTTATTTC	120
ACATTTAATT	TAAAGTGACT	TTTAGCACTA	AAATGCCTAG	AAGATTTTAC	TCCAGACCTA	180
TAAGGAAATG	TTTAGTTTTT	ATGAAAAATG	ACAAGTCGAT	GGTTAAACTT	CTCATGTCTT	240
TECTECTTE	CCCCTAATAG	CACTGGACAA	CACCACGACC	ACATGGAAAC	እጥለ ጥጥጥጥ ርር	300

346

AAGCAAAACT TTAATTTTAT ATAACGTATG CTATGGAGAA CTCGAG

(2) INFORMATION FOR SEQ ID NO:892:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 95 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:	
GAATTCGGCC AAAGAGGCCT AGTGGAGAGT GAAGCTTAAG ACTGCAATTG CAGAAAAAGT CCATGAGGAG AGAAGAAGGA GAAAAGGGGG AAGAG	60 95
(2) INFORMATION FOR SEQ ID NO:893:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 424 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:	
TTTTTTTTT TTTTTTTAA ATACTTCGCA TACTCTCCAA TGCCCAAAAA TAGCAAGGTG	-
GTAAAAAGAG AATTAGATGA TGATGTTACT GAGTCTGTCA AAGACCTTCT TTCCCAATGA	60 120
AGACGCAGCT GATGATGCTT TTAAGACAAG TGAACTAATT GTTGATGGCC AGGAAGAGAA	180
AGATACAGAT GTTGAAGAAG GATCTGAAGT CGAAGATGAA AGACCAGCTT GGAACAGTAA	240
ACTACAATAC ATCCTGGCCC AAGTTGGATT TTCTGTAGGT TTAGGAAATG TGTGGCGATT	300
TCCATACCTA TGTCAGAAGA ATGGGGGCGG TGCATATCTT TTACCATATT TAATACTACT	360
TATGGTAATA GGTATTCCCC TTTTTTTCTT GGAACTCTCT GTGGGTCAAA GAACCACTCT	420
CGAG	424
(2) INFORMATION FOR SEQ ID NO:894:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 390 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:	
GCCAAAATCA AGCAAAGTAT GAAGAAAGAT AAAGAAGGGG AAGAAAAAGG GAAGCGAAGA	
GGATTCCCCA GCATCCTGGG ACCCCCACGG AGACCAAGCC GTCATGACAA CAGTGCAATT	60 120
GGCAGAGCCA TGGAACTACA GAAGGCGCGC CACCCTAAGC ACTTATCCAC ACCCTCATCT	180
GTGAGTCCTG AACCTCAGGA CTCTGCCAAG TTGCGCCAGA GTGGGTTAGC AAATGAAGGA	240
ACAGACGCTG GATACCTGCC TGCCAATTCC ATGTCTTCTG TAGCTTCAGG GGCCTCTTTT	300
TCCCAGGAAG GAGGGAAAGA GAATGATACA GGATCAAAGC AAGTTGGAGA AACATCAGCA	360
CCTGGAGACA CCTTAGATGT CACCCTCGAG	390
(2) INFORMATION FOR SEC ID NO. DOC	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 595 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GAATTCGGCC	TTCATGGCCT	AGTAGCTGGT	ATTTATTCCC	CAAAGTAATA	ATGTTGAAGT	60
ATGGGTCTCA	TCATTCCCAT	ACACAGAAAC	ACAAAACACT	TTGATCATAA	ACTTTTTTCT	120
TCAGAAGCCA	AACTAACTTG	CAGAATAATA	GAGCCACTGG	TTTAATGTTT	CCTCAAGATA	180
GGTTTTAGTG	TAAGCTAGTA	TTCTGTGTGT	TCGTAGAAAT	GATTCAATAC	CTGCAGCTGG	240
TGAATTAGGA	ATTGTATTTG	TTGCCTTTTT	TATATTAGAT	GAGGTGCAAA	AATTTTAATG	300
CTAGTCAGTA	TGCACCACCA	CAGGAAAGTT	AGATCCCATT	AGCACTTGAA	ACTACAGCTT	360
TGGAAACTTA	GGCTAAGTTA	ATTTGGATTT	GTTACTTGAT	TCACCTACTG	ACCTTTTCTT	420
TTGTTTGAAG	TGCTTATCAG	CATAATGAGC	TAAGTGTCAT	GCATATTTGT	GAAGAAACAC	480
CCTTTTTGGT	CCCTTTTGGG	ACAGAGAGGT	ACTCCTTGAT	CTTTATGAAT	GACAGGTTAC	540
TGTTTTGCCT	TATTGCTTAA	CTTAATGTAG	TGAAATAAAG	CAGACGAGGC	TCGAG ·	595

- (2) INFORMATION FOR SEQ ID NO:896:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

GGCTGATCCG	CGTGAACATG	GAGGACTTGC	GAGAGCAGAC	TCACACCCGC	CACTATGAAT	60
TGTACCGACG	CTGTAAGCTT	GAAGAGATGG	GGTTCAAGGA	CACTGACCCT	GACAGCAAAC	120
CCTTCAGTCT	TCAGGAGACA	TATGAAGCAA	AAAGGAATGA	ATTCCTGGGA	GAACTGCAGA	180
AGAAAGAAGA	AGAAATGAGA	CAAATGTTTG	TTATGAGAGT	GAAGGAGAAA	GAAGCTGAAC	240
TTAAGGAGGC	AGAGAAAGAG	CTTCACGAGA	AGTTTGACCT	TCTAAAGCGG	ACACACCAAG	300
AAGAAAAGAA	GAAAGTGGAA	GACAAGGAGA	AGGAGCTCGA	G .		341

- (2) INFORMATION FOR SEQ ID NO:897:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

GAATTCGGCC	TTCATGGCCT	ATGCCTTAAT	TTTGCTGTTT	GCCCTCGGAT	CTCTGGGTTT	60
GATTTTTGCG	TTGACTTTAA	ACAGACATAA	GTATCCCCTT	AACCTGTACC	TACTTTTTGG	120
ATTTACGCTG	TTGGAAGCTC	TGACTGTGGC	AGTTGTTGTT	ACTTTCTATG	ATGTATATAT	180
TATTCTGCAA	GCTTTCATAC	TGACTACTAC	AGTATTTTTT	GGTTTGACTG	TGTATACTCT	240
ACAATCTAAG	AAGGATTTCA	GCAAATTTGG	AGCAGGGCTG	TTTGCTCTTT	TGTGGATATT	300
GTGCCTGTCA	GGATTCTTGA	AGTTTTTTTT	TTATAGTGAG	ATAATGGAGT	TGGTCTTAGC	360
CGCTGCAGGA	GCGCCACTCG	AG	•			382

- (2) INFORMATION FOR SEQ ID NO:898:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

GAATTCGGCC	TTCATGGCCT	ACGAGCCTCA	CATCACTTGT	ACAAGCCACC	TGGGAGAAGT	60
GGCCCTCAGG	AAGATCCTAA	AACCAATACA	CAAATACAAC	TTTTTCATTT	CATTAATACA	120
TCAAGTTCAT	ATAAGAGTCA	AACAGGTAAA	AGCAGCATCC	CAAACTGTTT	TCTCCTCGTA	180
CATGTCAGTT	CCACGATCCT	CAGTCTCATA	AAGTCAGGGA	CTAGAGACCA	ATGTAATTAT	240
CAATACGTAC	CTGCCTTTGA	GTGAACCTTC	AATGCCAACT	AGGAAGGGCG	CTTCCAAAAC	300
GACGTTATTT	GTAACTCCTA	GGAAGACAAA	CACGGGTCAG	AACCCATACT	CTGCGGGCCT	360
TGAAATGGAA	AATCTCTCCT	CTAGACAGAC	TCATCCTGGC	CGTAAATATC	AGGAGACTCG	420
AG						422

- (2) INFORMATION FOR SEQ ID NO:899:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 806 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	60
NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	120
NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	180
NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	240
NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	300
NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	NNNNNNNNN	360
NNNNNNNNN	NNCNTTGCAN	${\tt GNTTTGGTTC}$	CNTTTNTTCC	TTGTTTNTTT	TTTTGCACAA	420
TATTTCAAGN	TTTACNAGGC	ATACATCAAT	CCAAGTTCGG	AATTTTAATT	AAGAATTCGG	480
CGTTCATGGC	NTAAAAGAAN	TTGATGCTAC	CCCCGGAAAT	GCCAGAAGAG	GANATACATT	540
GAAATAGACN	GTGATGAAGA	GCCCAGGGGT	GAATTACTTT	TTNTTCGGGA	CANTGAACGC	600
NTTCATAAAA	AGCCAAAGTC	TGACAAAGAG	ACAAGAGTNG	CAANTNCAAT	GGNTGGANAG	660
ACAGACCGAA	AAGAATTTNT	GAGGAAGAAA	ACCAAAACAA	ATCCATNNTC	CAGNTCGACA	720
AATNAAGAGA	AGNAAANACA	GAAGAACTTT	ATGATGATGC	GGTATAGCCA	GAATGTCCGG	780
TCAAAAAATA	AGCATTCCTT	CTCGAG				806

- (2) INFORMATION FOR SEQ ID NO:900:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GAATTCGGCC TTCATGGCCT AGGAGGGCCT GTTTCAGAAT TGCTTTAATA GTTCCCTTCC AGTTGAATTT ACCTTTTGCA GGAGCCTCAT CGTCTTCTGG TCTCCGCCC TCAGGATGCT CTGGGAGCTT CATCTTTTC TTCTTAGAAT CTGTTTCAAC TTCCCAGGTGC CTCCGCTTCC TCTTCCCTCG CCCACGCGTG CCTCTTCCTC ACTGGCGCTG TCCTTGCGCT GCTTCTTT CTTGCTCCTC TCCCTCCAG AGCCATTGGC CTCAGGGACT TCCTCCCCAC CAGCCTCAAG GTCAGCCTCC TGCCTCGAG	60 120 180 240 300 319
(2) INFORMATION FOR SEQ ID NO:901:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:	
GAATTCGGCC TTCATGGCCT AAGAAAAGAC AAGGTCCCCA TAAGAGTGGC GAGAGGAACA GAGCCAGGAC ATCGGAAAGC AAGCCCCTGT GTTCCCAAAC CGCAGAAAGAG GGAGCTCTGA TGTTAGACAA GCCACCCTCC TACAAGCGAA GGGAAAGTAA CTTTGAGCAA AAATGAGCAA CAGAAAAATGA GATCAAGGTC AGATCTCATA CAAAGTTGCA AGATGAAAGA ATGAGCAGCA GAATAACCTC CCTGTGATGT GGAAAGTGTG CCAGGAAAAC AGACCCAAAC GCTCGAG	60 120 180 240 297
(2) INFORMATION FOR SEQ ID NO:902:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 429 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:	
GAATTCGGCC TTCATGGCCT AGGGGTTCTT TCTCCTGCAC GATGCCAGGT GGTACTGGAA TCTGCTGAGT GGGATTCGGT GGTGAGGATC ATAAGGGCAA ATTTCAAAGG CTTCTGGCTC CATGAGAAAT TCTTGAAGCA GGGTATCTCA CTGCTAGAGT CTAACGGAAA TGCTTCTTGT GGAGAAGCCC TTTTGTAAGA AGGATGGAGT TGTCCTCTGC CCAGTTTTGG CCCTTGGGAT TCTGTAGGTG ACGGTCTTAA CTTGTGGTCT GTTCTCTAGG ACTGTGAGTG GTGGATTAGA AGAGAGATGA GGAGCTGCCA AAAGCAGCTA CACAGAGAAC AGAGTTAGCA AATGCCACCC GAGACAGAAC TATAGCAGAT GCAAGAGCCA AAAACCCACA GCCGCATTGA ATTCTAGACC TGCCTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:903:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 307 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SECTIFACE DESCRIPTION, SEC ID NO. 903.	

GAATTCGGCC TTCATGCCTT GTAACCATCA GGTAGATACA GCACCAACGG TAGTGGCTCT

TTATGACTAC ACAGCGAATC GATCAGATGA ACTAACCATC CATCGCGGAG ACATTATCCG AGTGTTTTTC AAAGATAATG AAGACTGGTG GTATGGCAGC ATAGGAAAGG GACAGGAAGG TTATTTTCCA GCTAATCATG TGGCTAGTGA AACACTGTAT CAAGAACTGC CTCCTGAGAT AAAGGAGCGA TCCCCTCCTT TAAGCCCTGA GGAAAAAACT AAAATAGAAA AATCTCCAGT CCTCGAG	120 180 240 300 300
(2) INFORMATION FOR SEQ ID NO:904:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 322 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:	
GAATTCGGCC TTCATGGCCT AGGACCTCGT AGGTCCCTAC AGCACCACAG TGCTCTTCAT CTCTCAGAGG ACTGAACCAC CAGCCAGCAC CAACAGAGAC ACTGTGGAAA GCACAAGGAC CCGACGGCA CTGAGTGACG AGCAGTGTGC TGCCGTCATC CTTGTGCTGT TTGCTTTCTT TTCCATTTTG ATTGCCTTTA TCATTCAGTA CTTTGTAATC AAGTGAAAAT ATAACTTTAT TTTTTAACTC TATTACATTT TATTTTGTCA TGTACTAAAA TTATTTCTGT ATTGCTTTNA TAAAAAAACAG TGGCACCTCG AG	60 120 180 240 300 322
(2) INFORMATION FOR SEQ ID NO:905:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:	
GAATTCGGCC TTCATGGCCT AAAAAAACAC ATAATTTGAA TCAACACAAC CACCCACAGC CTAATTATTA GCATCATCCC TCTACTATTT TTTAACCAAA TCAACAACAA CCTATTTAGC TGTTCCCCCAA CCTTTTCCTC CGACCCCCTA ACAACCCCCC TCCTAATACT AACTACCTGA CTCCTACCCC TCACAATCAT GGCAAGCCAA CGCCACTTAT CCAGTGAACC ACTATCACGA AAAAAACTCT ACCTCTAT ACTAATCTC CTACAAATCT CCTTAATTAT AACATTCACA GCCACAGAAC AACTCGAG	60 120 180 240 300 318
(2) INFORMATION FOR SEQ ID NO:906:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 553 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:	
GAATTCGGCC TTCATGGCCT ACAGGAAACA TACAAAGCTG CTCATAGTGG GAGTCTTTTT GCTCATGTTC GTGTGCGGCC TCTTCTTCAC TCGACCTTCA GGCAGCTACT TCATCAGACT GCTGAGTGAC TACTGGATAG TCTTCCCCAT CATCGTCGTT GTCGTATTTG AAACCATGGC	60 120

TGTATCC	TGG GCCTATGGGG	CCAGGAGGTT	CCTTGCAGAC	CTGACGATCC	TGTTGGGCCA	240
CCCCATC	TCT CCCATCTTTG	GTTGGCTGTG	GCCCCATCTG	TGTCCAGTTG	TGCTGCTAAT	300
CATCTTT	GTG ACCATGATGG	TTCATCTTTG	TATGAAGCCG	ATCACCTACA	TOTCOTOCOA	360
CTCNACC	ACC TCARAGGG	TCOTTCC110	Intornocco	ATCACCIACA	HODGIOOTE	200
CICAMOC	ACC TCAAAAGAGG	TGCTTCGACC	ATACCCACCG	TGGGCACTGC	TCTTGATGAT	420
CACCCTI	TTT GCCATTGTCA	TCCTCCCCAT	CCCTGCATAC	TTTGTATACT	GCCGCATACA	480
TAGGATT	CCC TTCAGGCCCA	AGAGCGGAGA	CGGGCCTATG	ACAGCCTCCA	CATCCCTACC	540
	CTC GAG		0000011110		CATCCCIACC	340
CCIAAGI	CIC GAG					553

- (2) INFORMATION FOR SEQ ID NO:907:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 557 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GAATTCGGCG	TTCATGGCCT	AGTAGAGAAG	ANNNTATTGC	NGTGACAATG	AGGTTTCTAC	60
		GTTATTCTGA				120
ACAACTTTAT	TCCACAGCCA	ATTGGAAAAT	GCAAGCGTGT	ATTCCAAGCA	TTGCTACCTT	180
ACGCTGTGGA	AGAATTGTGC	AACGTAGCAG	AGTCACTGAT	TGTTCCTGTC	AGAATGGGGA	240
TTGCTCGTCC	AACTGCACCA	TTTACCCTGG	CTAGTACTAG	CATAGATGCC	ATGCAGGGCA	300
GTGAAGAATT	ATTTTCAGTG	GAACCACTAC	CACCACGACC	ATCATCTGAT	CAGTCTAGCA	360
		TCCTACATCA				420
AGTCACAGCC	CGTTCGGGGC	AGAGATGAAG	AACAGGATGA	TATTGTTTCA	GCAGATGTGG	480
AAGAGGTTGA	GGTGGTGGAG	GGTGTGGCTG	GAGAAGAGGA	TCATCATGAT	GAACAGGAAG	540
AACACAGGAA	GCTCGAG					557

- (2) INFORMATION FOR SEQ ID NO:908:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

GAATTCGGCC TTCATGGCCT	` AAAAAAGTCA	GCCAGGTGTG	GTGATGTGCG	CCTGTGGTCC	60
CAGGTATTCA CGAGCTGAGC	TGGGAGGATC	ACCTCAGCCC	GGGAGGTGGA	GGTTGCAGTG	120
AGCCCATATC CCGCCACTGC	ACTCCAACCT	GGGAGACAGA	GCGAGACCCT	GTCTCCAAAA	180
AAAAAAAAA AAAATCCGGC	ATCTATTTAT	GTAACTACTA	GAATCTTAAG	TTCAGAATTT	240
ACTCCATAAG AGTATATAAA					300
ATAGGTCTAA GTCTTGTACT	TTTCTGTCCT	GTCCACAGAG	CCTTGAAAAT	AATTTAGAGC	360
TCAGTCATTC AGTTTGGATT	TATGTATAAA	TTGAAATATA	TTAATTACTT	ATTTATAGTG	420
CAGCTCGAG					429

- (2) INFORMATION FOR SEQ ID NO:909:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

GAATTCGGCC	TTCATGGCCT	AGTCCCTGAA	ААААААААА	GAAAAAAAA	ATTTAAATAG	60
AGGAAATACT	AGCTAAGTTT	AATGTAGGCC	AGTTCTAAAA	TAATGATTTA	TTGCTGCTGT	120
TGTTACATAA	TTTTCTTAAA	TATTTTAAAG	ATTGCACACT	GTCTGCTCGT	AGGCCATGAA	180

- (2) INFORMATION FOR SEQ ID NO:910:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

TACCTGCAGT	TGTACCGGGT	CACATGTGAC	CAAACCTACC	TGCTCCGATC	CCTGGATTAC	60
GTAAAAAGAA	CACTTCGGAA	TCTGAATGGC	CGCAGGGTCA	CCTTCCTCTG	TGGGGATGCT	120
GGCCCCCTGG	CTGTTGGAGC	TGTGATTTAT	CACAAACTCA	GAAGTGACTG	TGAGTCCCAG	180
GAATGTGTCA	CAAAGTGAGT	TTTAGAACTG	GAAACATTTT	CTCCCAATTC	CCAGTGGAAG	240
CTCTTGCTGT	AGAAAGATAT	TCAGAAAGGA	AACTATTTTT	CCATTCATCC	ATTGTTGTAA	300
ACAGATCACT	CCAAAATGTT	AATCTTGAGC	ATAGTGGTGG	GATCATATGC	CCTCTTTTTA	360
	TGTGTGCCGG				COLCILITIA	387
						30/

- (2) INFORMATION FOR SEQ ID NO:911:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

GAATTCGGCC TTCATGGCCT	AGTGTCTTGA	CAATGGTTGA	GCTGGTTTGG	ATCACAGGAA	60
CATTTATTTG ATAACGATGG	AAGGAAAAA	CAGTGCTGTA	ATAAGTCGCT	TCTTAAAATG	120
TGGGGTGTTA TTAAAAGAAT	AATGGGAAAG	TGCTACTGGG	AAGGCAAACA	CAGCAATTGT	180
ACTCTACAGA CAGGGATTCT	CCTATTGGCC	ATTTTAGAAA	CATTCCCCAG	GCAACATGAG	240
ATTATCCAAG TGGAGAGAAC	CAGAGTCAGA	GCCATTTCCT	AGGCCGACAG	AGCAGCGCTC	300
CAGATGAGAT ACTGAAGGTT	TGAACTCAAG	TGATGGCAGT	AAGATCAGAA	AGCAAAAGGC	360
ATATCACAAA GAAACCATAA	GATTCTCCAT	CTGGATATAT	AGAAGATAAA	TGGAAAGAGA	420
AACTCGAG					428

- (2) INFORMATION FOR SEQ ID NO:912:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

GAATTCGGCC 1	TCATGGCCT	AGAAAACCAA	ATACTGCATG	TTCTCACTCA	TAGGTGGGAA	60
CTAAACAATG A	AGAACACTTG	GACACAGGGC	TGGGAACACC	ACAACTTCTT	TTTCAGTTCA	120
TAACTCATAG 7	CCACGATCC	ATGTGCTCTT	TGACTTGACT	TTTCTTAAAC	TCCTATTTTA	180
TGTGCTTCTG A	ACTTGCTTTC	CCTTCTTATT	TGTAATCCAC	ACTAGCCTCA	AAAGATGCAT	240
GAACTGTGAA 1	TTTCACTTC	CAGGGCCATG	GATAGTTGAA	CATCTAGTAG	TGAATTTCCT	300
CTTTCAGAAG A	TAAATAAAT	TCATTCATTC	CCCTGGATCT	AGAAGGACAC	ACTCGAG	357

- (2) INFORMATION FOR SEQ ID NO:913:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

CAGCCTGGGT GGCAGAGCAA GACTCCA	ATTT CAAAAAAAA AAAAAAAAGC CCAAGTCACT	60
TGCTGTTTCT GGATCCAGTA ACGCTGC	CCTC AAATTTGATT CAGTCACCTC ACATACTTAA	120
CATTCTGGCT TTCCTTTCCT CTGTTTC	TGG CATCTGGAGA TTTCCTTTTT TTGTGTGTGA	180
GCTCATTTAT GGTTATCTGT TGTTATG	STTT AATACAACCA TTCCTGGCTG AGGCTGCCAC	240
ATCTAGAGCT GGTAAACTCG AG		262

- (2) INFORMATION FOR SEQ ID NO:914:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

GAATTCGGCC	TTATGGCCTA	GTGATATGTC	ATAATCCCTT	CTGTGGGCTG	GGCCCACATA	60
AGGAGAGTCA	AATCACTTGG	GTGCTGGGAA	GAGGCACATG	TCACACGTGC	AAGAAGGTCC	120
AAGGATGAGA	TTAAAAATTC	CACAAAGGTC	CAAATTCTAG	GGCCCAGACA	GAAGAGAAGA	180
GTCACATCAT	CTAGATGATG	AATGAAAAGA	TATGTCATTA	TTCTCCTTTG	GGCAGTGCTT	240
CTGCAGAAAA	GTTGCACCTT	CTAGGTGTTG	GACTCAGCAA	TATATCACAA	TGTCTGCAGT	300
ATTTTGGAAG	GAGAGGAGAG	TCACCATTAC	TTAGGTGCTA	GGCCCAGCAA	TACATCTCAA.	360
GCACTTCTTG	GGCAAAGCCC	AAGCAGTAAA	AAAGAGTCAC	ATTACCTAGG	TTCTGGGTAT	420
AGCAATATGT	CACAAATGCC	CCTAAGAAGA	GGGCCCAGGA	AAAGACTCGA	G	471

- (2) INFORMATION FOR SEQ ID NO:915:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

A CONTROL OF STREET OF STREET AND ADDRESS OF STREET ADDRESS OF STREET AND ADDRESS OF STREET ADDRESS OF STREET AND ADDRESS OF STREET ADDRESS OF STREET AND ADDRESS OF STREET AND ADDRESS OF STREET AND ADDRESS OF STREET AND

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GAATTCGGCC	TTCATGGCCT	AGAGTGCCTG	ACCTTCCCTG	TTCAAGAATT	TATAAAGATT	60
CCTAACAGCA	ATTCTAGAAA	AAGGATAAAG	ACCTCCACTT	GGCTTTCAGA	AGCCTCCAGC	120
N TOTO COOK				COCITICA	ACCCICCAGC	120
ATCTGGCCCA	AGCTAATACA	GCCTTAAAAC	TAATCTGGTT	ATAGCCCAGC	CCCTCATTTC	180
ACAAAGAAAA	CTGAGACCCC	TCCCTATCTA	TTAACTCCCT	CCARCORRA	ACATCATCTA	
		LOCCIMICIA	TIMMCICGCI	CCAACCAAAC	ACATCATCTA	240
TCCCCTCTCT	TCCTCCAGAT	AACACTCACT	TACCAGGCTA	CACTGACCTC	CACGTCTCTG	
			cundocin	CHGIGHGGIC	CACGICICIG	300
ATATGAGGCT	CCTGTCCACA	AGTTTGGTAA	CCTTCATCTG	CCTCATCACC	AGTGAGCACC	360
CACCACOMO	01.0momo			coronica	MOTONGCACC	300
CAGCACTTAG	CACTGTGCCC	GACACAGAAA	TGAACACTCT	GCTCCTCCGG	GCCGGCGTGG	420
CTCCCCCCCT	GCGGCCACCG	0010000000			222020100	420
GIGCGCCGCI	GCGGCCACCG	GCAGCGCTCG	AG			452

- (2) INFORMATION FOR SEQ ID NO:916:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

TTCATGGCCT	ACAAATGGTT	GGTTTATGTT	ATGATAGCAA	TTTTCTGCAT	60
ATGAGTCTGT	ACAACTGTCT	TGCTGCACTA	ATTCATAACA	TACCATATCC	120
ATTGCATGTC	GTGGCAAAAA	CATGGAAGTG	ACACTTATOS	TACCATAIGG	
GCAGTAGCTG	TTGTTTGGGC	TCTCTTTCCA	AUMCITATIT	TICICICIGG	180
GATATCTTCC	CCATTCCTTC	CTCTCTCCA	AATGAAGACA	GGTGGGCTTG	240
AACTCATCTC	WCAMA COM	CIGICIGAAT	TTAATTAAAA	CACTGAAGTT	300
AAGICAIGIG	IGATACTTCT	AGGCCTTCTC	CTCCTCTATG	ATGTATTTTT	360
ACACCATTCA	TCACAAAGAA	TGGTGAGAGT	ATCATGGTTG	AACTCGCAGC	420
GGAAATAATG	AAAAGAATGA	TGGAAATCTC	GAG		463
	ATGAGTCTGT ATTGCATGTC GCAGTAGCTG GATATCTTGG AAGTCATGTG ACACCATTCA	ATGAGTCTGT ACAACTGTCT ATTGCATGTC GTGGCAAAAA GCAGTAGCTG TTGTTTGGGC GATATCTTGG GGATTGCTTT AAGTCATGTG TGATACTTCT ACACCATTCA TCACAAAGAA	ATGAGTCTGT ACAACTGTCT TGCTGCACTA ATTGCATGTC GTGGCAAAAA CATGGAAGTG GCAGTAGCTG TTGTTTGGGC TGTGTTTCGA GATATCTTGG GGATTGCTTT CTGTCTGAAT AAGTCATGTG TGATACTTCT AGGCCTTCTC ACACCATTCA TCACAAAGAA TGGTGAGAGT	ATGAGTCTGT ACAACTGTCT TGCTGCACTA ATTCATAAGA ATTGCATGTC GTGGCAAAAA CATGGAAGTG AGACTTATTT GCAGTAGCTG TTGTTTGGGC TGTGTTTCGA AATGAAGACA GATATCTTGG GGATTGCTTT CTGTCTGAAT TTAATTAAAA AAGTCATGTG TGATACTTCT AGGCCTTCTC CTCCTCTATG	TTCATGGCCT ACAAATGGTT GGTTTATGTT ATGATAGCAA TTTTCTGCAT ATGAGTCTGT ACAACTGTCT TGCTGCACTA ATTCATAAGA TACCATATGG ATTGCATGTC GTGCAAAAA CATGGAAGTG AGACTTATTT TTCTCTCTGG GCAGTAGCTG TTGTTTGGGC TGTGTTTCGA AATGAAGACA GGTGGGCTTG GATATCTTGG GGATTGCTTT CTGTCTGAAT TTAATTAAAA CACTGAAGTT AAGTCATGTG TGATACTTCT AGGCCTTCTC CTCCTCTATG ATGTATTTTT ACACCATTCA TCACAAAGAA TGGTGAGAGT ATCATGGTTG AACTCGCAGC GGAAATAATG AAAAGAATGA TGGAAATCTC GAG

- (2) INFORMATION FOR SEQ ID NO:917:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

GAATTCGGCC	TTCATGGCCT	AACGTACTTG	AAAAGGCTTT	CCTTTACACT	TCCAGGACCA	60
AACAGCAACT	TCCTGCCACA	CACTTCCACC	CTATCACTGG	GAGAAATCCT	TTTCTGGACA	120
TGAGCCTTTG	ACCTGGGTGG	GGCAGAAAGA	ACCACAAACT	CCATCTCCCA	ATAGAACTTT	180
GAAATTCACT	CAGCTTTTCC	TTTCATGCTG	TTTGTTGCCT	GCTTGTTGCA	CTCCTCCTGC	240
CCCAGAACTG	CAAGATTTTT	AGCTTCACCC	CTTTCTGAGA	CTAATCTTAT	CTCCTCCTGC	300
AATCAGTATC	AGTTCCCCTG	TATTCTGTGC	TTCATCCAAT	TUCCAACACE	CITTIATCAG	
AAGCATTTAA	TTCACTCCCA	GAATCTCCAC	TICKICGAAI	TIGCAAGACI	GACCICITIT	360
		CARTCICGAG				390

- (2) INFORMATION FOR SEQ ID NO:918:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

				AGCACACCAC		60
GATGAGGAAG	AGGATGATGA	TGGCTGTGAC	CTTTTTGCTG	ACTCTGAGAA	GGAGGAGGAA	120
GATATTGAGG	ACATTGAAGA	AAATACTAGA	CCTAAAAGAA	GCAGACCTAC	ATCGTTTGCA	180
GATGAGCTGG	CTGCCCGCAT	CAAGGGGGAT	GCCATGGGTC	GAGTGGACGA	GGAGCCGACA	240
ACCTTACCCT	CAGGAGAAGC	AAAACCTCGG	AAGACACTCA	AAGAGAAGAA	GGAAAGGAGA	300
ACTCCTTCAG	ACGAGTCTTC	ATCATCCAAA	CCTGGAAAGA	AAATCCCAGC	AGCTCTCGAG	360

- (2) INFORMATION FOR SEQ ID NO:919:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

GAATTCGGCC	AAAGAGGCCT	AGTGCTATTG	AAACATTGGT	AACAGCAATT	TCTTTAATTA	60
AACAATCCAA	AGTCTCTGCA	GATGATCGTT	GCAAAGTTCT	TATTAGCTCT	CTGCAGGATT	120
GCCTTCATGG	AATCGAGTCC	AAGTCCTATG	GGTCTGGATC	CAGACGTGAA	CGATCAAGAG	180
AACGGGACCA	TAGTAGATCA	CGGGAAAAGA	GTCGTCGCCA	TAAATCTCGG	AGTAGÂGATC	240
GCCACGATGA	CTATTACAGA	GAGAGAAGCA	GAGGTCGAG			279

- (2) INFORMATION FOR SEQ ID NO:920:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

GAATTCGGCC	TTCATGGCCT	ACAGAACTTG	AAGCCATCAA	TAAAAGAGTA	AAAGACACTA	60
TGGCACGATC	AGAAGATTTG	GACAATTCCA	TTGATAAAAC	AGAAGCTGGA	ATTAAGGAGC	120
TTCAGAAGAG	TATGGAGCGC	TGGAAAAATA	TGGAAAAAGA	ACATATGGAT	GCTATAAATC	180
ATGATACTAA	AGAACTGGAA	AAGATGACAA	ATCGGCAAGG	CATGCTATTG	AAGAAGAAAG	240
AAGAGTGTAT	GAAGAAAATT	CGAGAACTTG	GATCACTTCC	CCAGGAAGCA	TTTGAAAAGT	300
ACCAGACACT	GAGCCTCAAA	CAGTTGTTTC	GAAAACTTGA	GCAGTGCAAC	ACAGAATTAA	360
AGAAGTACAG	CCATGTTAAC	AAAAAGGCTT	TGGATCAGTT	TGTAAATTTC	TCCGAGCAGA	420
AAGAAAAGTT	AATAAAGCGT	CAAGAAGAGT	TAGATAGGGG	CCCACTCGAG		470

- (2) INFORMATION FOR SEQ ID NO:921:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

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GAATTCGGCC	TTCATGGCCT	AGCAGTGGCG	TTGGAAGGAG	ACGCGGAGGG	GCAGTGGCGT	60
TGGAAGGAGA	AACGGAGGG	CAGTGGCGTT	GGAACGGGGG	CAGTGGCCTC	GGAAGGGGAC	
GCGGAGGGGG	ACTOCCOTTO	0110010101		CHOIGGCGIC	GGAAGGGGAC	120
CCGGNGGGGC	MG 1GGCG 1 1G	GAAGGAGAGA	CCAGGGCCGC	GGGGCTGCTT	CTTGTAAAGG	180
GCCAAGCTGT	GAGGACTTCG	GGCTTTGCGG	CCCCTTTTTCT	CTATGTCCCA		
mamman		000111000	ccccitiidi	CIATGTCCCA	TCTCCTTCTT	240
IGTTTTGTTT	TTCTCAAACC	CTTTAAAAAC	GTGAAAACCA	TTTCTAGCTT	CCCCCCCCTA	300
TAAAAATACC	CCTCCCTCCC	CCD3 CDD		cimocii	GGGGGCCCIA	300
CONTENENT	CCICGCIGGC	CCTAGTTTGA	TGACCCCTGA	AACAGACAAT	TCAAGGAGAA	360
GCTTAGTGAA	AGAGTCACTT	ΔΤΔΟΟΤΤΟΔΤ	****	GAAGATATAG		
			MAMAMI AAGA	GAAGATATAG	TATCCATAAA	420
ATAATAATAA	GATTGTATCC	ATGAGGTTCC	TCGAG			455
						455

- (2) INFORMATION FOR SEQ ID NO:922:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 333 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GACATGACCC	TGGACAAAGA	ACAAATAGCG	AAGGATTTGC	TTTCAGGGGA	AGAAGAGGAA	60
GAGACGCAAT	CATCTGCTGA	CGACCTCACC	CCCTCCCTCX	22200007	GGCCTCCGAC	60
CTCTTCCCTA	ACCCCACTCC	ATOMOGRAM	CCGTCCGTGA	CCTCCCACGA	GGCCTCCGAC	120
CICIICCCIA	ACCOGAGIGG	ATCTCGTTTC	CTGGCTGATG	AAGACAGAGA	GCCTGGCTCT	180
TUTGUCTUUT	CCGACACCGA	GGAGGACTCT	CTTCCTGCCA	ACAAATGTAA	GAAGGAGATC	240
ATGGTGGGAC	CTCAGTTCCA	AGCTGACCTC	AGCAACCTGC	ACTOCA ACCC	GCACTGTGAG	
AAGATCTACG	AGAACGAAGA	CAACCTACTC	030	ACTIONACCO	GCACIGIGAG	300
	HOMEOGRAGA	CAMOCIACIC	GAG			333

- (2) INFORMATION FOR SEQ ID NO:923:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 263 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

GAATTCGGCC	TTCATGGCCT	AAGCAGCCTT	TCACCAGGGC	TCCATCTCTC	AAGAGTCTCA	
GCCATGACTT	TGAGCTGAGC	TTCCCACAAC	Thankson	recarrend	GCCCTTGCCC	60
CTCACACOTO	CONSCIONSC	TIGGGAGAAG	TAAAGCAACT	GTTAAGGCCA	GCCCTTGCCC	120
CICAGACCIG	CCATGAAAGG	AATGAGCCCT	AGACTGACTC	CTGCAGCACC	CCCGGGACAG	180
GCTGGGACCA	GCTGTTTGTC	TCCAGGTGTC	AGAGTCCCTC	CTCCTCCTCC	AACCTCTCCA	
TTGAATTCTA	GACCTGCCTC	CAC		CICCICCICC	AACCICICCA	240
	onceracere	GAG				263

- (2) INFORMATION FOR SEQ ID NO:924:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 467 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

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	CCAAGAACCT GTACAAGGAT TTGTG			60
TCGACATCTT	CAAGCCAGTG CGCAAGCACT TTGAT	ATGCC TCATGATATT	GTTGCATCTG	120
AAGATGGGAC	TGTGTACATT GGAGATGCTC ATACC	AACAC CGTGTGGAAG	TTCACCTTGA	180
CTGAGAAATT	GGAACATCGA TCAGTTAAAA AGGCT	GGCAT TGAGGTCCAG	GAAATCAAAG	240
	AGTTGTTGAA ACCAAAATGG AGAAC			300
AGATGCAAGA	GAAACAGAAA CTGATCAAAG AGCCA	GGCTC GGGAGTGCCT	GTTGTTCTCA	360
	TCTGGTTATT CCGGTGGTTG TCCTG		TTTATTCGGT	420
GGAAAAAATC	AAGGGCCTTT GGAGCAGATT CTGAA	CACAA ACTCGAG		467
(2) INFORM	ATION FOR SEQ ID NO:925:			
(i)	SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 310 base pair	s		
	(B) TYPE: nucleic acid			
	(C) STRANDEDNESS: double			
	(D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:925:		
	÷			
GCCATCCTCT	GACAAAAGAA AGAATATGTA CTCAG	GTGGA GAGAATGTTC	AGATGAATGG	60
GGATACGCCC	CATGATGGAG GTCACGGAGG AGGAG	GACAT GGGGATTGTG	AAGAATTCCA	120
GCGAACTGGA	CGGTTCTGTG GTGGACTAAT TAAAG	ACATA AAGAGGAAAG	CGCCATTTTT	180
TGCCAGTGAT	TTTTATGATG CTTTAAATAT TCAAG	CTCTT TCGGCAATTC	TCTTCATTTA	240
TCTGGCAACT	GTAACTAATG CTATCACTTT TGGAG	GACTG CTTGGGGATG	CCACTGACAA	300
CATGCTCGAG				310
(2) INFORMA	ATION FOR SEQ ID NO:926:			
(5)	SEQUENCE CHARACTERISTICS:			
(1)	(A) LENGTH: 287 base pair			
	(B) TYPE: nucleic acid	S		
	(C) STRANDEDNESS: double			
	(D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ	ID NO:926:		
GAATTCGGCC	TTCATGGCCT AGTGGAGACC TGGCC	AAGGT ACAGAGAGCT	GTGTGCATGC	60
TGAGCAACAC	CACAGCCATT GCTGAGGCCT GGGCT	CGCCT GGACCACAAG	TTTGACCTGA	120
TGTATGCCAA	ACGTGCCTTT GTTCACTGGT ACGTT	GGGGA GGGGATGGAG	GAAGGTGAGT	180
TTTCAGAGGC	CCGTGAGGAC ATGGCTGCCC TTGAG	AAGGA TTATGAGGAG	GTTGGTGTGG	240
ATTCTGTTGA	AGGAGAGGT GAGGAGAAG GAGAG	GAAAA CCTCGAG		287
(2) INFORMA	ATION FOR SEQ ID NO:927:			
(i)	SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 332 base pair	·s		
	(B) TYPE: nucleic acid	-		
	(C) STRANDEDNESS: double			
	(D) TOPOLOGY: linear			
(ii)	MOLECULE TYPE: cDNA			
(xi)	SEQUENCE DESCRIPTION: SEQ 1	ID NO:927:		

60

CCGCGCACCA ACAACAGCAA CAACTCCACT GCGCCGGGCT GAGGAGCAGG AATTAGGAGC

TCGCGAATAA TATGAAAGGG ATCCGCAAAG GGGAAAGCCG AGCAAAGGAA TCCAAACCCT GGGAGCCTGG CAAGCGAAGA TGCGCTAAAT GTGGCCGCCT AGACTTCATC CTGATGAAGA AAATGGGGAT TAAAAGTGGA TTTACGTTTT GGAACCTCGT CTTTTTATTG ACGGTGTCTT GTGTGAAAGG TAGGTCTGCT TTGGGGGTCC CCTCCGCTTT GGATGGAGGT GGGCTGACTT GTAGATGGAG AGAGGCTGGC AGCTTACTCG AG	120 180 240 300 332
(2) INFORMATION FOR SEQ ID NO:928:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:	
AGCCTGCCAT CCCAGGCTTC AGATTGGAGC CGATACTCAA GCAGCTTACT GGAATCCGTC TCTGTTCCTG GAACACTAAA TGAGGCTGTT GTAATGACTC CATTTTCATC GGAACTTCAA GGAATTTCAG AACAGACCCT CCTGGAGCTG TCCAAAGGAA AGCCCTCCCC GCATCCCAGA GCCTGGTTTG TGTCTCTTGA TGGAAAGCCA GTTGCACAAG TGAGGCACTC CTTTATAGAC CTGAAAAAGG GCAAGAGAAC CCAGAGCAAT GACACCAGTC TGGACTCTGG GGTGGACATG AATGAGCTTC ACTCAAGTAG AAAGCTCGAG	60 120 180 240 300 330
(2) INFORMATION FOR SEQ ID NO:929:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 266 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:	
GAATTCGGCC TTCATGGCCT AGTGAGTGGG TGATATCTGT AAAGTGCATT GTCTTCAGTT GTAGGTGGGG TAGGTGTAAG GGAATGGCGG GGGGGCATGC AATATGGGTG AGGGAGGGCA GTGCCCTTCT CATCCCAGAC CTGAGCCCCC CCCAAAACCT GTCTGGACTT TGATCAGGAT AAGAACGTTG CAGGGCGAGG CAAGTTCCTG AAGCCGAAGA GGTCTGGGCT GGGGCCTACT GGAGAAAGGG CATAGACTGG CTCGAG	60 120 180 240 266
(2) INFORMATION FOR SEQ ID NO:930:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 319 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:	
GCGAAAATAA CCTTTTCTAA TGAGGATGTC TGATACTGTT ACTGTAAAAG ATGAAACTGC AACAATGAAG GATTTGGAGG CAGAAGTGAA AGATACAACC AGAGTTGAAA ATCTTATCAA ATCAGAAAAC TATGGGAAGA TTTTGGTAGA GAAGAATGAA CATTGTATTG AGAACAATAT AGATTTGCAG GAGAAAATTC AGATCCAGTT AACACAATCA TTTGAGAAAG AAGAGAAGCC	60 120 180 240

AAGAGATCCC AGTCTCGAG	319
(2) INFORMATION FOR SEQ ID NO:931:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 255 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:	
GAATTCGGCC TTCATGGCCT AAAGAAGAGC AGGAAGTCCA ATGTGGCCGA AGCAGAGTGA GCAAGGGCAG GAGTACCAGA GGAGGAGATA GGACGCCAAA GAGTTAAGAA AAGGAGGAAT GCAGAACCTT TCCATCAAAA ATAAAATAAT ACATAACCAT GGTTATGTGG GGTGGGGTTG TCTCTTTCTT TTGGAAAGAA GAAGGGCTTT CTGGGAATAG ATGGCCAGGC CAGGCAGCAA GCTGCTAAAC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:932:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 588 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:	
GAATTCGGCC TTCATGGCCT AGCATTTCA AAAATTCAGT GCAAGCGCCA GGCGATTTGT GTCTAAGGAT ACGATTTTGA ACCATATGGG CAGTGTACAA ACCATTGCAC CTGATCAAGG AGCAGTGCTT CTCCATTTGT TTTGCAGAGA AATGTTTTCC ATTTCCCGTG TGTTTCCATT TCCTTCTGAA ATTCTGATTT TATCCATTTT TTTAAGGCTC CTCTTTATCT CCTTCTTAA GGCACTGTTG CTATGGCACT TTTCTATAC CTTTTCATTC CTGTGTACAG TAGCTTAAAA TTGCAGTGAT TGAGCATAAC CTACTTGTTT GTATAAATTA TTGAAATCCA TTTGCACCCT GTAAGAATGG ACTTAAAAGT ACTGCTGGAC AGGCATGTGT GCTCAAAGTA CATTGATTGC TCAAATATAA GGAAATGGCC CAATGAACGT GGTTGTGGGA GGGGAAAGAG GAAACAGAGC TAGTCAGATG TGAATTGTAT CTGTTGTAAT AAACATGTTA AAACAAACAA AAATTGTTAT TTTTCTTTTC CTTCGGTCAG AGCCTCGAG	60 120 180 240 300 360 420 480 540
(2) INFORMATION FOR SEQ ID NO:933:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 520 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:	
GAATTCGGCC TTCATGGCCT AGGGGAAGGA AAGGCCCGTG TGGAGGAGCA TGGAGCCATC TGCTCATGAA GGAAAGGCAG GGATGGGGCA GAGGTGTTGG GGCTTCCGTG CGACTCCAGA GGCCAAGCCC AGAGCTGTGT GTGGAGCCCA TGAGGAGCAG AGATTTTCCA GCAAAGGTGC	60 120 180

ATTTGTGGGC CTCCAGATGG AGGCCCTACC TTCTCAGCAA GGGAAGAAAC CCCTCTCTCT TTGACCTCTC TCCCCTGCAC AATTAGAAGG TTCTGAAGAG TGACTTCATT ATTGGTGGGT GAGTATATGT TTATTGGGCA TCTGTGGTGT GCCAGATGTT GTGTTGAGTG CTGGGTGCAG AGGTAAATGG GATATCTGGT TACCGCCCAC ATGGGGCTTA TAGTGGGGGA AGTGGGGGAG TAAGTCAGGA CACACGTAAG CAAACGCTAG AATGGATAGA TATTGTGATT AGAGCATTGG AGAGAAAGAA CAGGATGTT CAAGAAAGGA CAGTCTCGAG	240 300 360 420 480 520
(2) INFORMATION FOR SEQ ID NO:934:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 259 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:	
GAATTCGGCC TTCATGGCCT ACTTTTTTC TCAAGGTGCA ATGAAAGCCT TCCACACTTT CTGTGTTGTC CTTCTGGTGT TTGGGAGTGT CTCTGAAGCC AAGTTTGATG ATTTTGAGGA TGAGGAGGAC ATAGTAGAGT ATGATGATAA TGACTTCGCT GAATTTGAGG ATGTCATGGA AGACTCTGTT ACTGAATCTC CTCAACGGGT CATAATCACT GAAGATGATG AAGATGAGAC CACTGGGGAG TTTCTCGAG	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:935:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 413 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:	
AACAAAATGA AACAAACAAA AGACAGAGGC CAAGAAAGGC TAAGTAACTT GCCTAAGACT ATATAATAAG TCACAGGGCA GGGAATAAAA CTCAGTTTC CTGACTTCCA TTAAGGTTGT CTTTTCCTCA CTCCACATTG CCTGTCATTT TTTTTCTGAT TATTCTTAAG AAGGAGTGAG GAGAGAGAAT AGAGAAACAG ATTTTTTTCT CGGACTATCT TTTCTGTAGG GAAAAACCAC TGAAGCCCTA TTAGCCTGGA AGCTGCTTAT AGGGTTACAA TACTGTGTGT CCTGCAGAAC CTGTGAAGCT CTTCTGTATT TTCTGGACTT TCCTGGAAAG TCATTTAGAT ATAATGTAAT AAATATAATA AAGTAGTTTA GATATAATGA GGTTTTCAAT AGGCTTCCTC GAG	60 120 180 240 300 360 413
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 259 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:	
GAATTCGGCC TTCATGGCCT ACCCTGAGAG TAAGCCAAAA AAGGAAGAAA AAAATATGGA AGTAAATATG AAAGAGTGGA TTTTACGATA TGCTGAACAA CAAAATGAAG AAGAAAAGAA	60 120

TGAGAATTCT AAAAGTTTAG AAGAGGAGGA AAAATTTGAC CCTAATGAAA GGTACTTACA TCTTGCAGCA AAACTGCTGG ATGCAAAAGA ACAAGCAGCT ACCTTTAAAC TAGAAAAAAA CAAGCAGGGC CGTCTCGAG	180 240 259
(2) INFORMATION FOR SEQ ID NO:937:	•
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 263 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:	
GCGAAACCGT GGTCAGCTGC AAGAAGGCAC AGGAGAACAT GAAGCAAAGG CACGAGAACG AAACGCACAC CTTAGAAAAA CAAATAAGTG ACCTTAAAAA TGAAATTGCT GAACTTCAGG GGCAAGCAGC AGTGCTCAAG GAGGCACATC ATGAGGCCAC TTGCAGGCAT GAGGAGGAGA AAAAACAACT GCAAGTGAAG CTTGAGGAGG AAAAGACTCA CCTGCAGGAG AAGCTGAGGC TGCAACATAA GAGGGAGCTC GAG	60 120 180 240 263
(2) INFORMATION FOR SEQ ID NO:938:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 384 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:	
GAATTCGGCT TCATGGCCTA TTCCACTACT AGGCTGACAT GCAAAATCCT AAGAGAAGTC AGTCTTCCAG GATTGATCCT GGCATTTGTG CTTGCTGTTC CCCGTGCCTG GAGCACCTGT CCCAGCTCCC CTGTGGCTGG CTCCTTCTCA CCATCCAGGG TTCAGTCCAA ATATCTCCTT CAAAGAGAGA TCTTCCAGGG TCACCTAATC CAGAGAGTGC CCTCTATGGT TGCCACATCC CCCCGACCCA CCACCCACCA CCCCCCACTT CAACTCCTTT ATGGCACCTG CCCCTCCCTG AAATTCTCAC TGTTGCTTAT TTGTTATCTA GCCCTCTCAT CAGAATGTAG ATCCACTGGT GACAGGGGAC TTGTGTGCCT CGAG	60 120 180 240 300 360 384
(2) INFORMATION FOR SEQ ID NO:939:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 262 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:	
GAATTCGGCC TCCATGGCCT AGTTGTGTTT TTTGGGCTTG CTATTAATGC AAACTCTGAT TGCAAATGGA TGTCATGTTT CATACCTTTT TTATCAGGAA AAAGCAGCA AGCCTTCAGG TGTTCCAGTG ATGCCTGACA CAATTGAGCT GGACTTTATG CTGCTCTTTA CAGTAAGAGG TGTTGCATTG TATGTGGGGA CTATGTGCAC TGGCGTCTAA GACAGTGACC TCAACAATAT TAGCTTTGCA CAAACCCTCG AG	60 120 180 240 262

## (2) INFORMATION FOR SEQ ID NO:940:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 300 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

GAATTCGGCC TTCA	TGGCCT AGTGGAGGAC	TGCTTTTGTG	AACATGAGAA	AGCAGCGCCT	60
GGTCCCTATC TATT	TGGGTC TTATTTACAT				00
COLCCCIATO TATI	TOGGIC TIATTIACAT	CCTTCTTTAA	GCCCAGTGGC	TCCTCAGCAT	120
ACTCTTAAAC TAAT	САСТТА ТСТТААЛАД	AACCAAAAGA	CTTTTCTCCA	TECTOCOCCO	180
ACACCTCCTA CARC	G1G11= G=G1====		CITICICA	199199919	190
ACAGGICCIA GAAG	GACAAT GTGCATATTA	CGACAAACAC	AAAGAAACTA	TACCATAACC	240
CAAGGCTGAA AATA	ATGTAG AAAACTTTAT	TOTOTOTOTO	10m10101		
	MIGING WHANCILIAI	TITIGITICE	AGTACAGAGC	AGAACTCGAG	300

- (2) INFORMATION FOR SEQ ID NO:941:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 194 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

GAATTCGGCC TTCATGGCCT TTTCATTCTG AATGAGGTTT TGATTTGCTT TACATTCCTT TGAACACCCT CGAG	CTTTTTTTGA	TTTTCTTTAA	AAAAAAAAAA	CAACCTGCTT	120 180
TGAACACCCT CGAG					194

- (2) INFORMATION FOR SEQ ID NO:942:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 581 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

G11mmccccc						
GAATTCGGCC	TTCATGGCCT	AGTGAGGATA	AAGATAAGGA	ACAGGCCAGG	CACAGTAGCT	60
CACGCCTGTA	ATCCCAGCAC	TCTGAGAGGC	CGAGGCAGGT	GGATCACATG	GGGCCAGGAG	120
TTTGAGACCA	CCCTCCACAA	CATCOTONA	~~~~~~~		333551100710	
I On On CO	GCCTGGACAA	CAIGGIGAAA	CCCCGTCTCT	ACTAAAAATA	GCCAGGTGTG	180
GTGGCACACA	CCTGTAATCC	TAGCTACTTG	GGAGGGAAGG	TOCON NORTH		
0010001000			GGAGGCAAGG	IGGGAAGIII	GTTTGAACCA	240
GGAGGCAGCG	GTTGCAGTGA	GTCAAGATCA	TGCCACTGCA	CTCCAGCCTG	GGTGACAGAG	300
<b>ፕልሮርልርፕሮ</b> ፕሮ	TCCCAAAAA				OO TOH CHOMO	300
INCONCICIO	TCCCAAAAAA	AAAAAAAAAG	ATAAGGAACA	GACCCAACCC	GAATCCACAC	360
AACCTGACAC	ACAGGAAAGT	CTTGCCCATC	CATICCACCITA	CCMCCCCC > C	G1 G1 GG1	
		CITOCCCATC	CATCCACCIA	CCTCCCCAAC	CAGAGTAGTG	420
AAGCTATAAC	CCCAGAGAGA	TACCTTTGAT	GTGAGCACTG	TCCAGCATGG	CCACCAACCC	480
A TWO A COMO O	MCG3 GG3 GH-			1003003100	GCACCAAGGC	400
ATTCACCTGC	TCCAGGAGTG	CAACCTGGGA	AAGGATAAAC	TGCTCCTCTA	AAGCAAAAAT	540
GGACAAGATA	GTTGCAGTGA	ACCABACCTC	CCC3 mmccm3	~		
	GITCCAGIGA	MOCHMACCIG	GGCATTGCTA	G		581

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

(4) Daganca Cimarciania(16);	
(A) LENGTH: 259 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double -	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:	
GAATTCGGCC TTCATGGCCT AAAACAGGCA ACAATGACCT TTTATTTTCT GTTTGTCCCC	6
ACCTCCCCAG CCTTCCACCT CCTGTTCTTC CTACCTTCTT CCTTTTTGAC TAAATAATCC	12
CCACCTCCCT TGATCATACA GTGAGGCTAC AGTGACTGAG GGGAGAATCC CCTCCTGTTC	180
ACTCTCCCAA CCCTGCTCCA GCCCCTCAGC TTCCCAGACC CTCATGCAGT TGGTTGTAAA	24
TTCTCCCAGT GAGCTCGAG	25
(2) INFORMATION FOR SEQ ID NO:944:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 360 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:	
the sage and beschill total bag in houses.	
•	
GAATTCGGCC TTCATGGCCT AAAACCTCAC GTGGCCTCTG ATTTCATTGT GGGTGCATCC	60
ACAGGTGGCC CGAGCTGTTC TTTCAGCTGC TCCAAGGATT GAGACCCAAG TCATCATGAA	120
AAAGGCCCAA GTACAGTCTT AATGCGATAA ATCCACTAGC TAAGACGTCG AGTGCCAAGA	180
CCAGCCTTCC AGCCGAGGTT TGGACAAAGT CTCAGGTTCC CGTGACTCAG GGTAAGGTGC	240
TGGGGCTGCC AGAGGACCTG CCCCAGCAAG ATTTTTGTCA AGAGCGAGAC TCCATCAGCC	300
CAGGCAGACG GGAGCAGGTT CTTGGCCAGC GTAGACAGCA GCAAACAGCA GCTCCTCGAG	360
(2) INFORMATION FOR SEQ ID NO:945:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 206 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:	
CAATTCCCCC TTCATCCCCT ACTCCACCACA ACCCCCCA ACCCCCCACACACA	.=.
GAATTCGGCC TTCATGGCCT AGTGCAGGAG ACGCCCTCAC CGGAGATGGG GACCGAGTCC ACACGGCTCT CACTGCAAAT GCTTTGGGAA AAACAAGACA GTGTACTTTG TGATCATATA	60
AAACAGCAAA ATAAAATAGT CGTGGGCACA GGGCCAGTGA TTCTGCAGTT AGAGCCGTGT	120
GGACTCGGTC CCCTCTCCGG CTCGAG	180
CONCIEGOTE CECTETCES CICONS	200
(2) INFORMATION FOR SEQ ID NO:946:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 272 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

GA	ATTCGGCC	TTCATGGCCT	AGGTTCCCCG	GCGTGGCATG	GATGATGACA	GAGGCCCTAG	60
AC	GTGGTCCT	GAGGAAGATA	GGTTCTCTCG	TCCTCCCCCA	CACCATCACC	GGCCTTCCTG	
CC	מיים ארא מיים	CATCATCACA	GGGGGGGGG	1CG1GGGGCA	GALGATGACC	GGCCTTCCTG	120
00	GIANCACA	GATGATGACA	GGCCTCCCAG	ACGAATTGCC	GATGAAGACA	GGGGAAACTG	180
GC	GTCATGCG	GATGATGACA	GACCACCTAG	ACGAGGACTG	GATGAGGACA	GAGGAAGCTG	240
GC(	GAACAGCT	GATGAGGACA	AAGGACCTCG	A.C.		01.00/11.0010	
							272

- (2) INFORMATION FOR SEQ ID NO:947:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 294 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

GTTTTGCTTA GATTTTGCTT	'TGGTTAGGTT	GCGTTTTGGG	GTTTGCCTTT	TTTTCTTCTC	60
GCTTAAATGC AATTTGGTTG	TAAAGATTTG	V.L.L.C.C.L.L.L.L.C.L.	CTTCATCTCT	TOGGOOTTOTO	
AGCGGTCCAT CTCACCCTCT		ATTCCTTTGT	GITCATCIGI	receerrere	120
AGCGGTCCAT CTCAGCGTCT	CCCTTCAGGA	ACCGCTGAGT	GTCCTCTCTT	AACATCCAAG	180
CCTTTTAATG AAATCGTACT	GAAATCTGTA	TCAGCTAAGA	GTCCTCCAAT	CCTGGTCCCA	240
TTAACTCCAA GTGCCTTTT1	GACAGTGACA	ACAGACAGTC	CCTCCCCACT	CCAC	
		"ICTONCHOTC	CCICGGCACI	CGAG	294

- (2) INFORMATION FOR SEQ ID NO:948:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 462 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

GAATTAGAAT CTCTAAAGAA	ACAGGAGGGA	ממממידירים	<b>ስ</b> ፓስምምርክርርም	CTCN CNTCNC	
GAATTTTCAA AAATGAAACA	ATCTAATAAT	CIICIIAAA	AIAIICAGGI	CICACAICAG	60
AATTENACOUR COCCERTAGE	MICIAMIAMI	GAAGCTAACT	TAAGAGAAGA	AGTTTTGAAG	120
AATTTAGCTA CTGCATATGA	CAACTTTGTT	GAACTTGTAG	CTAATTTGAA	GGAAGGCACA	180
AAGTTTTACA ATGAGTTGAC	TGAAATCCTG	GTCAGGTTCC	AGAACAAATG	CAGTGATATA	240
GTTTTTGCAC GGAAGACAGA	AAGAGATGAA	CTCTTAAAGG	ACTTGCAACA	AAGCATTCCC	300
AGAGAACCTA GTGCTCCTTC	AATTCCTACA	CCTCCCTATC	ACTCCTCAGG	AGGREGATE	
CATGCACCAA CTCCTCCAAC	TCCACCCCC	CCIGCOINIC	AGICCICACC	AGCAGGAGGA	360
CATGCACCAA CTCCTCCAAC	TCCAGCGCCA	AGAACCATGC	CGCCTACTAA	GCCCCAGCCC	420
CCAGCCAGGC CTCCACCACC	TGTGCTTCCA	GCGTATCTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:949:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 624 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

	GAATTCGGCC	TTCATGGCCT	ACTCAAAGAG	ACAACAAATA	GCATGGTAGA	ATCAATTAAA	60
					ATCCCGTAGA		120
	CAACCTAGTC	CTTTGGAACC	TGTGATCAGC	ACAATGCCTT	CCCAGACTGT	GTTACCTCCA	180
•	GAACCTGTTC	AGTTGTGTAA	GTCAGAGCAG	CGTCCATCTT	CCCTACCAGT	TGGACCTGTG	240
					GTACAGGCAG		300
					TGTCTCCAAA		360
					CTGATGAATT		420
	GGCTCATCCC	CAAAGCGCTT	AATAGATTCT	TCTGGATCTG	CCTCAGTCCT	GACACACAGC	480
					CACTTAATTC		540
	AATGGAACAA	GTGATGCTGA	CCTGTTTGAT	TCACATGATG	ACAGAGATGA	TGATGCGGAG	600
	GCAGGGTCTG	TGGTGAAGCT	CGAG				624

## (2) INFORMATION FOR SEQ ID NO:950:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 371 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

GATTCTAGAC	CTGCCTCGAG	CACGCTTGGA	GAAGCCCCGT	CTCTACTAAA	AATACAAAAT	60
				CTGGAGGCTG		120
ATCACTTGAG	CCCAGGAGGT	GGAGTTGAGG	TGAGCCGAGA	TCGTGCCATT	GCACTCCGGC	180
CTGGGTGACA	GAGTGCAACT	CCGTCTCAAA	ААААААААА	AAGCATTCAC	GTCAATGTCA	240
				ATAGGTTGGA		300
ACTGGGATCA	AGCTTGGGTT	CCACTTACCA	GCTGTAGTAT	GTTGAGCAAA	TTATTTAATC	360
TAACACTCGA						371

- (2) INFORMATION FOR SEQ ID NO:951:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 283 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

CCCAMMOAAM	moma accomm	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT				
GCGATTGAAT						60
					AGCCCCGGCT	120
TTTTTTTTT						180
ACTTTATTAC	TATGTCACCA	GAAGTCACCA	CCTTCACTTG	GTTCACCACA	GATGGATGGA	240
TGTCATAAAG	GAGGGTGCCA	CGGGGCCACT	GGATTCACTC	GAG		283

- (2) INFORMATION FOR SEQ ID NO:952:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 285 base pairs

- (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

	GCTTGGCAGA	TCCTAACTTC	ATCCA ACATO	OTT 1 TT 001 1		TCTCTGCCCC	
	oci i occion	TOCIANCIAC	AIGGAAGAIG	GTAATAGGAA	CAGATACTGC	TCTCTGCCCC	60
	TGCTTCTTGG	ATTCTTCAGC	TCCTACCGCT	GATTCGGATT	ATCCCCTTTT	GACCCTCTTG	120
•	GGGATCCAGA	CTGCTGCCAG	GAGGCTGAGT	AGATACCTCA	GTTATCTGTA	TGTTATTTCT	180
	CACACCCTTT	CCCCCATOOM	COMMON COMMON			TOTIMITE	100
	SAGAGGCTTT	GGCGGAICCI	CITCACTIGG	CATCCTGTGG	CATCCCTAGG	GTCTGGTGGT	240
	AGCAGTAATA	GCAACAATGA	TATCTTACAT	CTGGAACAAC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:953:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 614 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

GAATTCGGCC TTCATGGCCT	AATTCTAGAC	CTGCCTGTCT	TGAGAGGAAC	CTTCCCTGTG	60
CTGGCTCCTG TTGTTATCTG	TACCTAAGTT	ACTCAGTTCT	GAGTGCATGT	CTGGTAAATG	120
CTGGCCATTT CTTTGAAGTT	CTGACTCAGA	ATCGGCCTCC	ATTAGAGAAC	TCAGTTCTCC	180
AAACCCAGTC ATGATCTGCC	TTAAAATTGA	CCGAAGAGCC	ACTGATGATG	GCTCAACAAG	240
CTCATTCTCA GAAATCCTAC	GAAGAGGAAC	TGTTATGGTA	CTAACATAGG	TTCGAATACC	300
TGACCGCTCT AAACGAGAAA	TGGTTCGGCG	AAAGCCCCCA	CTATTCCTTT	CAATACTCAC	360
TGTATTTCT GCTAGCCCTA	CTCTGGATCG	AGTTCTATTT	CCAATACTAT	CCCCATCTCT	
ATTTTCTCCA GGACGGATCC	TTCTCACTTC	AACCTCCACT	CTCAMMCTMC	CCCGATCTCT	420
TACAGCAGTT GAGGATCTGC	TCCACTIC	TECTIFICATION	GIGATIGITG	GATGTCGTCG	480
CCTTCAATTA CACAATCCCC	TATATOGA	TCCTTCTTCT	ACTGTTATTC	TIGACACAAG	540
CCTTGAATTA GAGAATGGGG TAAAAAGACT CGAG	TATATGCAGT	ACCTCTGCGT	TCTCGTTCTC	TATCTTGCTC	600
INVANAGACI COAG					614

- (2) INFORMATION FOR SEQ ID NO:954:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

GAATTCGGCC	TTCATGGCCT	ACAAGGATTT	CAGGATGTTC	TTCCTCTGGA	CTGCTCTGTT	60
CTGGGGTGGA	GTCATGTTTT	ACTTGCTGCT	CAAGAGATCC	GGGAGAGAAA	TCACTTGGAA	120
GGACTTTGTC	AATAACTATC	TTTCAAAAGG	AGTAGTAGAC	AGATTGGAAG	TCGTCAACAA	180
GCGTTTTGTT	CGAGTGACCT	TTACACCAGG	AAAAACTCCT	GTTGATGGGC	AATACGTTTG	240
GTTTAATATT	GGCAGTGTGG	ACACCTTTGA	ACGGAATCTG	GAAACTTTAC	AGCAGGCGCT	300
CGAG						304
						304

- (2) INFORMATION FOR SEQ ID NO:955:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 242 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

C	BAATTCGGCC	TTCATGGCCT	AGTAGCTATT	AATCTGTGGC	TATGAAATGA	TCAGAAATGC	60
7	TAAGTGAGAT	CAATATTTGT	TTGGAAAAA	AATCTTGGGA	AACAACCCAA	GGGTTTTCGC	120
3	GTTGTTGTT	TTTCTTTTTC	TATTTTTGTN	NACTTAGTCC	TTTAGCTAGT	GGATTTAATT	180
7	TGTTGTGCC	TGCTTCATTT	TGCAATAACA	ATGCAGTAGA	ATTTAAAACT	TGGACGCTCG	240
	\G		*				242

- (2) INFORMATION FOR SEQ ID NO:956:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 293 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

${\tt GCTGCGCTGT}$	ACTTCAGATA	CTTTTTTCGA	GGAACATTTG	TGATTTGTGG	CATAAAGTAA	60
CTGTCTAAAG	GAAATCTTCT	GAGAGGATCT	GGTCATTTTA	TGAAAGGGGC	AATTAAGGGG	120
AAATGGAAGC	AGATCTTTTA	AAGAAGGAGC	ATTTGAAATT	AGCCCAGGAA	TCATGTCCGG	180
CGAGTCCTGC	TCTTTTGTAC	CTGGGCATAA	TAGTCAGCCA	CACAGAGCTA	GAGTTAGTTC	240
AAGAATTGTC	TTTCCTGATC	GTGCTATATT	TTTGGAAACA	CGCCGTACTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:957:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 253 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

GCAAAGAATG	GTAACGTGCT	TATCATGGGA	GTGTTTTGAG	AAACTTAGCC	AAAGCTTCAG	60
CAGAAAAATC	CCCGAGAAAG	ACCAGAGAGT	TCTTCACCAC	AACAATGTTC	CTGCTCATCC	120
CTCTCATCAA	ACAAGGCCAT	TTTGCAAGAG	TTTTGATGGG	AAATCACTAG	GCATCCACCC	180
TACAGTCCTG	GTTTGGCACC	TTCTGACTTT	TTGTTTCCTA	ATCTTAAAAA	AATTTTTCAG	240
GGCAACTCTC						253

- (2) INFORMATION FOR SEQ ID NO:958:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 466 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

CAAACTACAA AAGCTCCTCT AGTCTTCAGC ATGACCCTAA TACAACATCA CCTCCCCGAG	TTCATGGCCT ACAACATCAG CTCCTGTCTG GTTCTCCAGC TGCACGACCT CCTCAGCTCT TCCCCGAGTC TTCTGCTGCA TGACCCTCAA TCTAGAACAT CTGGATGTCC ACCTGAGGG ACCTCAAATT AGAACGTCAG CTCCTCCCAG TGCATGACCC TCAATCTTTA ACATCAGCTC CTCTCCAGGT CTGCAGCTCC AAATACATGA GCAGCTCCTC CCTGAATCTT CAGCTGTACG ACCCTCAAAC GCTCCTGTCT GCACCTCCAG CTGCAGGGCC CTCAAACTAG AATATCAGCT TCTTCAGCTG CACGACCCTC AAACTAGAAC ATCAGCTCCT GTACAGATTT GGCCCTCAAA	60 120 180 240 300 360 420 466
(2) INFORMA	ATION FOR SEQ ID NO:959:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 137 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: CDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:959:	
GGAGCATGTC TTGCTTATGA CAATCTGCAG	CTGTTATTTA TTTAACTTTT CCATTTTCAT TTTTTATTTG GGTAAGATAA TAAGCCTTGG GTGTGGAGAG CCGGTGCATA CAGAGTGGCG AGGCAAGCTT TCTCGAG	60 120 137
(2) INFORMA	TION FOR SEQ ID NO:960:	
(i) :	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:960:	
CATCTGTAAC GCTCCAGTTC TTCCCTCCTG	TTCATGGCCT AGAGCCGCGG CTCATGCGCG GTGCACAGAG GCTTGTTTCA AACAGGAGGA GGCCCAGCCT CGTGATGAGG AATAGCAAGG AGAGAATTCA AAAAGCCTAC AAAATCTGAG ACTGTCATTG CTTTTATAAG GATTCCAGCT GCCAGAAATG TTCAGCCTGG ACTCATTCAG AAAAGATCGG GCCCAGCACA GTGCAAACTT CCCCCACCCC GCCTTCCACC CATGTGTGTC AACCCTACCC CCTCGAG	60 120 180 240 300 317
(2) INFORMA	TION FOR SEQ ID NO:961:	
(i) S	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 470 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:961:	
	TTCATGGCCT ACTCTGCTCA ACCTGCACAT CACCCACCAC AGTCACCAGC ATGCAACTAC AGCACGAATT ACAACGCAA GCCGCATTCT TTCACCCTCA	60

GTTTCTAAAC	CCAGCCTTTT	TGCCTCATTT	TCCTATGGCC	CCAGAAGCAC	TGCTGCAGTT	180
					GCTTGGGGCC	240
AGATTTGGGC						300
CTCCTTGCTT	GAAGACCTAA	AGCAGCAGAT	TCAAACCCAA	CATCACGTTG	GTCAAACTCA	360
ACTCCAGATA	CTACAGCAAC	AAGCACAACA	ATACCAAGCC	ACACAGCCCC	AGCTGCAGCC	420
TCAAAAACAA	CAGCAGCAGC	CACCACCTCC	ACAGCAACAA	CAAGCTCGAG		470

- (2) INFORMATION FOR SEQ ID NO: 962:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 603 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

GAATTCGGCC	TTCATGGCCT	AGGAGAANGA	CGTGCTGGTG	AACGTGAACC	TGGTGGATAA	60
GGAGCGGGCA	GANAAAAATG	TGGAGCTGCG	GAAGAAGAAG	CCTGACTACC	TGCCCTATGC	120
CGAGGACGAG	AGCGTGGACG	ACCTGGCGCA	GCAAAAACCT	CGCTCTATCC	TGTCCAAGTA	180
TGACGAAAAA	CTTGAAGGGG	AGCGGCCACA	TTCCTTCCGC	TTGGAGCAGG	GCGGCACGGC	240
TGATGGCCTG	CGGGAGCGGG	AGCTGGAGGA	GATCCGGGCC	AAGCTGCGGC	TGCAGGCTCA	300
GTCCCTGAGC	ACAGTGGGGC	CCCGGCTGGC	CTCCGAATAC	CTCACGCCTG	AGGAGATGGT	360
GACCTTTAAA	AAGACCAAGC	GGAGGGTGAA	GAAAATCCGC	AAGAAGGAGA	AGGAGGTAGT	420
AGTGCGGGCA	GATGACTTGC	TGCCTCTCGG	GGACCAGACT	CAGGATGGGG	ACTTTGGTTC	480
CAGACTGCGG	${\tt GGACGGGGTC}$	GCCGCCGAGT	GTCCGAAGTG	GAGGAGGAGA	AGGAGCCTGT	540
GCCTCAGCCC	CTGCCGTCGG	ACGACACCCG	AGTGGAGAAC	ATGGACATCA	GCACACTCTC	600
GAG						603

- (2) INFORMATION FOR SEQ ID NO:963:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 415 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

GAATTCGGCC	TTCATGGCCT	ACAACAGCGT	TAGGTTTTTT	TTTTNGTTNG	TTNGTTNGTT	60
TNGTTTTTTT	CCAACCCTCT	TTCGGATGGA	CGGGGAAAGA	GAGAAAGAAA	AANCGAGGGA	120
AAATCNACAA	AATGTGCGAT	GCAAAGAGTC	GATTTTCGCG	GGGTTTGTCA	ACTTCGCCAC	180
TGCCGCACGC	GAATCGACGT	CGTCACGTGA	CGGTCTGCCT	CCGCCCTTAT	TAACTCTCAG	240
CCCAGCGGCG	GTTTCCAGGA	CCTCAGACTT	TTTGCCGAGG	CGGCAGTCCC	TAGACGAAGC	300
GAAGGAGGCG	GCGCCTGCCC	CGCCCACAAG	AGCTGCCGCG	CGCGGGTGTT	ATAGCTCCAC	360
CCCATCTGCA	AAGGAAGGGG	GAGCGGAAAG	AGCGGGATCT	AGCGGGGAAC	TCGAG	415

- (2) INFORMATION FOR SEQ ID NO:964:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 241 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

GAATTCGGCC	TTCATGGCCT	AGCGGGTCTT	CAGACAACTC	CARARCOTOR	GAGAGGAGAT	
G1 GGGGGG1 G			CAGACAAGIG	GAAAAGGIGA	GAGAGGAGAT	60
CAGGGCGCAG	AGCCCCGTGG	AGGCTGAGTT	TCCATATGGG	CAACTGAGCA	CATCCTGCCA	120
CTCCCACCTC	GTGCCTCAGA	ATNGACACCA	GGCTACTCAT	CTGGAGGTGA	CCAAGCAGCC	180
AACCAATCCC	CTCCCCCC			0.000.00107	CCANGCAGCC	190
	GICCCCTGGA	GGTCCTCAAA	TGCCTCCCCA	TACCTTGTTC	CAGACCTCGA	240
G						
						241

- (2) INFORMATION FOR SEQ ID NO: 965:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 485 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

GAATTAATAG CCTGCAGGT	T AATTACTCCC	TGAAGGGTAT	TGTGGAAAAG	TATAACAAGA	60
TCAAGATCTC TCCCAAAAT	G CCAGTATGCA	AAGGACACTT	GGGGCAGCCT	CTCAACATTT	120
TCTGCCTGAC TGATATGCA	G CTGATTTGTG	GGATCTGTGC	TACTCGTGGG	GAGCACACCA	180
AACATGTCTT CTGTTCTAT	T GAAGATGCCT	ATGCTCAGGA	AAGGGATGCC	TTTCACTCCC	240
TCTTCCAGAG CTTTGAGAC	C TGGCGTCGGG	GAGATGCTCT	TTCTCCCTTC	CATACCTTCC	
AAACTAGTAA GAGGAAATC	C CTACAGTTAC	TGACTANAGA	TTCACATAAA	CTCAACCAAM	300
TTTTTGAGAA GTTACAACA	CACACTGGATC	DARACARCA	TCABAIAAA	GIGAAGGAAI	360
AGACCATGAA ACTTGCTGT	r arccaaccar	ATCACCCACA	CAMCALCIG	TCTGACTTTG	420
TCGAG	I MIGCANGCAI	ATGACCCAGA	GATCAACAAA	CTCAACACGC	480
					485

- (2) INFORMATION FOR SEQ ID NO:966:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 330 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GAATTCGGCC	TTCATGGCCT	AACGGCTCCC	TCACTTGTGA	ATTAAAGTCA	GACACTGCCG	60
TAAGGTTCTT	CTGGTTCCTG	CTTTGTGGAG	AAAGCTTTCA	GCAGCAATAT	CTGGGATCAC	120
TGGTGTATTA	AATGTCAGGC	CTCGCATCAT	TATTCTCCCC	TGAGCTGATG	GTAAACCGGG	
CACCCAGCCT	TTTAGCTTTC	ATCCAGCACC	ACCCA ACTOC	COMMONON	TGACACGTAC	180
AAGTCAAAAA	ACCTCACACT	CACCACCACG	AGGGAACTIG	CCTTCAGATG	TGACACGTAC	240
AAACCAAAA	AGCICAGAGI	CAGCICCAAC	GTCTATTGGA	TCCCACTCTA	TCGCCTTTAA	300
AAAGGAAAAG	AAAATCGAAA	CGAACTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:967:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

GAATTCGGCC	TTCATGGCCT	AGGGTCGCAG	ACTCAAATGC	CCACAGGGGC	CAGGTTAGGT	60
TAGCGGCTGA	AGCAGTCTGG	GGAGAGGCAA	AAAGCAATGG	CAGGGAGGTG	GGACAGAGGA	120
ATGTGGGCCC	CAAACTATGG	GGGCAGCTGC	TACTCAGTGC	CAGCTGTTCG	TCGCCATGGG	180
GGGAAGCGGG	ACCAGAGCCG	CCGGGTCTTC	GGCTTTTTCA	AGAGGACGCA	TAACTCCGGA	240
TTGTTATTTG	AACTGTCCTG	ACTTTGGTAA	GACTCTGTGA	CGGTGACAGT	GAAGGAGGCC	300
GACTCATCGT	CAATTTCACA	CAAGTACTCG	CCGGAGTCCT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:968:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 531 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

GAATTCGGCC	TTCATGGCCT	AGGATGCAGC	CGAAAAGGAT	CGCAAGCTTC	AGGAGAAAGA	60
	GAAGAGCTGA					120
GAAAATGCAA	CTTGAGGTTG	AAAAACGAGG	GCAGCAGCAG	CGGCCCCTGG	AAGCCCAGCC	180
CAGTGCCCCA	GGTCATTCTG	TCAAGTCAGA	TCAGAAGCAC	GGCAGCCTTG	GCTCCTCCAT	240
CAAAGATGAG	GCCTCACTCC	CTGACTGCTC	CAGCTCCAGG	CAGCCCATCC	CAGTAGCCAG	300
CCACGCTGTA	GGCCAGCCCG	TCTCTACAGG	TGGCCAGACC	CTTGTTGCCA	AAAAGGCTGT	360
AGTTATCAAG	CAAGAGGTCC	CTGTGGGCCA	GGCAGAGCAG	CAGAGTGTCG	TCTCGCAGTT	420
TTATGTGAGT	TCCCAGGGAC	AGCCACCGCC	TGCTGTTGTT	GCTCAGCCCC	AGGCTTTACT	480
GACCACGCAG	ACTGCTCAGC	TGCTGCTCCC	AGTGTCCATC	CAGGGCTCGA	G	531

- (2) INFORMATION FOR SEQ ID NO:969:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 388 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

GTGCCTCGAG	AAACTGCCTA	TTCAGAAACA	CAGAAACACC	GAGACCTCAA	AATCCCCTGA	60
GAAGGACGTT	CCCATGGTAG	AAAAGAAGAG	CAAGAAACCC	AAGAAGAAAG	AGAAAAAACA	120
CAAAGAGAAA	GAGAGAGACA	AGGAGAAGAA	GAAGGAGAAG	GAGAAGAAGG	CTGAGGACCT	180
GGACTTCTGG	CTGTCTACCA	CCCCACCGCC	TGCCCCCGCC	CCCGCCCCCG	CCCCCGTTCC	240
ATCCACGGGG	GAGCTCAGTG	TGAACACTGT	CACTACCCCG	AAGGACGAGT	GTGAGGACGC	300
CAAGACGGAG	GCGCAGGGCG	AGGAGGACGA	TGCCGAGGGG	CAAGACCAGG	ACAAGAAATC	360
TCCCAAGCCT	AAGAACAAGA	AGCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:970:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 365 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GAATTCGGCC	TTCATGGCCT	AGCTTACACT	GGGCCAAGTG	CTTGCCAAGG	ATTCTCATGT	60
GACATTTCTT	TCAGTCCTGC	CGAGGACTTT	ATGAGGGAAG	CACCCTGTTT	TACAGAGGGA	120
AGGGGGCCTA	TGGGGTCTAC	AGCAGTGAGA	GCCTAGAGTT	CAGTCTGCGT	CTCTCTGATT	180
CCAAAGCCTG	TGATTGTGAC	TTCCATACTC	TCCCTAAGAC	ACATTCATAC	ATTCAACTCA	240
ATATTTATTG	AGCACCTACT	GTGTGCTAGG	GATAGAGCAG	TAAATGAATC	ACCCANANA	300
TATTTACATT	CCACTGGGGC	TGACAAACCC	AAACAAGGAA	GAGGTGTAGT	CCTTCCCCCTC	360
TCGAG				CAUGIGIAGI	GCTTCGGGTC	365

- (2) INFORMATION FOR SEQ ID NO:971:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 332 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

GCAAAAGTAA TATGATTTGT	TTAAAATACT	CAGTCAACAG	GTATTTCCTG	AAAATATTTT	60
CCATAGAAAG TAGAATATGG	TTCTCCCGAA	TAAAAACTGA	TCCATTTTAC		120
CCCTTTTGTT TNNGGTATTT	<b>ԱՎԻՆԻ ԱՎԻՐԻՐԻ</b>	The state of the s	COMMENTAL	CITITICITI	
CAGCCAAAGG CTTCTATGAT	CTTCATCCTT	TARACTANA	COMMON	TTTAACTTTC	180
GCCAGTTGGT TCCCTCTAAT	CTTOATGCTT	IMMATGAAGC	IGCITGGACA	AGTGCCCACA	240
GCCAGTTGGT TCCCTGTAAT	GITIGIGGC	GTACCTTCCT	GCCAGACAGA	CTGATTGTTC	300
ACCAACGATC TTGTAAACCC	AAAGCTCTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:972:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 273 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

GCGCCCTCA	CCCTCCAATC	CCCCCTCTGA	CCCCCTCTTC	CTCACATGGG	GTCGGGGGCC	60
TGGGAGTTC	TTCTGGACCA	GCCCACCTAT	CTCCATTTCC	TTTTATACAC	ACTTTCACAC	120
TTGCCATCAC	CACAGCACAC	AGCAGCAGCG	TTTCCCTTTTCC	TTTTATACAG	ACTITICAGAC	
TOTOLOGO	· ATTCCCCCTCT	CCCALLOCACCC	TICCCCTGAG	GCCGGTGGGG	AGGGGACAAG	180
TOTCAGCAGG	ATTGGCGTGT	GGGAAAGCTC	TTGAGCTGGG	CACTGGCCCC	CCGGACGAGG	240
TGGCTGTGTC	TTCACACACA	CACACACCTC	GAG			273

- (2) INFORMATION FOR SEQ ID NO:973:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 274 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

GAATTCGGCC TTCATGGCCT ACTCTGTCTC AAAAAAAAAT AGTAAGTTGT GTAAAGAAA ATATTAATTA TATAATATGG CAGTTCCTAT GAGAGTGTGG CAAAAATCAA GAGGGCTTGG AAGTTTTTTC TTTGCTCTTG CAACTGGCTG GATGCAGTTC ATATATTTTT CAACCAGTAG GGCTTGGGCA AGCCTAATTT TTTGCAGTTG TAACCTGGTG GCAGAAGGGG CAGGACTGAGGCTGGCCAGAGGGCA AGACTGTTAT GCCAAGTTCT CGAG	G 120
(2) INFORMATION FOR SEQ ID NO:974:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 145 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:	
GAATTCGGCC TTCATGGCCT AGTGAGATAG TACCAGATTT AGAATATAAT TTTATCTTTCTTTCTTTAGCAACA AGCCCTAACA ATATCCAAAC TAAATAAAAT CATTACATGA ATTTACTTTTTACAATCATT CTCCTAAGGC TCGAG	
(2) INFORMATION FOR SEQ ID NO:975:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 242 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:	
GAATTCGGCC TTCATGGCCT AGGAAATAAC AGTTATTTCA TCATAAAACA GTCCCTTCA ACACACAATT GTTCTGCTGA AGAGTTGTCA TCAACAATCC AATGCTCACC TATTCAGTTC CTCTGTGGTC AGTGTGGCTG CATAGCAGTG GATTCCATGA AAGGAGTCAT TTTAGTGATC AGCTGCCAGT CCATTCCCAG GCCAGGCTGT CGCTGGCCAT CCATTCAGTC GATCATCTCAGC	G 120
(2) INFORMATION FOR SEQ ID NO:976:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 116 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:	
CATGTGCACA CTCGCACATG CACATATGGG CACGTGGGAA GACGGGAGAA GTACTGTCA AGTATAAGGA ACTGCAGAGG TTGGGATTTA CTGGAAGGGA AGGGAGCACA CTCGAG	A 60
(2) INFORMATION FOR SEQ ID NO:977:	

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<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 461 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:	
GAATTCGGCC TTCATGGCCT AGCATGGCAA CAGATATGTG GAGCATTGGA GTGTTAACAT ATGTCATGCT TACAGGAATA TCACCTTTCT TAGGCAATGA TAAACAAGAA ACATTCTTAA ACATCTCACA GATGAATTTA AGTTATTCTG AGGAAGAATT TGATGTTTTG TCTGAGTCGG CTGTTGATTT CATCAGGACA CTTTTAGTTA AGAAACCTGA AGATCGAGCC ACTGCTGAAG AATGTCTAAA GCACCCCTGG TTGACACAGA GCAGTATTCA AGAGCCTTCT TTCAGGATGG AAAAGGCACT AGAAGAAGCA AATGCCCTCC AAGAAGGTCA TTCTGTGCCT GAAATTAATT CGGATACCGA CAAATCAGAA ACCGAGGAAT CCATTGTAAC CGAAGAGTTA ATTGTAGTTA CTTCATATAC TCTAGGACAA TGCAGACAGT CAGAACTCGA G	60 120 180 240 300 360 420 461
(2) INFORMATION FOR SEQ ID NO:978:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 108 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:	
GAATTCGGCC AAAGAGGCCT AATGATGATG AATAAGTTGG TTCTAGCGCA GTTTTTTTT TTTCTTGTCT ATAAAGCATT TAACCCCCCT GTACACAACT CACTCGAG  (2) INFORMATION FOR SEQ ID NO:979:	60 108
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 505 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:	
GATGGCGTCG GGCAGCGGGA CAAAAAACTT GGACTTTCGC CGAAAGTGGG ACAAAGATGA ATATGAGAAA ATATGAGAAA CTCCCCGAGA AGAGGCTCAC GGAAGAGAGA GAAAAGAAAG ATGGAAAACC AGTGCAGCCT GTCAAGCGAG AGCTTTTACG GCATAGGGAC TACAAGGTGG ACTTGGAATC CAAGCTTGGG AAGACAATTG TCATTACCAA GACAACCCCT CAATCTGAGA TGGGAGGATA TTACTGCAAT GTCTGTGACT GTGTGGTGAA GGACTCCATC AACTTTCTGG ATCACATTAA TGGAAAGAAA ACCTGGGCAT GTCTATGCGT GTGGAACGTT CCACCCTGGA TCAGGTGAAG AAACGTTTTG AGGTCAACAA GAAGAAGATG GAAGAGAAGC AGAAGGATTA TGATTTTGAG GAAAGGATGA AGGACCTCAG AGAAGAGAGG GAAAAGGCCA AAGCGTACAA GAAAGAGAAAA CAGAAGGAGC TCGAG	60 120 180 240 300 360 420 480 505
(2) INFORMATION FOR SEQ ID NO:980:	
(i) SEQUENCE CHARACTERISTICS:	

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- (A) LENGTH: 314 base pairs(B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

CGAGGGACAT	GAGGCTGAGC	TGGTTCCAGG	TCCTGACAGT	ACTGTCCATC	TGCCTGAGCG	60
CCGTGGCCAC	GGCCACGGGG	GCCGAGGGCA	AAAGGAAGCT	GCAGATCGGG	GTCAAGAAGC	120
GGGTGGACCA	CTGTCCCATC	AAATCGCGCA	AAGGGGATNT	CCTGCACATG	CACTACACGG	180
GGAAGCTGGA	AGATGGGACA	GAGTTTGACA	GCAGCCTGCC	CCAGAACCAG	CCCTTTGTCT	240
TCTCCCTTGG	CACAGGCCAG	GTCATCAAGG	GCTGGGACCA	GGGGCTGCTG	GGGATGTGTG	300
AGGGGGACCT	CGAG					314

- (2) INFORMATION FCR SEQ ID NO:981:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 379 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

GAATTCGGGC	TTCATGGGNT	ACTCATTGCT	ACATTGCTAG	TTGACCCGCA	GTTATATTTC	60
CTTTTTTTCT	TTTTAATAAA	AGGCAAGAGA	AACAATCCGT	TTTTGCCTTT	TCCTACCACA	120
TCTTTGACTT	TTCTGATTCC	TGCAAGTTTA	AGTTAAAAAC	ATCCTACCTT	CAAGCTACAA	180
AATGCAGCAC	ATCCCAGGAC	ATCCCTCACC	TGCTTTGCTT	GTTTATTAGA	CACAAGTGGC	240
TTTGTTCAGA	AAGTTACTGG	GAACCGCTAA	GGATAGTCAA	GGTGGAGAAC	ACAGGGTGGG	300
GTCTCAGAGT	CTGAGGCCTT	GGTTCAGGTT	CCTGATAACA	TTAAATATAG	AAAATACACA	360
GCACAAGGCC	AAACTCGAG					379

- (2) INFORMATION FOR SEQ ID NO:982:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 362 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

GAATTCGGCC	TTCATGGCCT	AGAAGATGGT	AAGGTTCGAA	TCTTTCGGGT	GATGGGAGTT	60
AAGTGTGAAC	AGGAACTGGG	ATTTAAGGGC	CACACTTCAG	GGGTATCCCA	GGTCTGCTTT	120
CTCCCAGAAT	CCTATTTGCT	GCTTACTGGA	GGGAATGATG	GGAAGATCAC	GTTGTGGGAT	180
GCAAACAGTG	AAGTTGAGAA	AAAACAGAAG	AGTCCCACAA	AACGTACCCA	CAGGAAGAAA	240
CCTAAAAGAG	GAACTTGCAC	CAAGCAGGGT	GGAAATACTA	ACGCTTCAGT	AACAGATGAG	300
GAAGAACATG	GCAACATTTT	ACCAAAGCTA	AATATTGAAC	ATGGAGAAAA	AGTGAACTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:983:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 574 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

GAATTCGGCC	TTCATGGCCT	AGGCCACTGA	TATTTTTCTA	AGTTAGCAAG	GCTCACTTGC	60
TTGCTTTCTT	GCCTCCCTTG	CCTCCATCCC	TCTCCCTTCC	TACCTTCTCT	ATTTACCTAT	120
TTCTCTCCCT	CCCTCTCTTC	TCCTCTCTTT	TTTTTTCCCC	CGCATATGCA	GCTTTTTGAT	180
TGTACTTGAT	TTTATAGAGA	CTGCACAGTT	CCAGCAAGAT	TGGGAGTCAG	GCATGGAGCA	240
GGCATCTCAG	GCTACCAGAA	AGAATTGGTC	ACCTAGACTT	TCAGTCAGGC	ATCCTCGTTT	300
GCATTGTCCT	GTAAGTCAAT	TAGTTGATAA	ATAGTTCCCC	CTTCATCCCT	TAAGTTTTGT	360
TTTTGTTTTT	GTTTTTAATA	TAGGTAAGTG	GGACTCTACC	TAAAATTTTG	CATCATACTT	420
ATGGGTAATA	TCTTTTTCAT	ATATTATTTA	TCAAAGTATG	AAGTTGAGTA	TTTTGCTTGT	480
ACCATTTCAA	TTCTGCATTA	TAGTAGTTCA	TTGTATAACT	GAAAGAAATG	ATTTCTTCAT	540
AAGTGACATT	AAATATGAAC	ATTCATCTCT	CGAG			574

- (2) INFORMATION FOR SEQ ID NO:984:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 274 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

TTCATGGCCT	ACGATTGAAT	TCTAGACCTG	CCCCCTCCCT	CCATGCCTCA	60
CCTCCAGTCA	TGCCGCAGCA	GGTTAATTAT	CAGTACCCTC	CGGGCTATTC	120
TTCCCACCTC	CCAGTTTTAA	TAGTTTCCAG	AACAACCCTA	GTTCTTTCCT	180
AATAACAGCA	GTAGTCCTCA	TTTCAGACAT	CTCCCTCCAT	ACCCACTCCC	240
AGTGAGAGAA	AGTCCCCACT	CGAG			274
	CCTCCAGTCA TTCCCACCTC AATAACAGCA	CCTCCAGTCA TGCCGCAGCA TTCCCACCTC CCAGTTTTAA AATAACAGCA GTAGTCCTCA	CCTCCAGTCA TGCCGCAGCA GGTTAATTAT TTCCCACCTC CCAGTTTTAA TAGTTTCCAG	CCTCCAGTCA TGCCGCAGCA GGTTAATTAT CAGTACCCTC TTCCCACCTC CCAGTTTTAA TAGTTTCCAG AACAACCCTA AATAACAGCA GTAGTCCTCA TTTCAGACAT CTCCCTCCAT	TICATGGCCT ACGATTGAAT TCTAGACCTG CCCCCTCCCT CCATGCCTCA CCTCCAGTCA TGCCGCAGCA GGTTAATTAT CAGTACCCTC CGGGCTATTC TTCCCACCTC CCAGTTTTAA TAGTTTCCAG AACAACCCTA GTTCTTTCCT AATAACAGCA GTAGTCCTCA TTTCAGACAT CTCCCTCCAT ACCCACTCCC AGTGAGAGAA AGTCCCCACT CGAG

- (2) INFORMATION FOR SEQ ID NO:985:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 366 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

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GAATTCGGCC	TTCATGGCCT	AGATAAGGAG	ACTTCAGAAG	AGAAGCCGCC	AGCTGAGGGA	60
AGTGAGGACC	CTAAGAAGCC	ACCCCGCCCT	CAGGAGGGAA	CAAGATCTAG	CCAGCGAGAT	120
CAGATACTCT	ATCTCTTTGG	GAGAACTGGC	CGAGAAAAAG	AGGAATGGTT	TAGGAGATTT	180
ATTCTGGCAT	CTAAGCTAAA	GTCGGAAATC	AAGAAGTCAT	CGGGTGTCTC	TGGAGGTAAA	240
CCAGGGCTTT	TGCCTGCACA	CAGCAGACAC	AACAGTCCGT	CCGGGCACCT	GACCCACAGC	300
CGCAGCAGCA	GCAAAGGCAG	TGTGGAGGAG	ATCATGTCAC	AGCCAAAGCA	GAGGGAGCTA	360
CTCGAG						366

(2) INFORMATION FOR SEQ ID NO:986:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 451 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GAATTCGGCC	TTCATGGCCT	ACTCTCTTCC	AACCAAAAGT	CTTAATATGG	GAATATCCCT	60
CACCACGATC	CTAATACTGT	CAGTAGCTGT	CCTGCTGTCC	ACAGCAGCCC	CTCCGAGCTG	120
CCGTGAGTGT	TATCAGTCTT	TGCACTACAG	AGGGGAGATG	CAACAATACT	TTACTTACCA	180
TACTCATATA	GAAAGATCCT	GTTATGGAAA	CTTAATCGAG	GAATGTGTTG	AATCAGGAAA	240
GAGTTATTAT	AAAGTAAAGA	ATCTAGGAGT	ATGTGGCAGT	CGTAATGGGG	CTATTTGCCC	300
CAGAGGGAAG	CAGTGGCTTT	GCTTCACCAA	AATTGGACAA	TGGGGAGTAA	ACACTCAGGT	360
GCTTGAGGAC	ATAAAGAGAG	AACAGATTAT	AGCCAAAGCC	AAAGCCTCAA	AACCAACAAC	420
TCCCCCTGAA	AATCGCCCGC	AGCATCTCGA	G			451

- (2) INFORMATION FOR SEQ ID NO:987:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 334 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

GAATTCGGCC	TTCATGGCCT	AGAGAAACTG	AGCAAAAATA	GCTGCCAAGA	GAAGAGGGAA	60
CGAGTGCTCG	GGGCGGGTTG	GAGGCAGATA	ACGAGAAGGC	AAGAAAATTC	TTTGTCTTTG	120
GCTCCTGCTG	TCAGCTCAGA	GGGGTCATCT	TGAGATGAAA	AAGAAAAGTC	CCCAGCCTTG	180
GGGAAGGAAA	GGAGAGGGTG	CCCCACGCAG	ATATGAAGCA	AAGCCATTGG	CAAGATATTC	240
TCTCTAAGGA	GAGCAGCGGT	CTTGCCAAAG	GCATCTTCTA	TTGTGTATTG	CCGTCATAAA	300
CCCTACCCTT	CCATGTAGAT	AGCCAGGACT	CGAG			334

- (2) INFORMATION FOR SEQ ID NO:988:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 509 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

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	GAATTCGGCC	TTCATGGCCT	AAGAGAAACA	AAAATGATTT	TGCTTTCCAA	GCTTGGTTTG	60
	${\tt TGGCGTCTCC}$	CTCGCAGAGC	CCTTCTCGTT	TCTTTTTTAA	ACTAATCACC	ATATTGTAAA	120
	TTTCAGGGTT	TTTTTTTTTG	TTTAAGCTGA	CTCTTTGCTC	TAATTTTGGA	AAAAAAGAAA	180
•	TGTGAAGGGT	CAACTCCAAC	GTATGTGGTT	ATCTGTGAAA	GTTGCACAGC	GTGGCTTTTC	240
	CTAAACTGGT	GTTTTTCCCC	CGCATTTGGT	GGATTTTTAT	TATTATTCAA	AAACAAAATG	300
	AAAAGGTTAT	TTACTTTTTT	TTTCCTGAAA	TGCTGACAAT	ATGTGATATC	TTAATATCTG	360
	TAATTCTTAG	TGAAAGTTAT	GGTATAGTAT	AGGTGAAGCT	GTAGTGTTTA	TATCAATAGA	420
	TGTGAATTCA	AATGAGCAAT	CTAATAATTA	TTTACTATTC	AATTATGTTA	ATTTTCTTCT	480
	CTTTGTCTCC	CATTGTATCT	GCACTCGAG				509

- (2) INFORMATION FOR SEQ ID NO:989:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 409 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

GAATTCGGCC	TTCATGGCCT	AGGCTTGTGG	GCAGGGCCCG	TGCAGGTCAT	GGAGCCGGTA	60
GCATCTCAGA						120
CCCTGCACAG						180
TGCCACCCGG						240
GCAAAGCTGA						300
GAGTGAGACA					TTTTACAGCC	360
CCGAGAAATT	GCTCACTAAT	AGCCAGACAG	ATGCTCCCCC	TGCCTCGAG		409

- (2) INFORMATION FOR SEQ ID NO:990:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 210 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

GAATTCGGCC	CATGGCCTA	CCCAAATCTG	AAGTCTTTGG	ATATGTTACT	GCTGAAGTTT	60
CTATCACTTC T	<b>ICACTCCTGG</b>	TTCCTTGTTT	CCCTGTATGC	TTTTTTTTT	TTTCCATGAG	120
TTCACTTTTT T	<b>FAAATTATAG</b>	TTCTTCAAGG	CCTAGGATGC	AGGTGTGTTC	TTCCATAAAG	180
GGCTATTTTG (	CCTCTGCCGA	GGTCCTCGAG				210

- (2) INFORMATION FOR SEQ ID NO:991:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 447 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

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${\tt GAATTCGGCC}$	TTCATGGCCT	AGTAGATAGT	ACAAAATTCA	ACAGATATCA	AAGTGTGTTA	60
AGTTTACCTT						120
ACGTATATTC						180
TACACAAATG						240
GTCGTGATGA						300
GTAGAATTGC	TAGAACAAAG	ATTTATGCAT	TTTAAATATT	CCTTTATTAT	AAAACTAATG	360
AAAGTAAACA	TGTTGGCTAT	GACCACGTAT	GCTCTATGCT	CAGTTTTTCT	AGAGTTGTGT	420
ATGCTTAATA	TAGGAGCCTG	CCTCGAG				447

(2) INFORMATION FOR SEQ ID NO:992:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 303 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

GAATTCGGCC	TTCATGGCCT	AGCCCATTGT	TGTTTATTTT	GAATTAATTT	CAAGCTTACA	60
GAAGAATTAT	AAGAATTATA	CAAAGAGCCC	TTGTATAGCC	TTCATCCAGA	TTCCTCATTA	120
ATAGTTATCT	CCCCCACACA	CGTAATGCAC	AGACACTGCA	TGCATTTTCC	TTTTCTTTTT	180
TCTCTTCTTT	CTTTTTCTTT	TTCTCTCTTT	CCCTTTCTCT	TCTCCCTCCC	CTCCCCACCC	240
$\mathtt{CTCCCCTCCC}$	TTCCTCTCCC	TTCCCCTCCT	CCTACTTCAG	CCTCTAGAAT	AACTAGACTC	300
GAG						303

- (2) INFORMATION FOR SEQ ID NO:993:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 359 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

GAATTCGGCC TTCATGGCCT	AGGATTTGGT	AGGGTAACTT	GAAAACTGAG	TTAAATGAGA	60
AAGGTAGAAA AAATTCGTAC	TTTTTCTCCT	CCCCACAAAA	AATAAAAACA	GTAAAATCTT	120
TACCAACTGA AAAAGCTGTT	GAAATTTTCT	GTATGTTAAA	AAAATGAGCT	TTGCAGTAAC	180
TCTTAAAATC ACCTAGCAAA	ATAGGAACTA	TAATGTGCAT	CTTTCCTTCA	CTAAAACATT	240
TATTGCATCT CTTCTTGATG	CTGATGATTG	AGGACACACA	TTCTGCTTTC	CTGGGGCTTA	300
TGGTTTTATA TAAAAACCAA	AGCAAAGTAG	AAAGTATACC	TCCTACCAAG	GGGCTCGAG	359

- (2) INFORMATION FOR SEQ ID NO:994:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 406 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

GAATTCGGCC	TTCGGCCTTC	ATGGCCTAGA	GGAGGACCAA	GGCTTCAAAG	GCCCCTGCCC	60
GCGCGTCCTG	CAGGTTCCCA	TTGTCCGTGT	TAATAGCCTC	AGATGGGCAT	CAGTTGCCCT	120
GATGGGCTTG	GGCTCCACGC	CCGGGCTTGC	ATGTTTGGCA	AAATTACTCA	AGAGCATTTC	180
TTTTTTTTT	CTTTGAGACT	CCGTCTCAAA	АААААААА	AAAGAGATCC	TCAGCTGTTG	240
TTTCTTGAAT	CAGATATTTG	GATCACTCTA	GCATCCAATC	ATGCAGCTCC	TAAATATGCT	300
CCTAAATCAT	GCAGGTCCAA	TCACGCACCT	GTTTTACGGT	TTATCAATTT	GTGCTCATCC	360
TGAACTAAAT	AAACAAATCC	ATGAGCCAAC	TGCAGCACCA	CTCGAG		406

- (2) INFORMATION FOR SEQ ID NO:995:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (=) Idio2001. Illica

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

GAATTCGGCC	TTCATGGCCT	ACCATCTTGG	AACCTCCTCC	CATGATTGCC	TTATTATTTT	60
AAATACATTA	ATGTAGATCA	ATGAAGAATA	AGAAAATAAG	CAATTTTATT	TTACCTTAAT	120
TTATTCTGTT	TCTGATGCTC	TTTGTCTCTC	TATGTAGGTC	TGACTTTTTG	ACCTACATTA	180
TTTTCTTTCC	CTCCTAGGAA	TTTTTAAAAG	CATTTCTTGT	AAGGCAGGGC	TACTGAAAAC	240
AAATTTCCTC	AATATTTGCT	TGTCTACAAA	AGTCTTTATT	TCTCCTTTAC	CTTTTAAGGG	300
AAATTTCACA	ACCTACAGAA	TTCTAGGTTG	GTGGGTTTTT	TCCCCCTCAA	TCCCTTAAGT	360
ATTTAATTCC	TCTCTTCTTG	CTTGCATGGT	TTGTAAGGAA	GAGTCAGATG	TAATTTTTAT	420
CTTTGCTTCT	GTATGGGTAG	GGTGCTTTTT	CTTCTAGATT	TTTTTTCCAG	AGTTTTTTC	480
TTTATCTTTG	ATTTTCTGTA	CTTCAAATAT	ATTATGCCCA	GGTATAGATT	GTTTTTTGTT	540
	TTTCATTTGG	CATTTGTTCT	GCTTGGTGTT	CTCTGAGCTT	CCCGGATCTC	600
GAG						603

- (2) INFORMATION FOR SEQ ID NO:996:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 461 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

				CTCACATTCT		60
TAAAAAAAT	CATATCAGAT	GGTGATGAGC	TTTTCGGTTT	TCTATTTCTA	TTTATGAAGA	120
ATAAAATAAG	GTAATAGAGA	TAATGTGATG	AAAATTCTAA	CATTCTCTAC	CTTTCCTGAA	180
TTCTTAATCT	ATACCTTCTG	TTCTTACATT	TTCTACTTAA	TTTTATTTAA	TACAACTTGT	240
AGCTAAACTT	TTATTTTTCT	TTCACTCCTG	ATTCTTAACC	CCTATCCATG	CTAATTTTTG	300
CCTTCACTAT	TCCACAAAAC	TTACCCACTG	TCGTATTATT	ATCTTCTATT	AAAAGCCAGT	360
ATTCTCTTTT	CAGTTTTTAT	CCTTCTTGAT	CTACACTGAA	CATGATTGCC	TTTCTCTCTC	420
TTATATCACT	TGCTGCTATC	TGCAGTCCAA	CTAGCCTCGA	G		461

- (2) INFORMATION FOR SEQ ID NO:997:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 470 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEO ID NO:997:

GAATTCGGCC	TTCATGGCCT	AGTGATTTGG	GTACAGACAC	AGCCAAACCA	TATCATTACA	60
GATATAAATC	TCTGAGTAAA	TCCGGTGTTT	GATTTCTTCT	AGCTTTTTAG	CTTATGAGTA	120
GAGGTCTTTC	TCCTCTACTC	CAAGAATTTT	CATAGACACA	CCACTTAGTA	CTTACGTTTA	180
CCACCATTGT	TATTATTTT	AAGAATGTAC	TACTTTATAT	TTTTAAACAT	GAAGGACTAG	240
CTCAAAATTT	TGTAGCTTCC	CCCCCCCCCC	CAATCTTTTT	TTTTTTTTTG	ACTCCTTTGT	300

TACATAATTC AGCCTATGAA CATGTATCTG GCAAGAGAAA TTCCTGATCT GTGGTTCGGC 4	60 20 70
(2) INFORMATION FOR SEQ ID NO:998:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 350 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:	
TAACTGTCGG TTTTTACCTG CATTCCTAGG TGCTAAAACT TACAAGTGTA TCTCTTGAAC  ACAGGCATTG ATCCTCTACC AATGAATAAT TGAGAGAGGT AGGAATGACT GATTTTCTA  GTTGTAGTTT GAAAGATTAA TTTGATGAAT TGGAAAGTAT GGAAACTATT CTGTTACTAT  TGCAAAGAAA GATTTATTTT TTTAAAAAAAT TTATTTTTAT TTATTTTTATT TTATTTTTT	60 20 80 40 00 50
(2) INFORMATION FOR SEQ ID NO:999:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 266 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:	
TGTTTATTCA GAATCTCCTG TGGGAAAAGA ATGTGAGAAA CAAGGACAAT CACTGCATGG 1 AGGTCATAAG GCTGAAGGGA TTGGTGTCAA TCAAAGACAA ATCACAACAA GTGATTGTCC 1 AGGGTGTCCA TGAGCTCTAT GATCTGGAGG AGACTCCAGT GAGCTGGAAG GATGACACTG 2	60 .20 .80 .40
(2) INFORMATION FOR SEQ ID NO:1000:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 309 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:	
GAGCTGGAGG TGGAGTGCAT GGAAGAGCCT AATCACCTTG ATGTGGACCT GGAGACCCGG 1 ATCCCTGTCA TCAATAAGGT GGATGGTACT TTGCTGGTGG GTGAGGATGC CCCTCGCCGG 1 GCTGAACTGG AGATGTGGTT ACAGGGTCAT CCAGAGTTTG CTGTTGATCC CCGATTTCTA 2 GCGTATATGG AGGATCGCAG AAAACAGAAG TGGCAAAGAT GTAAAAAAAA TAATAAGGCA 3	60 120 180 240

GGACTCGAG

- (2) INFORMATION FOR SEQ ID NO:1001:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 306 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

CACGTCAGGA	GAATAGAATG	GAAAATTTTT	ATTTCAACAG	AAAGAAGTTA	ATTTAGAAAA	60
TTAGTTTAAA	ATACATTTGA	AAACTTAAAG	AGCAAAAAGC	ATTTGTAAAC	AAACAAAAA	120
TAAACCAAAA	AAACCCTGAT	GAGGTTACTA	CTAATAGTAA	CTGTAGGAGG	CATCTACCTC	180
CCTAGATTGG	GGAAAGAAGT	AGTGGTTGAA	TTATCAGAAC	CTAGAAGCAC	AGAACAGGGG	240
CCCCTCAGAA	TGTGTTCTCA	GACTCCTGAG	GGAAGGATGC	TACCCAGCTA	CAGCTGGTTC	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:1002:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 541 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

GAATTCGGCC TTCATGGCCT	ACACCCTGCT	AATTTTTGTA	TTTTTTTTTG	TAAAGGCTGG	60
GTCTCACTAT GTTGCCCAGG					120
GGGTTCAAGC AATCCTGCCT	CGGCCTCCCA	AAGGGCTGGG	ATTACATGCA	TGAGCCATCA	180
CATCTGGCCC CCACCCATCT	TAAAAGTCAG	AAATAAAAGC	CAGAGCCCCT	CCTTGACCTC	240
CTGGCCCCCT CCGCTTTATC	ACCCCACCTC	TCTGCCTGTC	TTTATTGCAA	AACCCCCAGA	300
AGGTTATCAG GCTCATGGTC	TTCCCTCCTG	TCCACACTGC	CCCAACTACA	CAATGAGATG	360
CCCCCATTCC AACTCCCCAG	CCTCCTCTGC	TGGCGTCTCC	TCCTTCCTAA	TCTCTGAACA	420
TTGTCCCATC CAAGGGCTCA	GTCCCAGGTC	CGTTCACCCC	TTGTCCACAC	TCACCCTGAG	480
AGCTTCCAGT CTGTGGCCTC	CATGCCCTGG	AATGAGCCCC	TGTAAGATCC	ACAATCTCGA	540
G					541

- (2) INFORMATION FOR SEQ ID NO:1003:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 602 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

GAAACGCCTC	CTGATTTTGT	CTTACAATGG	AACTTAAAAA	GTCGCCTGAC	GGTGGATGGG	60
GCTGGGTGAT	TGTGTTTGTC	TCCTTCCTTA	CTCAGTTTTT	GTGTTACGGA	TCCCCACTAG	120
CTGTTGGAGT	CCTGTACATA	GAATGGCTGG	ATGCCTTTGG	TGAAGGAAAA	GGAAAAACAG	180
CCTGGGTTGG	ATCCCTGGCA	AGTGGAGTTG	GCTTGCTTGC	AAGTCCTGTC	TGCAGTCTCT	240
GTGTCTCATC	TTTTGGAGCA	AGACCTGTCA	CAATCTTCAG	TGGCTTCATG	GTGGCTGGAG	300

GCCTGATGTT GAGCAGTTTT GCTCCCAATA TCTACTTTCT GTTTTTTCC TATGGCATTG TTGTAGGTCT TGGATGTGGT TTATTATACA CTGCAACAGT GACCATTACG TGCCAGTATT TTGACGATCG CCGAGGCCTA GCGCTTGGCC TGATTTCAAC AGGTTCAAGC GTTGGCCTTT TCATATATGC TGCTCTGCAG AGGATGCTGG TTGAGTTCTA TGGACTGGAT GGATGCTTGC TGATTGTGGG TGCTTTAGCT TTAAATATAT TAGCCTGTGG CAGTCTGATG CGACCCCTCG AG	360 420 480 540 600
(2) INFORMATION FOR SEQ ID NO:1004:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 378 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:	
GCGGCAATGA TACCCACTGC CAACCAACAA AAATTGGCTG CAACCATCCC CTACCAGGAC CGAGCCCTA CAGGTGAGC GCTCTGCCAG GCCCTGGCTC CTGCCCGCAT GCACCCAAGC CGGAGCCTGG GGCAGCTCCT ACGAGGCTCA CCAGGGCCCC AGCAGGATGC CTGGGTCCCC TGCTCCTGCT TGGCCAAAGG GAAGAGGAAG CAGCAGGCAG GGGCTGGGGA GGCCTTCATG AATTACATGA ATTATCCTTC TTTTTTTTT TTTCCCCTTT TTTTTTTT	60 120 180 240 300 360 378
(2) INFORMATION FOR SEQ ID NO:1005:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 208 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:	
GAATTCGGCC TTCATGGCCT ACTGTTTTAT TTCCCGCTTT TATTTTGCTT TTGAAATCTT TTTCCTTGGT GGATTTGTAC GTGTCTTCAC TAGATGCCTC AAATTAAGTC TGACCACAAT CCTACTCTAC TTTCTACAGT GGAGAGACCA TCCTCCCTGC CCCAGGGCTG TCTCCACCCA CCCCCCCTTC CCCACCCGCA CCCTCGAG	60 120 180 208
(2) INFORMATION FOR SEQ ID NO:1006:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 396 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	

60 120 180

CTGATCTGTG AACCTTACAC GAGCAAGGAA TTATTCCGGG TTTTGGATAC ACCCTACTTA
CTAAATGAAG ACTGGGAATA CTATCTCTCT GGGAAGCTAT TTAATAAATC AAAAATGAAG
CTCACTTTTG AACAAGTTTA CAGTGACTGC AAAAAAAATA GAGGCACTTA CGGCACTCTT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

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CACCTGCAGA ACAGCTTCAA TATCAGTGAA CATCTCAACA TTAATGAGCA TACTGGAAGC ATAAGCAGTG AATTGGAAAG TCTGAAGGTA AATCTTAATA TCTTTCTGTT GGGTGCAGCA GGAAGAAAAA ACCTTCAGGA TTTTGCTGCT TGTGGAATAG ACAGAATGAA TTATGACAGC TACTTGGCTC AGACTGGTAA ATCCCCCGGCT CTCGAG	240 300 360 396
(2) INFORMATION FOR SEQ ID NO:1007:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 290 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:	
GAATTCGGCC TTCATGGCCT AGATGGGGGC TAGTTTTTGT CATGTGAGAA GAAGCAGGCC GGATGTCAGA GGGGTGCCTT GGGTAACCTC TGGGACTCAG AAGTGAAAGG GGGCTATTCC TAGTTTTATT GCTATAGCCA TTATGATTAT TAATGATGAG TATTGATTGG TAGTATTGGT TATGGTTCAT TGCCGGAGA GTATATTGTT GAAGAGGATA GCTATTAGAA GGATTATGGA TGCGGTTGCT TGCGTGAGGA AATACTTGAT GGCAGCTTCT GTAGCTCGAG	60 120 180 240 290
(2) INFORMATION FOR SEQ ID NO:1008:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 311 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:	
GTGGTTCTGA AATCACCCTT CCTTTTCACT CCTCTGCCCT GACTTCCTCT CTCACCATGC TCTCCTGCTC TCCACCCTTCA CCCTCTTCAG TGGGATTTCTT GCATTTCAGC CAGAGGGACC TGTCTGCAGC TACCAGATGC TCCCCACCCT GGGAGAGCTC AGCGGCATGT CTGCACATGG GCCTTTTCAG CCTTCTTCAT CCCGCAATTG GAACTGACTT TCCCACTCC ATCTCACACT TGAGAATCTC TGTTTCTTGT TTCTTGTTTT TTATTTTATT	60 120 180 240 300 311
(2) INFORMATION FOR SEQ ID NO:1009:	
(2) INFORMATION FOR SEQ ID NO:1009:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 391 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 391 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 391 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

GCAGAGTTGG AGCACCTCTT ATTTGCTGTG AAATTAAGCT AAAAGACTGG CAAGAAGGCG GTTNTACAAT TAATGACAAG CCAAACTCGA G	360 391
(2) INFORMATION FOR SEQ ID NO:1010:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 415 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:	
GGGGAAGAAA GGCGTAAGGA TGGTGAAGCT GAACAGTAAC CCCAGCGAGA AGGGAACCAA GCCGCCTTCA GTTGAGGATG GCTTCCAGAC CGTCCCTCTC ATCACTCCCT TGGAGGTTAA TCACTTACAG CTGCCTGCTC CAGAAAAGGT GATTGTGAAG ACAAGAACGG AATATCAGCC GGAACAGAAG AACAAAAGGGA AGTTCCGGGT GCCGAAAATC GCTGAATTTA CGGTCACCAT CCTTGTCAGC CTGGCCCTAG CTTTCCTTGC GTGCATCGTG TTCCTGGTGG TTTACAAAGC CTTCACCTAT GATCACAGCT GCCCAGAGGG ATTCGTCTAT AAGCACAAAC GCTGTATCCC AGCCTCCCTG GATGCTTACT ACTCCTCCCA GGACCCCAAT CCCAGAAGCC TCGAG  (2) INFORMATION FOR SEQ ID NO:1011:	60 120 180 240 300 360 415
(1) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 407 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:	
GCCAGACTAC CACAAGCCCC ACCCACACTA TGCCAAGCCC TACCCATACC ACAGCAAGCC CCACTCATAC TTCCACAAGC CCCACCACAAG TCCCACCAC AAAACCAGTA TGTCACCTCC CACCACTACA AGTCCTACCC CCAGTGGTAT GGGCCTAGTC CAGACTGCCA CCATCCCAC CACAAGCCCC ACCATCACA ACAGCCCCA CCCATCCCAC CACAAGCCCC ATCCTTATAA ATGTAAGCCC TTCCACTTCT CTAGAACTTG CTACCCTCTC CAGCCCCTCC AAACACTCAG ACCCCACCCT CCCAGGCACT GACTCCCTTC CCTGTAGTCC CCCAGTCTCC AATTCCTACA CTCAGGCAGAACTC CCCACCCAAG TCTCGAG	60 120 180 240 300 360 407
(2) INFORMATION FOR SEQ ID NO:1012:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 291 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:	
GAATTCGGCC TTCATGGCCT ACGCCGCCGC CACAATGGGC CGCGGAGTTT GGGAATCTGA CGCGGATGCG GCATGTGATC AGCTACAGCT TGTCACCGTT CGAGCAGCGC GCCTATCCGC ACGTCTTCAC TAAAGGAATC CCCAATGTTC TGCGCCGCAT TCGGGAGTCT TTCTTTCGCG TGGTGCCGCA GTTTGTAGTG TTTTATCTTA TCTACACATG GGGGACTGAA GAGTTCGAGA	60 120 180 240

GATCCAAGAG GAAGAATCCC GCTGACCATT GAATTCTAGA CCTGCCTCGA G	291
(2) INFORMATION FOR SEQ ID NO:1013:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 351 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:	
GAATTCGGCT TCATGGCCTA TGGATTACCT GAGGAAGAAG AGATCAAGGA AAAAAAACCC ACCAGTCAAG GAAAGTCAAG TAGCAAGAAG GAAATGTCTA AAAGAGATGG CAAGGAGAAA AAAGACAGAG GAGTGACGAG GTTTCAGGAA AATGCCAGTG AAGGGAAGGC CCCTGCAGAA GACGTCTTTA AGAAGCCCCT GCCTCCTACT GTGAAGAAGG AAGAGAGTCC CCCTCCACCT AAAGTGGTAA ACCCACTGAT CGGCCTCTTG GGTGAATATG GAGGAGACAG TGACTATGAG GAGGAAGAAG AGGAGGAACA GACCCCTCCC CCACAGCCCC GGCAGCTCGA G	120 180 240
(2) INFORMATION FOR SEQ ID NO:1014:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 596 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:	
GCTCGAGTCG GATCCTCCT GAATGTGGAG CCAGCAGCT ACAAGAAAG ACCCTTGCAT TCCTCCCTGC ATCTCTCCCT TTTGGGTCCT ACTAATGTCT CTTGTCTGT TCCCAGAGCC GCAGGACTCT CTTGTCTGT CTTAGCTTGT CTTAGCTGT TCCCAGAGCC GCAGGACTCT CTTGTCTTT CTAAGCTGTG TTGTGTGTTT CCAGGACT CCAAAGATAA ACATGACTAA GGATTGGAAA GGAGGAAAGG CCGCGCAGAT CCCCGGATTTA CCCCGGATTTA CCTCCAAAA ATGCTTTATT TTTGGAGAAA AGCAATAGAC AGCAATAGAC CCCGGATTAACG CTTGCAGGA AGCCTTCCC AGGAGTGAC CTTGCCACC AGGAGTGAC CTTGCCACC AGGAGTGAC CTTGCCACC CTCGAG CTTGCCACC CTCGAG CTTGCCACC CTCGAG CCCCTTCCCC CTCGAG CCCCTTCCCC CTCGAG CCCCTTCCCC CTCGAG CCCCTTCCCC CTCGAG CCCCTCCC CTCGAG CCCCTTCCCC CTCGAG CCCCTTCCCC CTCGAG CCCCTTCCCC CTCGAG CCCCTCCC CTCGAG CCCCTCC CTCGAG CCCCTCCC CTCGAG CCCTCCC CTCGAG CCCCTCCC CTCGAG CCCCTCC CTCGAG CCCCTCCC CTCGAG CCCCCCC CTCGAG CCCCCCC CTCGAG CCCCCCC CTCGAG CCCCCC CTCGAG CCCCCC CTCGAG CCCCCCC CTCGAG CCCCCC CTCGAG CCCCCC CTCGAG CCCCCC CTCCCC CTCGAG CCCCCC CTCGAG CCCCC CTCGAG CCCCCC CTCGAG CCCCCC CTCGAG CCCCCC CTCGAG CCCCC CTCGAG CCCCCC CTCGAG CCCCC CTCGAG CCCCC CTCGAG CCCCC CTCGAG CCCCC CTCGAG CCCCC CTCGAG CCCCCC CTCGAG CCCCCC CTCCC CTCCCC CTCCC CTCC CTCCC CTCC	480
(2) INFORMATION FOR SEQ ID NO:1015:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 353 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:	
GAATTCGGCC TTCATGGCCT ACTTGGTTTT GCTGACCAAC AAATATGCAT AGTGTCTATT CACAGTTATA CAGTAATAGG TTAGAACAGA AATAAATGCC AGCTTCTTAT GATGCCTTTG CCAACAATCA GGCCATGTGT TTCAGGACCC TTCCTTCCTC TGACTTGTGT AGCATTACAC	60 120 180

and a series of the common of

CTCAGCACAC GACTTCTTGA AAGAGTGAAC CTCCAGGGCT TGCTCTCTCA GATGCACCTG GGCAGCAGCA GGAACTGTCT GACAGTCTCT CCTGTCTCCA TAAAGTAGCG GGCTGGCTCT TTCCTCCCAC TCATCCACC GACAGTCTC CTCCATCACAC TTAAAGTAGCA GGCTGGCTCT	240 300
TTGCTGGGAG TGATGGAGC CACAGATACG TGCATGGAAG TTACTGCCTC GAG	353
(2) INFORMATION FOR SEQ ID NO:1016:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 300 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:	
GAATTCGGCC TTCATGGCCT AATTATTAAG TAAAATAAGG GTTCCTTGAA TATAGGCACT GCAAATACCA TGACAGTGAT CTGATCACTG AGCTAACTAC TGAGTGACTC AGAGGCAGGT GATGTATACT GTGTGGAGTG GAATGGTGAG AGATTTCATC ACACTACTCA GAATTGCATG AAACTTAAAAG CTTATAAATT GTTTAATTCT GGAATTTTC ACTTAATATT TTCTGACTGA GATTGCCCAC GGGTAACTGA AACTGTGGAA AGCGAAACTG CAGATAATGG CGGACTCGAG	60 120 180 240 300
(2) INFORMATION FOR SEQ ID NO:1017:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 491 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:	
GCGATTGAAT TCTAGACCTG CTCGATCTCA TGGGGCAGAT GAAATTCTCT TCCTTAGAGG AAAGGGAAAG GTGAGGCCCC AGAGGACTTA TCTCAGCTGT ACATGCTCTG CCTGTGGAGA CATGGCTTTT CTTTGTGCTG TGGCAGACTG GGGCTTTGGA AGTGGTGTAT GTTTAACTTA ACATTTTTGGCC TGTTATCCAG TAGAGAGAAA GTGACAGTGA AAGTAACGTG AGAGAGAAAG AGTGTGTGTG TATATGTGAG AGAGAGAAAG AAAGAGAAAG GAATGCTTGA TTGCTTGTTG TCACTGGGC CAGCTCTGAA ATCCAAAATC ATGCCTTGAT AACATTACAA AACCGTGATC CTGGGTTTGA GTGAATCCTA GAGACATTGT TCTTATGGCC GCCTGGTTTC CGCAGCATGA TCACCCCTCGA G	60 120 180 240 300 360 420 480
(2) INFORMATION FOR SEQ ID NO:1018:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 323 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:	
GCTTTTCCAT GAAAGGTGGA TCGAGATCTA CTGCCAGTGG GTCAACAGGT TCTAAATTGA AATCAGATGA GTTACAGACC ATCAAGAAAG AATTAACCCA GATCAAAACT AAAATTGACT CCTTGCTAGG GCGCTGGAG AAGATTGAGA AACAGCAGAA GAAGCTCAGA	60 120

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ATCACTCTAC	GGAAGAGAGT CTAGTGCTGA TCCAAGAGGA ATGTGTGTCA GAGATTGCAG AGAGGAGCCT GCTGAAGGAG GGCCAGATGC CGATGGAGAA GAGATGACAG GGTTGGACTC GAG	240 300 323
(2) INFORM	ATION FOR SEQ ID NO:1019:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 319 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: CDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1019:	
CCTTGTATTT TACCCCTACC ATCGAACTGT	TCCTTGCAGT CCAGGACTGG GCATACTCAT ATGCCTTCTG TGGTTGGCGT ACCCAGTTTT GGTTCTGGTT TCCTCTTTCA CACTTCCTGT CATTGCCTTA TGTGTCATTG GCCTTAACAA GGACTTAAAG ATGCCGAAAG TTCAGTATAA AAACCATCCA CATTTGCATA TCCTGCCCCT CTGGAAGTAC CAAAAGAAAA AAGGTTTCTA CTGCTGTATT ATCTATAACT GCCAAGGCTA AAAAGAAGGA GAACTCGAG	60 120 180 240 300 319
(2) INFORMA	ATION FOR SEQ ID NO:1020:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 450 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1020:	
GAGGTATTGC GGGGGGTGGG GCATGTCATG TTTGTGGAGC TGCTCCAGCC CAGGCTGAGG	TGTGTAGCCT ATGGGTGCTG CTCCTGGTGT CTTCAGTTCT GGCTCTGGAA TGGACACCAC CGGAGAGACA TCTGAGATTG GCTGGCTCAC CTACCCACCA ACGAGGTGAG TGTTCTGGAC GACCAGCGAC GCCTGACTCG GACCTTTGAG TGGCAGGGGC CCCTCCAGGC ACCGGGCAGG ACAATTGGTT GCAGACACAC GGCGCGGGGC CCCAGAGGGCG CACATTCGAC TCCACTTCTC TGTGCGGGCA TGGGTGTGAG CGCGGCACC TGCCGGGAGA CCTTCACCCT TTACTACCGT AGCCCGACAG CCCTGACAGC GTTTCCTCCT GGCACCTCAA ACGCTGGACC CAATTGCAGC AAGACTCGAG	60 120 180 240 300 360 420 450
(2) INFORMA	ATION FOR SEQ ID NO:1021:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 266 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1021:	
CTTTTTTTAA	TTCATGGCCT ACTAGACCTG CTTTTTGGAA GAGAATGCTT TTCACCTGTT TCCACCTGGC ACTTTCCTCA GGACCCAAAC TTGTTCACTC TGCTGCTTCT ATTTTGGGAC ATCACCTGTT GTCTCCTTGC TGTGAATGAT GAGGATTTGG	60 120

CCCATATTAC CCCCGTTCCT TCCCCGGTCA TTCTCTCGGT TGCCTTTGTC ACTTTAAATC ATTTACATAA ACCACAACTT CTCGAG	240 266
(2) INFORMATION FOR SEQ ID NO:1022:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 352 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:	
GAATTCGGCC TTCATGCCTA AGAAACTTAT TCGTCTTCAG CATGAGAATA AGATGTTAAA GCTTAACCAA GAAGGTTCGG ACAATGAAAA AATAGCCTTA TTGCAGAGCC TTCTAGATGA TGCAAATCTA CGCAAGAATG AACTGGAGAC AGAGAATAGG CTGGTGAATC AAAGACTTCT GGAAGTACAG TCACAAGTTG AAGAATTACA AAAATCTTTA CAGGATCAAG GCTCAAAAGC AGAAGATGCT ATTTCAGTCC TTCTAAAAAA GAAGCTTGAA GAACATCTAG AGAAGCTGCA TGAGGCCAAT AATGAACTAC AGAAGAAGAG AGCCATTATT GAAGATCTCG AG	60 120 180 240 300 352
(2) INFORMATION FOR SEQ ID NO:1023:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 249 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:	
GAATTCGGCC TTCATGGCCT ACAAAAGCCA CCAGGTGAAT AAATGCCATT TTCTTTTTGC CTAGACATTG TTCATTTACT GAAAATGAAC AAGGTAATGC TCAGCATACA AAAAAAAAATT AAAGTTCTCA AGATCCCATG CTTTCTGGAT TCCTCTGTAT TTATCACTCA AGTCATCCCC CTTTTTGTAA TCTCGCTTTT TGTCCTCGCT TTATTTAAAT CCTTTATATC ACTACCCCCA TCTCTCTGAG	60 120 180 240 249
(2) INFORMATION FOR SEQ ID NO:1024:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 267 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:1024:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 1024.	

(2) INFORMATION FOR SEQ ID NO:1025:

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:	
GAATTCGGCC TTCATGGCCT AGCCATCTTA TTTGAACTAT ATTTTTCCTT CAAAGAAGC	A 60
ATAGGTCTCA ACATAGTGTA GGTAGCATCA GGTGACAGAA AGCCAATTTT ATTTTCAAAT	120
TTAAGTTAAT TATCTTCGTG ATCCTATTTA TCCACAATTT CTTTCAGAAA AGACTGAAAA	1 180
AACACATTAT ATTCAGGAGA TATAATGAAA TTATTGGAAG GCATCACTCG AG	232
(2) INFORMATION FOR SEQ ID NO:1026:	
(i) OPOURNOR CUIDACERRA	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 153 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:	
Character and modern account and an account account account and account accoun	
GAATTCGGCC TTCATGGCCT AGATTGAATT AGACCTGCCT CGAGCCCCTA AAAATATCCT	60
AAATGCATTT CCTCCTCTGC ATTCTAACTA CTGCTGCCCT TGTTCTAGGA CTCCACTCTC	
CCACATCAAC CAACTTTTCT CCTTGGCCCC CTC	153
(2) INFORMATION FOR SEQ ID NO:1027:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 294 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:	
With adjusted pedentificat. SEQ ID NO:1027:	
GCGAGGGCCA GGGAGGGAGG AAGCAATAAA TAGGGGGAGA AAATGGCAAT AAGACGTTAT	. 60
ATAGCCCTTC TAACAAAAAT ACCAGAAGGG AGGGGTGAGG GACAAGGCTG TCTGAGGGAG	120
GGCAGGAGGT GAGGCCATGG CTTGGTCTCT TTTGCGCTTG GATGGCCGTC AGCTCAGCAT	180
GAGGCATCTG AAAGAACTAC CCAGATTGCA GAAGAGAGAG GTCCCAGCCT CCTTGGAAGG	240
ACATGATGGG GGAGGAGTGG AGACAACAGC TGAGTGTTAC CTGTAAAACT CGAG	294
(2) INFORMATION FOR SEQ ID NO:1028:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 285 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) forobodi: finedi	
(ii) MOLECULE TYPE: cDNA	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs

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GAATTCGGCC TTCATGGCCT ACATAATTTG AATCAACACA ACCACCCACA GCCTAATTAT TAGCATCATC CCTCTACTAT TTTTTAACCA AATCAACAAC AACCTATTTA GCTGCTCCCC AACCTTTTCC TCCGACCCC TAACAACCCC CCTCCTAATA CTAACTACCT GACTCCTACC CCTCACAATC ATGGCAAGCC AACGCCACTT ATCCAGTGAA CCACTATCAC GAAAAAAACT CTACCTCTCT ATACTAATCT CCNNACAAAT CTCCTTAATT ATAACATTCA CAGCCACAGA TCTCGAG	60 120 180 240 300 307
(2) INFORMATION FOR SEQ ID NO:542:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 353 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:	
GGATGGCGCC GCGGAGGGTC AGGTCGTTTC TGCGCGGGCT CCCGGCGCTG CTACTGCTGC TGCTCTTCCT CGGGCCCTGG CCCGCTGCA GCCACGGCGG CAAGTTACTCG CGGGAGAAGA ACCAGCCCAA GCCGTCCCCG AAACGCGAGT CCGGAGAGAG GTTCCGCATG GAGAAGTTGA ACCAGCTGTG GGAGAAGGCC CAGCGACTGC ATCTTCCTCC CGTGAGGCTG GCCGAGCTCC ACGCTGATCT GAAGATACAG GAGAGGGACG AACTCGCCTG GAAGAAACTA AAGCTTGACG GCTTGGACGA AGATGGGGAG AAGGAAGCGA GACTCATACG CAACACACTC GAG	60 120 180 240 300 353
(2) INFORMATION FOR SEQ ID NO:543:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 310 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:	
GGATACCCTA AAAAAACAAT CTATGTCAGA GGCTTCACTG GAGGTTACGT CACGTTATCG TATTAATTTA GAAGATGAGA CACAGGATTT AAAGAAGAAA TTAGGTCAAA TCAGAAATCA ATTGCAAGAA GCACAGGATC GACATACAGA AGCTGTCAGA TGTGCTGAGA AGATGCAAGA TCACAAGCAA AAGCTTGAAA AAGATAATGC CAAGTTAAAA GTTACAGTCA AAAAGCAAAT GGAACACAGAG GGAACTCGAG	60 120 180 240 300 310
(2) INFORMATION FOR SEQ ID NO:544:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 282 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:	

60

120

GTTTGGATGA TTGGTGGCGT GTACGCAGCT GCTATGGCCT GGGCCATCAT CCCCCACTAT

GGGTGGAGTT TTCAGATGGG TTCTGCCTAC CAGTTCCACA GCTGGAGGGT CTTCGTCCTC

GATACCAACA TGCGAGCCAA AGGACATCCT GAGCGACTCG AG

(A) LENGTH: 362 base pairs

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:545:

GTCTGCGCCT TTCCTTCTGT GTTTGCCATT GGGGCTCTGA CCACGCAGCC TGAGAGCCCC

CGTTTCTTCC TAGAGAATGG AAAGCATGAT GAGGCCTGGA TGGTGCTGAA GCAGGTCCAT

180

240

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:545:	
GAATTCCCCC	TTCATGGCCT AGAACTTTGT ACACCATGGA ATGTTCTACT TATTATTTTG	60
	TGTGCTGTTT CTTTTGTTTG AATTGCAGAT TGTCTACTAT GAAGGAGGGA	120
	CTGTGTCCTG GGGCTGCTGT TTATTATTCT GATGCCTCTG GTGGGGTATT	180
	GTGTCGTTGC TGTAACAAAT GTGGTGGAGA AATGCACCAG CGACAGAAGG	240
	CTTCCTGAGG AAATGCTTTG CAATCTCCCT GTTGGTGATT TGTATAATAA	300
	CATCTTCTAT GGTTTTGTGG CAAATCACCA GGTAAGAACC CGGATCCTCG	360
AG	Chieffelli dell'illette divirence dell'indiane confected	362
(2) INFORM	ATION FOR SEQ ID NO:546:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 315 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:546:	
TCGAGGGACA	TGAGGCTGAG CTGGTTCCAG GTCCTGACAG TACTGTCCAT CTGCCTGAGC	60
	CGGCCACGGG GGCCGAGGGC AAAAGGAAGC TGCAGATCGG GGTCAAGAAG	120
	ACTGTCCCAT CAAATCGCGC AAAGGGGATG TCCTGCACAT GCACTACACG	180
	AAGATGGGAC AGAGTTTGAC AGCAGCCTGC CCCAGAACCA GCCCTTTGTC	240
	GCACAGGCCA GGTCATCAAG GGCTGGGACC AGGGGCTGCT GGGGATGTGT	300
GAGGGGGACC		315
(2) INFORM	ATION FOR SEQ ID NO:547:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 449 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii	MOLECULE TYPE: cDNA	
(xi)	) SEQUENCE DESCRIPTION: SEQ ID NO:547:	
	TAAGAATTCG GCCTTCATGG CCTAATCGAG GAGAATGGAG ACCAAACCTG	60
	TCTCAAAACC CTCCTCATCA TCTACTCCTT CGTCTTCTGG ATCACTGGGG	120
	GGCTGTTGGA GTCTGGGGCA AACTTACTCT GGGCACCTAT ATCTCCCTTA	180
TTGCCGAGAA	CTCCACAAAT GCTCCCTATG TGCTCATCGG AACTGGCACC ACTATTGTTG	240
	265	

TCTTTGGCCT GTTTGGATGC TTTGCTACAT GTCGTGGTAG CCCATGGATG CTGAAACTGT	300
ATGCCATGTT TCTGTCCCTG GTGTTCCTGG CTGAGCTCGT AGCTGGCATT TCAGGGTTTG	360
TGTTTCGTCA TGAGATCAAG GACACCTTCC TGAGGACTTA CACGGACGCT ATGCAGACTT	420
ACAATGGCAA TGATGAGAGA ATGCTCGAG	449
(2) INFORMATION FOR SEQ ID NO:548:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 374 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(4)	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:	
GGGCTTTAAA GGCAGACATT GATGCTACAT TATATGAACA AGTCATCCTG GAAAAAGAAA	60
TGGGAACTTA TTTGGGCACC TTTGATGATT ACTTGGAGTT ATTCCTGCAG TTTGGTTATG	120
TGAGCCTTTT CTCCTGTGTT TACCCATTAG CAGCTGCCTT TGCTGTGTTA AATAACTTCA	180
CTGAAGTAAA TTCAGATGCC TTAAAAATGT GCAGGGTCTT CAAACGTCCA TTCTCAGAAC CTTCAGCCAA TATTGGTGTG TGGCAGTTGG CTTTTGAAAC GATGAGTGTT ATATCTGTGG	240 300
TCACTAACTG TGCGCTGATT GGAATGTCAC CACAAGTGAA TGCAGTCTTT CCAGAATCAA	360
AGGCAGACCT CGAG	374
(2) INFORMATION FOR SEQ ID NO:549:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 294 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:	
GTACAATCTG AATCCAGGTC TGACAGCTGG CCATACAAAG TCATACTTTC CCCACATCCC	60
TCCTCTTTGA TAGGCATTGT CATCTAGAGC AATAGCCTCG AAATAGACTG AACACCGTGG	120
CCCATAGCTT AACTCCGTTC CACCTCTATT TCAAAGTAAA CTTGGGCTGG GATTACAGGC	180 240
ATGAGTATGT TTTCATTTGT ACATAAAGAC TTTATACAAA TGCTCTTCCT AATATTTGCT ACTTATTTTT GCATTAGTTC AAATTCTTTG TCCTGTCATC CCAAAACTCT CGAG	294
ACTIVITIES OF THE PROPERTY OF THE PROPERTY CONTROL CON	
(2) INFORMATION FOR SEQ ID NO:550:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 303 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:	
GAATTCGGCC TTCATGGCCT ACACTGCACG GGGAACCCCC GAACCATCAT CGTGCCACCC	60
CTGAAAACCC AGGCCAGCGA AGTATTGGTG GAGTGTGATA GCCTGGTGCC AGTCAACACC	120
AGTCACCACT CGTCCTCCTA CAAGTCCAAG TCCTCCAGCA ACGTGACCTC CACCAGCGGT	180
CACTUTTURE GERCETCATO TOGRACIONTO ACCTACOGGO AGORGOGGO GUECCUCORO	240

TTCCAGCAGC AGCAGCCACT CAATCTCAGC CAGGCTCAGC AGCACATCAC CACGGCCGTC GAG	300 303
(2) INFORMATION FOR SEQ ID NO:551:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 375 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:	
GCCACAAGCC TGTCAGCAAG TGGGGCTACT TGGGTCCTCG GGCCTCAATC CACTCCTGGC CAGAGACAAC TTCCTCTCCC ATGGGAAAGG CTAACGCATG CCCATAAATT AAGACATTTG CTCTCCCTCC AAGCCCTGGA AACCTGGGAC TCTCTAACAT CTACCTCTGT TTTCTTTGGC CAGAGGATTG CAGAATCTAA TCCAGAAGGA AGAGTTTATC CAAATGTTGG TGGCCTTTCT CTTTTGGCGC ATTCTCTTCT GGTTCTGTCT TTTCTCAGGA GTCCTCTGAG CTTCCATGTA CCGGGCCCCC TCGAG	60 120 180 240 300 360 375
(2) INFORMATION FOR SEQ ID NO:552:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 390 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:	
GCAAGGGCAG GCGGGTCCCC CAGTCCCGCC ATTACGGGTT GTCAGACCGT CTGCGTGTGG CAGGGCTCCC AAGGGCAGGC GGGTCCCCCA GTCCCGCCAT TACGGGTTGT CAGACCGTCT GCGTGTGGCA TTTTTTGGCT TATAAGCTTC ACCCACTCAC CCCCAACCCA CACCCCACAT CCCCCTGCCG GCAGCCCTC AACCTAAGAA GGCCAGAGCA TATTTATTTT CGGAGGGAGC AGATTACTTC TCCCAGAGAA AGGAAAATCT TGGAAAAGAT TTAAAAACAC AAATCTAAGC CTTGACGGTT TTTTTTTCCC TTTTGACCCC CTTCCCATTT TTTCAGNATT TATTCCCATG	60 120 180 240 300 360 390
(2) INFORMATION FOR SEQ ID NO:553:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 620 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:	
GAATTCGGCC AAAGAGGCCT AAGCAGGCGC GAGGCGGCGG CAGCGAGCCG GGTCCCACCA TGGCCGCGAA TTATTCCAGT ACCAGTACCC GGAGAGAACA TGTCAAAGTT AAAACCAGCT CCCAGCCAGG CTTCCTGGAA CGGCTGAGCG AGACCTCGGG TGGGATGTTT GTGGGGCTCA TGGCCTTCCTT TACCTAATTT TCACCAATGA GGGCCGCGCA TTGAAGACGG	60 120 180 240

CAACCTCATT	GGCTGAGGGG	CTCTCGCTTG	TGGTGTCTCC	CGACAGCATC	CACAGTGTGG	300
CTCCGGAGAA	TGAAGGAAGC	TGGTGCACAT	CATTGGCGCC	TTACGGACAT	CCAAGCTTTT	360
GTCTGATCCA	AACTATGGGG	TCCATCTTCC	GGCTGTGAAA	CTGCGGAGGC	ACGTGGAGAT	420
${\tt GTACCAATGG}$	GTAGAAACTG	AGGAGTCCAG	GGAGTACACC	GAGGATGGGC	AGGTGAAGAA	480
GGAGACGAGG	TATTCCTACA	ACACTGAATG	GAGGTCAGAA	ATCATCAACA	GCAAAAACTT	540
CGACCGAGAG	ATTGGACACA	AAAACCCCAG	TGCCATGGCA	GTGGAGTCAT	TCATGGCAAC	600
AGCCCCCTTT	GTTCCTCGAG					620

- (2) INFORMATION FOR SEQ ID NO:554:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 600 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

GAATTCGGCC	AAAGAGGCCT	AGGACTTGTT	TCGGAAGGAG	CTGACTGGCC	AATCACAATT	60
GCGAAGATGA	AGGCTCTGTG	GGCCGTGCTG	TTGGTCACAT	TGCTGACAGG	ATGCCTAGCC	120
GAGGGAGAGC	CGGAGGTGAC	AGATCAGCTC	GAGTGGCAAA	GCAACCAACC	CTGGGAGCAG	180
GCCCTGAACC	GCTTCTGGGA	TTACCTGCGC	TGGGTGCAGA	CGCTGTCTGA	CCAGGTCCAG	240
GAAGAGCTGC	AGAGCTCCCA	AGTCACACAA	GAACTGACGG	CACTGATGGA	GGACACTATG	300
ACGGAAGTAA	AGGCTTACAA	AAAGGAGCTG	GAGGAACAGC	TGGGTCCAGT	GGCGGAGGAG	360
ACACGGGCCA	${\tt GGCTGGGCAA}$	AGAGGTGCAG	GCGGCACAGG	CCCGACTCGG	AGCCGACATG	420
GAGGATCTAC	GCAACCGACT	CGGGCAGTAC	CGCAACGAGG	TGCACACCAT	GCTGGGCCAG	480
AGCACAGAGG	AGATACGGGC	GCGGCTCTCC	ACACACCTGC	GCAAGATGCG	CAAGCGCTTG	540
ATGCGGGATG	CCGAGGATCT	GCAGAAGCGC	CTAGCTGTGT	ACAAGGCAGG	GGCAGTCGAG	600

- (2) INFORMATION FOR SEQ ID NO:555:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 262 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

GAATTCGGCC	TTCATGGCCT	AGTATTTCCT	TATCACAGAT	TTTGGGAGCA	ACAGTGTTTT	60
CCCATCTGGA	GGAGGCTGAG	TTAATTCTGT	GGAACACCCA	TTTGGTTGGA	AATAAAAACA	120
CAGCATGGAT	TTAATTCATG	CCACTTATTT	ATTTTTATTA	GGACTTGAGC	TTCTTTGTAT	180
TTTTTTTGCT	TTGCTTCCAC	TCAAAACCAG	ATTTGGTGGT	TGCTGTGTAA	ACAGTGAAAT	240
ACAACACAGG	CCAGGACTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:556:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 470 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GAATTCGGCC AAGAGGCCTA GTATTCTTTC GTTTCTCTCT AAAAGAAGAA AAATATAATT	60
TAGAAATACA TTGCGTATTT TCTAAAACAA TAAATTTATA GTGTTAATAT TCATAGGGTC	120
AATCAAAATG AAGCTTCTCC TTTGGGCCTG CATTGTATGT GTTGCTTTTG CAAGGAAGAG	180
ACGGTTCCCC TTCATTGGTG AGGATGACAA TGACGATGGT CACCCACTTC ATCCATCTCT	240
GAATATTCCT TATGGCATAC GGAATTTACC ACCTCCTCTT TATTATCGCC CAGTGAATAC	300
AGTCCCCAGT TACCCTGGGA ATACTTACAC TGACACAGGG TTACCTTCGT ATCCCTGGAT	360
TCTAACTTCT CCTGGATTCC CCTATGTCTA TCACATCCGT GGTTTTCCCT TAGCTACTCA	420
GTTGAATGTT CCTCCTCTCC CTCCTAGGGG TTTCCCGTTT GTCCCTCGAG	470
(2) INFORMATION FOR SEQ ID NO:557:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 432 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:	
GAATTCGGCC AAAGAGGCCT ATGCAGATTC TGTGGTTATA CTCACTCCTC ATCCCAAAGA	60
ATGAAATTTA CCACTCTCCT CTTCTTGGCA GCTGTAGCAG GGGCCCTGGT CTATGCTGAA	120
GATGCCTCCT CTGACTCGAC GGGTGCTGAT CCTGCCCAGG AAGCTGGGAC CTCTAAGCCT	180
AATGAAGAGA TCTCAGGTCC AGCAGAACCA GCTTCACCCC CAGAGACAAC CACAACAGCC	240
CAGGAGAGTT CGGCGGCAGC AGTTCAGGGG ACAGCCAAGG TCACGTCAAG CAGGCAGGAA	300
CTAAACCCCC TGAAATCCAT AGTGGAGAAA AGTATCTTAC TAACAGAACA AGCCCTTGCA	360
AAAGCAGGAA AAGGAATGCA CGGAGGCGTG CCAGGTGGAA AACAATTCAT CGAAAATGGA	420
AGTTCCCTCG AG	432
	432
(2) INFORMATION FOR SEQ ID NO:558:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 104 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(wi) CECHENCE DESCRIPTION OF TO MA SEC	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:	
GAATTCGGCC AAAGAGGCCT AAAAAGTATA TACATTTTAG TACTGCTTTG ATTTTGTTTA	60
CATACTGAAA AATGTATCTG AAAATGAGTT ATTTTGGACT CGAG	104
(2) INFORMATION FOR SEQ ID NO:559:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 203 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:	
OPGORNER DESCRIPTION: DEG IN MO1333:	

GTAAAAGGAC TCAGCCAACT ATGAAGTTTT TTGTTTTTGC TTTAATCTTG GCTCTCATGC TTTCCATGAC TGGAGCTGAT TCACATGCAA AGAGACATCA TGGGTATAAA AGAAAATTCC ATGAAAAGCA ACATGATCTC GAG	120 180 203
(2) INFORMATION FOR SEQ ID NO:560:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 484 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:	
GAATTCGGCC ACAGAGGCCT AGCCCAGTCT CGGGTATGTC TTTATCAGCA GCATGAAAAT GGACTAATAC AGTTGCTATG ATTATTAGTT TTTTGCTACT GAGTTGTAGG AGTATCTGAT ATATATTTTG GTAACTAATC CCTTATAAAA TATATTGTTT CCAATATTT TTTTCCCATT CCATAGGCTG CCTTTTCATT CTGTTGTTTC CTTTGCTTCA GGTAAGGGAT TCTGAAACAA CTATTTGGGC AGCAGAACAG CTTCTTTTGT TTGCTTTCTC ATTGTCTACT GTGTTCTGCA TAAATAAGGT TATGAATTAG CTGTTGTTCA TATGGGTGAA AGATTTGCAT CTGTGGACGC TTAGATAGCA CATATGGTAA ACCATAGAAC TTCACCATTT ATAACCTTTG AACAACTGAT ACACTTAGAA AAGCAGTTTT TGGCTGGGCG CGGTGGCTCA TGCCTGTAAT CCCTAGGCCT CGAG	60 120 180 240 300 360 420 480
(2) INFORMATION FOR SEQ ID NO:561:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 176 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:	
GAATTCGGCC AAAGAGGCCT ATTGAATTCT AGACCTGCCT CGAGCTGACA ACTATGAAGT TTTTTGTTTT TGCTTTAATC TTGGCTCTCA TGCTTTCCAT GACTGGAGCT GATTCACATG CAAAGAGACA TCATGGGTAT AAAAGAAAAT TCCATGAAAA GCATCAAGGA CTCGAG	60 120 176
(2) INFORMATION FOR SEQ ID NO:562:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 475 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:	
GAATTCGGCC AAAGGGCCTA ATTTTATTAA TAACATTTTA AAAACAACAA TTATGAAAAA GCAATTCGGT TTACCGCTGA TGCTTGCGTC AGCCCTCGCC TTCTCTGCTT GTAGCTCTGA TGATGTGGCC GAGAATGGCC CAAAGGACAT CGCAGCTCTT ACAGATGGTG GTTACTTGAA GATGTCTATC AATCTTCCTT CCCGTGCTGC TAATGGTGGC TTCAGAGCTA CGGAACAAGA CGGTTATGTT AACTTGGAAG ATGGATTGGC AAAAGAGTAC AATGTAAAGG ATGCTATCCT	60 120 180 240 300

CGTCCTTTTC CAAGGTGATA ATGAAGCAGA TGCCAAGTTC CATTCTGCAT ATGAACTTAC

TACATCAATG CAGAAGGATG GCTCTACGCA AATCACTTCC ACAACGAAAC TTGTTAAGAA TGTGAATATT GGTGGTCAGG GAAATCCTCT TAAACCTGCT GATGTTAAGC TCGAG 360 420

(2) INFORMATION FOR SEQ ID NO:563:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 204 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:	
GAATTCGGCC AAAGAGGCCT ACAATTATGG GGCTTATGGG GAACATGCTC ATTGTGTTTT ACCAATCAGG ACATGGAACT TAAACAATAT TTGTTGACTT ATAGTGAAAC CTGGCTAATT AGGACTCTTA ACCAGCACTC TTAATTAACT GACTTATTTT TCTCTGTGTC CACCCCTCTT AAAGAAAAAG AAGCGAAACT CGAG	60 120 180 204
(2) INFORMATION FOR SEQ ID NO:564:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 102 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:	
GAATTCGGCC AAAGAGGCCT ATAGGCCTCT TTGGCCGTAG GCCTCTTTGG CCGATTGAAT TCTAGACGCG GCTCGAGGCA GGTCTAGGCC TCTTTGGCCG AA	60 102
(2) INFORMATION FOR SEQ ID NO:565:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 285 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:	
GAATTCGGCC AAAGAGGCCT ACTCAATTGT TCCTTTCTTC CATCACCACC CTTTGAAGGT CTCTTTGCCT ACTTGTAGAT TTAGGGGGAC ATAACATTGA GACTGAGCAG TTTCTTGAAC CTCTCCTCTC	60 120 180 240 285
(2) INFORMATION FOR SEQ ID NO:566:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 259 base pairs  (B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GATAACTTGA	GATCAAATCA	GTCATATTTG	ACTCTTCTCT	TTTTCACTCC	TTTTATATCT	60
GATCAGTCAG	CAGTTTTTTG	AAACCCTGTT	CGAAGCAGTT	CTCAACACTT	GTGCACCCAT	120
TCTTTCTCCT	ACACCACTCA	ATCTAGACCC	TCACATGTGG	CTGTCCTGCT	TTCCTTCTCT	180
CCTACTTCTA	AGCTATTCTG	TGGAGAGATG	TCAAAGTAAT	CTTCACAAAA	AATCTGATTG	240
CATCACTTCA	CATCTCGAG					259

- (2) INFORMATION FOR SEQ ID NO:567:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 374 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GGGCTTTAAA GGC	AGACATT GATGCTACAT	TATATGAACA	AGTCATCCTG	GAAAAAGAAA	60
TGGGAACTTA TTT	GGGCACC TTTGATGATT	ACTTGGAGTT	ATTCCTGCAG	TTTGGTTATG	120
TGAGCCTTTT CTC	CTGTGTT TACCCATTAG	CAGCTGCCTT	TGCTGTGTTA	AATAACTTCA	180
CTGAAGTAAA TTC	CAGATGCC TTAAAAATGT	GCAGGGTCTT	CAAACGTCCA	TTCTCAGAAC	240
CTTCAGCCAA TAT	TTGGTGTG TGGCAGTTGG	CTTTTGAAAC	GATGAGTGTT	ATATCTGTGG	300
TCACTAACTG TGC	GCTGATT GGAATGTCAC	CACAAGTGAA	TGCAGTCTTT	CCAGAATCAA	360
AGGCAGACCT CGA	<b>\</b> G				374

- (2) INFORMATION FOR SEQ ID NO:568:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 250 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

GAATTCGGCC	TTCATGGCCT	AGATAAGTAA	ATAGACTTAC	AGAGGGAAAG	TAACTTGGCT	60
AAGGTGAACT	TGAACCAAGA	TGACTGACTC	CAGAGCTTCC	ATTTTTCTTT	TTCTTTCTTT	120
TTTTTTTTT	NGGAGACAGA	GTCTCACTCT	GTCGCCCAGG	CTGGAGTGCA	ACGGCGCGGT	180
CTCCACTCAC	TGCAGCCTCC	AGCTCCTGGG	CTCAAGTGAT	CCTCCCACCT	CAGCACCCCC	240
ACGTCTCGAG						250

- (2) INFORMATION FOR SEQ ID NO:569:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 367 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GAATTCGGCC TTCATC	GCCT ACAGGGAGGG	AGGGGTTCTG	AGAGCCTCAG	ACCACAGGGC	60
CTGAGGCCCA CAGTGG	SCCCA GAGTCCATCT	GGCAGCCCCT	GCTCTGCTGG	CCCAGGGGGC	120
TCTCCCCAGG GTGGAG	STAGG CAGGGGAGGG	TCGCTGGTCC	CCAGTCCCAG	CCTTCGAGAG	180
GTGGGGCCAG ACAGCA	AGGGC ACCCGTACCC	GAGACCACAG	TGCTCCCCAA	GGCCAGCTCT	240
CTCCCCAGTG AGGTCA	ACTCC TACCTCCGGG	GCCATTTGGG	GCGGGGGATC	CTGTAGATCT	300
CTGACTCTGC GGCGCC	CTTAT CTTGATGGCC	TGGCNCAAGA	AGGGAGGGCG	CTGCCCACTT	360
CCTCGAG					367

- (2) INFORMATION FOR SEQ ID NO:570:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 262 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

TTTTGACTGA CTCTTTA	AAT TAGTACAATT	TTTCTACTTG	TCATATAACT	CCTGGAACAA	60
TAGTACGGGA AGCCGTG	ATC CTTTTCCCTG	ACTCATGATT	TTAGTCTTTT	TCCAAATCGC	120
TGTTTTTTT TGGTTTT	TTT TTTTTTTGCT	GCTCCAACGA	CCAGCATGTG	TTGGAGCAGA	180
TCTCCATGGT AAGCCAA	AAG TGGACTTGTC	AGCCTATAAC	TACTCTGCAG	CTGCCACTAA	240
CTCTACAGGC ACAGAGC	TCG AG				262

- (2) INFORMATION FOR SEQ ID NO:571:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

CAGAAACTCT	TGGACTCAAA	AGAGAAAGAA	AAAAGTCAAG	CCAAGGAAAG	CACAAGAGGT	60
AAGACAGGCC	TAGTGATCTC	AGCAGGCAGA	ATTTATGGAC	ATATTTTGCA	GGCAAGTGGT	120
TCTCAATCAG	GGGTGATTTT	TGGCTTGTAA	GGACATTTAG	CAATATCTGG	ACACATTTTT	180
TGGTTGTCGT	AAGTGGATGG	GGGTTGCTGC	TATCATCCTA	CAATGCATAG	GTGCATTAGT	240
CTGTTTTCAT	GCTGCTGATA	AAGACATACC	GGAGACTGGG	CAATTTGCAA	ATGAGAGATG	300
GCTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:572:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 578 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

GAATTCGGCC	TTCATGCCTA	CAGCCATATT	AAAACTAAGT	AAACTCGTCC	CTGGGAACTA	60
CACTTTCAGC	TTGACTGTAG	TAGACTCTGA	TGGAGCTACC	AACTCTACTA	CTGCAAACCT	120
GACAGTGAAC	AAAGCTGTGG	ATTACCCCCC	TGTGGCCAAC	GCAGGCCCCA	ACCAAGTGAT	180
CACCCTGCCC	CAAAACTCCA	TCACCCTCTT	TGGGAACCAG	AGCACTGATG	ATCATGGCAT	240
CACCAGCTAT	GAGTGGTCAC	TCAGCCCAAG	CAGCAAAGGG	AAAGTGGTGG	AGATGCAGGN	300
TGTTAGAACA	CCAACCTTAC	AGCTCTCTGC	GATGCAAGAA	GGAGACTACA	CTTACCAGCT	360
CACAGTGACT	GACACAATAG	GACAGCAGGC	CACTGCTCAA	GTGACTGTTA	TTGTGCAACC	420
TGAAAACAAT	AAGCCTCATC	AGGCAGATGC	AGGCCCAGAT	AAAGAGCTGA	CCCTTCCTGT	480
GGATAGCACA	ACCCTGGATG	GCAGCAAGAG	CTCAGATGAT	CAGAAAATTA	TCTCATATCT	540
CTGGGAAAAA	CACAGGGACC	TGATGGGTGC	AGCTCGAG			578

### (2) INFORMATION FOR SEQ ID NO:573:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 623 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

			•			
GAATTCGGCC	TTCATGGCCT	AACTTTGTGT	GATCAGAGTT	TATGGGTTGG	GCTGCCCCAG	60
GCTTGGATAA	CTTAAAGGCT	TGATGAGGTC	ATCAATTTAT	GCTTGGCTAC	CCATGGCACA	120
GAAGCATAGC	CCCACTGTGA	TGGCTGGGGT	GGCTCCGGGC	ATCCTGGGCA	GTCAGGAGGA	180
<b>AACTCCATGA</b>	AGGAAGGAGC	TAACCTTTCT	GGGGGTACCC	CTATCCCAGC	ACAGACTTCC	240
TCATCTCATT	GGTCAGAACT	GGGTCACATG	AACATGCCTC	AGCCTATCAC	AGGCACAGGG	300
AATGAGACCA	TCATGGACCA	ATCAGGATTC	ACCACTCAAG	GTGGGGCCTG	CCATCCGGAT	360
GGATGCTCTC	CGCCACAGGG	AGGTGGGGGA	CCCAGAAGCT	GTGGGCAATG	GCCATGTGCA	420
CAGTAGGACT	GAGGCACTCA	GTCCCGTAGC	TGACCTACCT	GGGACAGGCC	TGGAGGCTGA	480
CTTAGGTGTG	AGGGGCAGAG	AGATTACTGT	GCACAGACCG	CTGTGTGACC	CCAGATCTAG	540
GTGGGATCCC	GGTGTGCCCC	ATCTGCCTGG	CTTACCCCAA	CCCCTCTGGA	ACCTGAACCA	600
TTGAATTCTA	GACCTGCCTC	GAG				623

## (2) INFORMATION FOR SEQ ID NO:574:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 277 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

GAATTCGGCC	TTCATGGCCT	ACTCCAGAAT	GAAGATCTTC	TTGCCAGTGC	TGCTGGCTGC	60
CCTTCTGGGT	GTGGAGCGAG	CCAGCTCGCT	GATGTGCTTC	TCCTGCTTGA	ACCAGAAGAG	120
CAATCTGTAC	TGCCTGAAGC	CGACCATCTG	CTCCGACCAG	GACAACTACT	GCGTGACTGT	180
GTCTGCTAGT	GCCGGCATTG	GGAATCTCGT	GACATTTGGC	CACAGCCTGA	GCAAGACCTG	240
TTCCCCGGCC	TGCCCCATCC	CAGAAGGCCT	GCTCGAG			277

## (2) INFORMATION FOR SEQ ID NO:575:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 251 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:	
GAATTCGGCC TTCATGGCCT AAGCTTTTGC TTTTTTAATA ACTTGTATAG CTAAAAACTT GACGGTGAAA AGCTCTCAGA TCAAAGCTGA TCCTTCTGTC AGTAATGATT CTAAAAATAA GCAAGATTT AATGGGAAT ATATTTTATT TCATTCTTAT CTCAAACCTA GGTACTGTGG TCGTTTTGAG TTCATTCGA GGCATTTCA ATGTGCCTCA GGCCACATCC AACCTCTCCC CAGAACTCGA G	60 120 180 240 251
(2) INFORMATION FOR SEQ ID NO:576:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 261 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:	
GAATTCGGCC TTCATGGCCT ACAGTCTAAG ACATTTCCTA TTCTGCCTTC TTGTCTTCCT CCCTCTCTTC CACATTGGTC AGACTTACAT CTTGGACAGC TCTCCCAGCC ATCTTCTACT GCCTCCCTAT TTTTCCCTCC CAGACTTTC CCCGCAAAAC ATCTGTTGCA GGTGGTATTA ATTTCCTATC ACGGCTGTGA CAAATTACCA CAAACTCAGT GGCTTAAAAC AATGCACATT TATTATCTGA CAGTTCTCGA G	60 120 180 240 261
(2) INFORMATION FOR SEQ ID NO:577:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 216 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:	
GAATTCGGCT TCATGGCCTA GCAAGACTCC ATCTCAAAAA AAGAAAGAAA GAAAAAAGAA AGTACAAGTT TATAAAGTAT TATAGTGAAA AATTCGCATT CTGGCTGATT TTAAGCCATT TAAAATTTAT ATAAAACAAC CTTCCATAAA AATTTGACAG GTGCCCAGAT GTTGCTTTCT CCATTTATTT TTTGTTTTT TTTAATCACA CTCGAG	60 120 180 210
(2) INFORMATION FOR SEQ ID NO:578:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 294 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

GCGATTGAAT TCTAGACCTG CCTCGAGTAA GTGCCGAAAA CTTCACTGTG CTCATCAAGA ACAATATCGA CTTCCCCGGC CACAACTACA CCACGAGAAA CATCCTGCCA GGTTTAAACA TCACTTGTAC CTTCCACAAG ACTCAGAATC CACAGTGTCC CATTTTCCGA CTAGGAGACA TCTTCCGAGA AACAGGCGAT AATTTTTCAG ATGTGGCAAT TCAGGTTGGT GGTGCTTTGT ACACTGGGAT GTGGGGCTGT GTGTCTAGGG ATGGAGGATG TCAAACAACT CGAG	60 120 180 240 294
(2) INFORMATION FOR SEQ ID NO:579:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 229 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(11)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:	
GAATTCGGCC TTCATGGCCT ACCTTCACAG AAAAATGCAT AGCTGGATGC TGCAGACTCT	60
AGCGTTTGCT GTAACATCTC TCGTCCTTTC GTGTGCAGAA ACCATCGATT ATTATGGGGA	120
AATCTGTGAC AATGCATGTC CTTGTGAGGA AAAGGACGGC ATTTTAACTG TGAGCTGTGA	180
AAACCGGGGG ATCATCAGTC TCTCTGAAAT TAGCCCCCCC GATCTCGAG	229
(2) INFORMATION FOR SEQ ID NO:580:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 205 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:	
	60
GAATTCGGCC TTCATGGCCT AGCTTACTTT ACAATTCTGC TGTTTGTCAA GTGTTCCTAT AGTTTTTTTT AAAGGTATGT TAACTATTTT TCCCTTTTGG TTTATATTTG TAGGAATCTT	120
TGCCTTTAAG TGTGCCCGTG CAGAAGAATT ATTTAACATG TTGCAAGAGA TTATGCAAAA	180
TANTACTATA AATCTCCACC TCCAC	205

(2) INFORMATION FOR SEQ ID NO:581:

TAATAGTATA AATGTGGAGC TCGAG

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GAAGTGTAAT	GTCAGACACA	CAAGAAAAGC	AAATCAGTGT	TGTAAGCTTA	AAGTACAATT	60
TCAAAGGTCA	TTACCAACAG	CAGGGTTTTT	TTTATACTTT	AAAAACATTA	TGCTACATAT	120
					AATGGAAATG	180
TCATCCAGCC	AGATCTCGAG					200

- (2) INFORMATION FOR SEQ ID NO:582:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 321 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GAATTCGGCC TTCATGGCCT	ACACAAATGT	TTGTTGAGTG	CTCATTGTAT	GTCTGGAGAC	60
CATTCTGTCT TCTTCCCTAA	GAGTGTTCAT	GCTGTTGGAC	CAGGTGTTAT	GATTTTGCTC	120
TGGAGAATAA GGTATTTCCA	CATGGAGCAT	GTGGAAAATA	TAGTGCCTAT	CTCCTGAAAG	180
GTCCAGGTGA TGCAAAGATG	AATGAGACAT	GATTGGAGGT	TTTTCTTCTG	TCTGAAATGC	240
AGACAGTTCT GGGTTGGGCA	GCTCTGTAAG	ATGCTGAACA	TGTGTCCTTC	CAAGAAGCAA	300
GGATCAGAAA GCAGACTCA	G				321

- (2) INFORMATION FOR SEQ ID NO:583:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 355 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GAATTCGGCC	TTCATGGCCT	ACACCATTGA	CTTCTTCTAC	CGGCCGCATA	CCATCACCCT	60
GCTCAGCTTC	ACCATCGTCA	GCCTCATGTA	CTTCGCCTTT	ACCAGGGATG	ACTCTGTTCC	120
AGAAGACAAC	ATCTGGAGAG	GCATCCTCTC	TGTTATTTTC	TTCTTTCTTA	TCATCAGTGT	180
GTTAGCTTTC	CCCAATGGTC	CGTTCACTCG	ACCTCATCCA	GCCTTATGGC	GAATGGTTTT	240
		TCCTGTTCCT				300
GGTTAAATCT	CTAATGTATT	GGCTAGATCC	AAATCTTCGA	TACGGCCACC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:584:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 374 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

AAGGAAATCG CAAAGAACGT GTTTGTGCAG AACATTTGAG GAAGTACAAT GAGGCCCTAC  AAATTAATGA CACAATTCGA ATGATAGATG CGTATACTCA TCTTGAAACT TTCTATAATG  AAGAGAAAGA TAAGAAGTTT GCAGTCATAG AAGATGATAG TGATGAGGGT GGTGATGATG  AGTATTGTGA TGGTGATGAA GATGAGGATG ATTTAAAGAA ACCTTTGAAA CTGGATGAAA  36	GGAAACTTCT	AGAAATAATG	ACAAGGATTC	AAACTTATTG	TCAAATGAGT	CCAATGTCAG	60
AAATTAATGA CACAATTCGA ATGATAGATG CGTATACTCA TCTTGAAACT TTCTATAATG 24 AAGAGAAAGA TAAGAAGTTT GCAGTCATAG AAGATGATAG TGATGAGGGT GGTGATGATG AGTATTGTGA TGGTGATGAA GATGAGGATG ATTTAAAGAA ACCTTTGAAA CTGGATGAAA 36	ATTTTGGAAC	TCAACCCTAT	GAACAATGGG	CCATTCAAAT	GGAAAAAAA	GCTGCAAAAG	120
AAGAGAAAGA TAAGAAGTTT GCAGTCATAG AAGATGATAG TGATGAGGGT GGTGATGATG AGTATTGTGA TGGTGATGAA GATGAGGATG ATTTAAAGAA ACCTTTGAAA CTGGATGAAA 36	AAGGAAATCG	CAAAGAACGT	GTTTGTGCAG	AACATTTGAG	GAAGTACAAT	GAGGCCCTAC	180
AGTATTGTGA TGGTGATGAA GATGAGGATG ATTTAAAGAA ACCTTTGAAA CTGGATGAAA	AAATTAATGA	CACAATTCGA	ATGATAGATG	CGTATACTCA	TCTTGAAACT	TTCTATAATG	240
	AAGAGAAAGA	TAAGAAGTTT	GCAGTCATAG	AAGATGATAG	TGATGAGGGT	GGTGATGATG	300
CAGATAGACT CGAG	AGTATTGTGA	TGGTGATGAA	GATGAGGATG	ATTTAAAGAA	ACCTTTGAAA	CTGGATGAAA	360
	CAGATAGACT	CGAG					374

(2) INFORMATION FOR SEQ ID NO:585:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

GAATTCGGCC	TTCATGGCCT	ACACACATAC	CCAACACACA	CACAGACACA	CACATACACA	60
GAATCAACAC	TCAACACGCA	AACACCCAAC	ACACACATGC	ACACACACTT	TCTGAAGATG	120
AGTTTTCTCA	TTTATGAAAT	GAGCTCATCT	GGACTTGCCA	TGAGGGTCCA	ACAGGTGCCA	180
TGCAATCAGG	TGTGCACTCA	GTATGGGCTG	GGTGGAGATG	GCCATCTCCT	TTCCCGTCCA	240
GGCCTGGTTC	CTGTGTGCTG	GGCCTCTGCT	CTTCCCCCCC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:1029:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 263 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ. ID NO:1029:

GACAAGCTGA GAAAATGA	AA GGAAAACTAG	AAGAATTGTC	TAATCAGTTA	CATCGCAGTC	60
AAGAGGAGGA AGGAACAC	AA AGAAAGGCCT	TGGAAGCCCA	<b>AAATGAAATA</b>	CATACCAAAG	120
AGAAGGAGAA GCTGATTG	AT AAGATTCAAG	AAATGCAGGA	GGCCAGTGAC	CACTTGAAGA	180
AACAATTTGA AACTGAAAG	GT GAAGTCAAGT	GTAACTTCCG	GCAGGAAGCA	TCCCGGCTCA	240
CTTTGGAAAA CAGGGAACT	TC GAG				263

- (2) INFORMATION FOR SEQ ID NO:1030:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 243 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

G.	AATTCGGCC	TTCATGGCCT	ACCTCCTACA	AATTTAATTT	TTTTATGAAA	TTTTTAGGTG	60
. A(	TTGTAAAT	TCTTCATGTA	TGAGGAGTTG	TGTTTATTAA	TGCTACTTTT	TAAATTTTCC	120
T	STGCCATGT	GGCAGATGTT	TATTCTCTTA	ATGCACTTCA	GGTTTGCTAT	CTGTAAAGCC	180
T	TGACCCAG	GCCTACTGAG	TCAAATCTAC	ATTCAGTGTA	ACATTAAAGG	CAGAAACCTC	240
G.	AG						243

- (2) INFORMATION FOR SEQ ID NO:1031:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 246 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

AATTCGGCCT	TCATGGCCTA	ATTGAATTCT	AGACCTGCCT	CGAGATTACA	GCCAGAGTCT	60
CCTAACTGCT	CTCCATCTAT	TCTCTAATCC	CAATAGCTAC	TCTCCATGCA	GCTGTCAGAG	120

TGGGCCTTAT AAAACATTGG TCAGGTCATG CCAGGCCTCC GATGGCTCCC ATCACACTCA GGGTAAGAGC CGAAGCCCCA TGTGGGTGTC TAAGGCCCCG TGTGATCCTT ACCCACTTCT CTCGAG	180 240 246
(2) INFORMATION FOR SEQ ID NO:1032:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 114 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:	
GAATTTACAC CTGCCTCGAG TACTCCCATG CCACTTTCAG CACAAATATC ACTTATTATG TGCTGCTTGA ATATTATTTT CTTTATTTCT AAGTTTGGTC CATTCAGTCT CGAG	60 114
(2) INFORMATION FOR SEQ ID NO:1033:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 302 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:	
GAATTGTTGT TCTTTTCTTT TCCATGATAT CATTATATGG ACAGTTTAGG GTGGTCTCAT GGATTATAAC CATTTGGATA TTTGGTTCAC TAACAATTTT CTTACTGGCC AGAGTTCTTG GTGGAGAAGT TGCATATGGC CAAGTCCTTG GAGTTATAGG ATATTCATTA CTTCCTCTCA TTGTAATAGC CCCTGTACTT TTGGTGGTTG GATCATTTGA AGTGGTGTCT ACACTTATAA AACTGTTTGG TGTGTTTTGG GCTGCCTACA GTGCTGCTTC ATTGTTAGTG GGAGATCTCG AG	60 120 180 240 300 302
(2) INFORMATION FOR SEQ ID NO:1034:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:	
GAATTCGGTC TTCATGGCCT ACCTGAGCAC TCTGCATTTT AATTCTGTGT TCTTTCCCTT TATCTATGTG TTGTCTCTGA GGAAATGTCC TTTAATGTCT TCCTCAGGCT TGATACCTAA TTTGAGATGG TTCAAACAAT TTTTTCCTTT TCCCTTCACT GGAAGCTTTG TTACTCATTC TGTTTGCTTT CATACTTTCA AATGCTGTCT TTTTATTTTT GGTGGTATTT TTTTTCTCTT TCTCAGGTGT AACATACCTC GG	60 120 180 240 262
(2) INFORMATION FOR SEQ ID NO:1035:	
(i) SEQUENCE CHARACTERISTICS:	

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(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) Totoboot. Tilled!	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:	
GAATTCGGCC TTCATGGCCT ACCTACTAGG CATGTTTTAT GACACAGATG ATGCGAGTTT CAAGTGGTTT GATAATTCAA ATATGACATT TGATAAGTGG ACAGACCAAG ATGATGATGA GGATTTAGTT GACACCTGTG CTTTTCTGCA CATCAAGACA GGTGAATGGA AAAAAGGAAA TTGTGAAGTT TCTTCTGTGG AAGGAACACT ATGCAAAACA GCTATCCCAT ACAAAAGGAA	120 180
ATATTTATCA GATAACCACA TITTAATATC AGCATTGGTG ATTGCTAGCA CGGTAATTTT	240 300
GACAGTTTTG GGAGCAATCA TTTGGTTCCT GTACAAAAAA CATTCTGATT CTCGTTTCAC	360
CACAGTTTTT TCAACCGCAA CCCTCGAG	388
(2) INFORMATION FOR SEQ ID NO:1036:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 258 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:	
GAATTCGGCC TTCATGGCCT ACTTTTTAGT AAAGAGCAAA CTCATAAATT TTGGCATCAG AGTTTGAGCT TTATTTTCT TAAATGAGTT TGAAATCAAT TTAATATTC TCTCCAATTC CCTAATGTCT CAGAAGTGAA TTTACAGTAT ACCTTTGTTT TTTCGTATTC TTAAGTAGTA TTTGGATTTT ATTTAGTAGT TGCAGTACTA AATAAGGAGT GGGGAGTTAA TTACAAAACG AATCAGGTGA CTCTCGAG	60 120 180 240 258
(2) INFORMATION FOR SEQ ID NO:1037:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 85 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:	
GCGATTGAAT TCTAGACCTG CCTCGAGTGA TTTGGCCTGC ATGGTTTTCC TCCTACCCCT TTTTCTTTGC CTGGGTCAGC TCGAG	60 85
(2) INFORMATION FOR SEQ ID NO:1038:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 248 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
424	

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

GGG3.00003.5.0						
GCGATTGAAT	TCTAGACCTG	CCTCGAGGGG	TTTGGAGCTC	TGTTGGGTGG	TGACCTCAGT	60
CCTCTTTTXCC	GGMGG33333					• • •
CCIGITIACC	CCTGCAGAAG	AAGGACCCAG	CCCAGTTCCT	GCAGGTACAT	GGCCGAGCTT	120
CCAACCTCCA	COMOGRAMMON					
GCAAGGIGCA	CCTGGATTCT	GCAGTCGCCC	TGGCCGCTGA	GAGCCCTGTT	AATATGATGC	180
CCIGGCAGGG	GGACACCAAC	AACATGATTG	ACCGATTCGA	TGTCCGTGCT	TAGGCCATGA	240
AGGTCGAG						210
AGGICGAG						248

- (2) INFORMATION FOR SEQ ID NO:1039:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 253 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

GAATTCGGCC TTCATGGCCT GGTGACTTTT GTTCTAGTAA GAAGATAGTT ATAACTGAGA GAGTGCTGTG GTGCGGTCAT CTCAACCCTC GAG	GTATTCTCAA TAGCGGTTTT	AGAAAAGAGA TGTTTTTGTT	GTGAGTAGCT TTTTGTTTTT	ATTTTGGGAT GGCCCAGGCG	60 120 180 240
CTCAACCCTC GAG					253

- (2) INFORMATION FOR SEQ ID NO:1040:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 232 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

GAATTCGGCC TTCATGGCCT	AGTTCAAAAA	TAAAGCAAAT	ATTTATTTTG	GTATTGTTTT	60
GAGCACAGCT GATTTTTAAC	ATTTTCTTTC	ATAACACTCA	GAAATCATTA	ACAATTGTTT	120
GCTCATTTGG TATGGGTTTT	TTGTTCTCTT	TTTTTTTTTG	GGTTCTTTTA	GGTGCTTTCT	180
TTTAACATTG GTCATGTTTC	ACCCTTTTTT	TTTTCATCCC	CCCAGTCTCG	AG	232

- (2) INFORMATION FOR SEQ ID NO:1041:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 272 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

GAATTCGGCC	TTCATGGCCT	ACAAGGACGT	TAAAGGCATT	TTATTCCAGC	GTCTTCTAGA	60
GAGCTTAGTG	TATACAGATG	AGGGTGTCCG	CTGCTGCTTT	CCTTCGGAAT	CCAGTGCTTC	120
CACAGAGATT	AGCCTGTAGC	TTATATTTGA	CATTCTTCAC	TGTCTGTTGT	TTACCTACCG	180

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TGGACTTTCT CCAAAGGCAC TGGACCCTCG AG

TAGCTTTTTA CCGTTCACTT CCCCTTCCAA CTATGTCCAG ATGTGCAGGC TCCTCCTCTC

240

272

(2) INFORMATION FOR SEQ ID NO:1042:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 286 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:	
GAATTCGGCC TTCAGGGCCT AGATTAAATC TCAAGGTGGA CTAGGAGAGA ACAAGCAGAC TTCTATAGAA CAGTGTCTTC CTTTGGTGTT GTTTACGATC AAGAAAAGAA	60 120 180 240 286
(2) INFORMATION FOR SEQ ID NO:1043:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 230 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:	
GAATTCGGCC TTCATGGCCT AGTGTAATCT TATTGGGAAC CTAAAACTGC TCTTAAAGTC TTTTTGAAAA CTCAGACATA TTTTTGGCAT TACCTTTTT TTATTGGAAA GGAAAAATGA AAACCTTTCA TTTTATTAAT AATTCTATAT TCCACTCCTG TATTTTCTTC TCTTGGATGA TGATGGTGAT ATTATTTCTC ACTTTTCAAA ATAATACCCT GGGACTCGAG  (2) INFORMATION FOR SEQ ID NO:1044:	60 120 180 230
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 238 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:	
GATTCGGCCT TCATGGCCTA GGGAAAATAA AAATGTATTC AGTAGCACGT GGGTTATGGT TTCTCATAGA CCAGGGGATA AGATTAAAAG TCACTGAAGA GTGGGAAAAT GCATGTTGAG AAGATGAGAA TGGCCTGTAT TTTCTCCAGG GGAATCTGTG TAATGTGCCT TTTCCCTCTC CAAATGCCTA GAACCATGGC ACTGTGTCTT ATTTATTTAA CCGTTGGGCC GTCTCGAG	60 120 180 238
(2) INFORMATION FOR SEQ ID NO:1045:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs	

<del>nami</del> i namini i mengangkan dinamakan m<del>ang mengangan di</del> palaut kalaut namini kalaut nalaut nalau di palaut n

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:	
TAATTCATCT AAGTTGTTGA ATTAGCATAA AGTTTTTAAT AAAATTTTAT GTAATTCCTT TTTAGAGAAC TAACTTTTGA AATTGCTGAT TTTCTGTTTT CCGTTTCAAC ATTTTACACA CTGGTAGTTA ATAGTTTTT CTCTCCAGCT TACTTCGTGT TTGATTTACT TTTCCTTTTC TGTCTTCTTG AGGTGGAAGC TTAGAGGATT AATGATTCCA TTTCTTTCTA ACGAAATCAC TTAAAACTAT AAATTTCACT CCAACTACTT CTTTAGCTAA ATTCCATAAA TTTTACTATG TTGTGTTTCC CTTTTCACT CCGTCTCCTC GAG	69 129 189 249 309 333
(2) INFORMATION FOR SEQ ID NO:1046:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 429 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:	
GAATTCTAGA CCTGCCATTG TGGGGAGTGG AAGTGGCATG ACCTCAGGAG CCAGTTCTGA GTCCAGGTGA ACCAAAGCTC AGTTTCTTC ATCTTTGAAC CTGAACCTCT TACCTCCAAG AAAAAGGGCC CAGGAATTTG GGCCTTCTTG TTTATTTGTC CTTCTGCCCC TCTCCCTATC TAACCCCTGG GTAAGGGTGA GCTTGAAGGT GATGGTGACA GTGGCTTCTG TGTGTGTCAG TCCACCCTCC AAGCAATGCT TAGAAACCAG TCCATAAGCC AATTAACACA TCATTTTTAG GGCAGATTTG CACATTCCA GTTGTTTACA TGTTTCGTTA AGTACTAACC TCCAAATTAA TAAAGCATGA CACATGACAT CACACATTTC ACAATTTGTA CCCCAAGCAAA GTTCATGGAG GTACTCGAG	60 120 180 240 300 360 420 429
(2) INFORMATION FOR SEQ ID NO:1047:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 65 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:	
. GCTTGGTAGA CCACATCCAA GGGACGATGA GGTTTCCCAG AGGAGGAGTG GTCACCATGA TCGAG	60 65
(2) INFORMATION FOR SEQ ID NO:1048:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 498 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

GAATTCGGCC	AAAGAGGCCT	AAATTTGGTT	TAATGTGTCA	TCAAACTTTG	TATTCAGCTA	60
TCTAGAGCCA	TTTTCTGGAT	TCATGCAATA	CATTTTCCCC	AAACCCTTTT	TATTTTGAAA	120
AAGCTCAAAC	ACAGAAAAGT	TGAAAGAATA	GCGTAAAGAA	CATCTGGATG	TGGTGCAGGG	180
			GGATTATTTC			240
GTAAGACCCA	ATGTCTACAA	AAATGTTTAC	GGATAAACĊA	GGCGTGGTGG	TGAGGTAGTC	300
CCAGCTACTC	AGGAGGCTGA	GGTGGGAGGA	TTGCTTGAGC	CCAGGAGTTC	AAGGCTGTAG	360
TGAGCAATAA	TCACATCACT	GCATTCCAGC	CTTGAGTAAC	AGTGAGACCT	GTCTCAAAAA	420
AAAAAAAAA	AACACCAAAA	ACAACCAACT	GTGTATATCT	TGCACTGATA	ATCCCCCGAA	480
TTCTAGACCT	GCCTCGAG					498

- (2) INFORMATION FOR SEQ ID NO:1049:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 443 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

GAATTCGGCC AAAGAG	GGCCT AAGCTGAGAT	GGGTGTTAAA	AGTTAAGACA	CAGCTTAAGA	60
CAGAAGCATT GTAAA	ACAGG AACAAATACT	GGCTTAAACC	TGATGTCTCT	AACTATATTC	120
CTCTATTTTA AGAATO	GTTTT AGTATCTGAT	AGTTTCATCA	GCCTTTCCAT	TTTCCAATAT	180
GTGACCTTTA TTCCC	ACCAT GTCCCAAATA	AACGAGTCCT	AGGATTTCCT	AGAAGGTGGA	240
CCTCAATTAT TGTGT	CCCTT TTATATATA	GGCAAACATT	GCTTTTAAGT	TCTGTTGGAA	300
CATGGGAACT TTCAC	TAGAA TGCTTAGAAT	GTTCAGAAAA	AATGTCCCAA	AGCTCTCTTC	360
TGGTCCATAC AAGAC	AATCA GAATGTAACA	CAGTAGCAGA	GGGTGTGGAA	CATACACTAG	420
TCATATTTGA TTCTC	ICTGT CAG				443

- (2) INFORMATION FOR SEQ ID NO:1050:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 68 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

GAATTCGGCT AAAGAGGCCT ACTTCTGGCT ATTTTCAAAT ATATAATATG TTATTGTTAA 60 CTATACTC 68

- (2) INFORMATION FOR SEQ ID NO:1051:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 278 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

GAATTCGGCC AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	ACAATTCCCC	ACCACCGGAA.	
CACECECECE COLLABORA		O' CO' L'OCCA	AUAAT I COOC	ALGAGGGLAA	60
GACTCTGTCT CCAAAAAAA	AAAAATTTAA	AAAAAAAAA	ATTTTTTAAA	AAATTTTANT	120
TAANGTAAAT TTAAAAATGT	TCAGTGAAAT	CCTAAAAAA	222222	~~~	
00000000000	1 CHO I ONHI	MAMAMATOO	AAAAAAAGAC	GCACAAAATA	180
CCTTCATGTT TCTCATCTCT	TTTTCCCTTC	AGATTCTGCC	TTTCTTCCAA	TTCACCTCTT	240
CTTTTCCAGT CTTTCAACCA	1001001001			TICAGCICII	240
CITITECAGI CITICAACCA	ACCACCACGA	CTCTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:1052:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

CTCGAGGACC	AAGGATGAAG	<b>Δ</b> GCδTδδCδδ	CATCAACADO	am	ATAAAATTAT	
		NOCHIMAGAA	GAIGAAGATT	GTAAACTTGT	ATAAAATTAT	60
CTTGGTGAGA	AGACAAATTG	TAAAGTAGAT	ATTTGTAATC	TTTTACCACT	TTGGGGTTGC	
The state of the s	CAATTCATCA	C 3 A OFFICE S		TTTTTCCACI	1100001100	120
1111110000	GMATICATCA	GAACTTIGAA	TTTTTTTTT	AAATGGGCTG	TTTTTAATGC	180
AGGGGCTTTT	CTTCCCTAGA	AACCCAATTC	TAAGCACAAA	7 7 CM 7 7 7 7 7 7	ACACCAAAAA	
TRABBARACC	222222222		*1210CAOAAA	VACIANAVANI	ACACCAAAAA	240
IMMMMACCC	CCCTCGTGCC	GAATTNTNGG	CTTCGGGGGC	CAAATTCCGG	CCTCTTTGGC	300
CGAATTC						
						307

- (2) INFORMATION FOR SEQ ID NO:1053:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 332 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

GAATTCGGCC AAAGAGGCCG GAATT	TTGGCC CTCGAAGCCA AGAATTCGGC A	ACGAGGGCAG 60
TTAAGATCTG GGTGATTCTT TAGGC	BAAACG GCTGGTTGAG AGGCTTTGAT G	COADGOCAG 60
TCTCTGCTGT GGCCAGAAGG TGGTC	CTAGA GGCCAGTCCC ACTTGGATGT G	GAATCCCAT 120
TCTGCCAGGA TTCAAACCAC AAACC	ACADE EGGLAGICCC ACTIGGATGT G	SACCCTGGCC 180
TCANACAC TCANACCAC AAAGA	ACATT TGGAACTGGG ATGTTTGCTT T	GAAGCAGCC 240
NAMACAAG IGAAAAGGAA ACCAA	GATAA CTCTCTCTC CTCCGCTGGC A	AGGATCAAA 300
AATACCTTGT GCAGGGAAGC CCGAG	SCCTCG AG	332

- (2) INFORMATION FOR SEQ ID NO:1054:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 389 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

GAATTCGGCC	AAAGAGGCCG GAATTCGGCC TCGAAGCCAA GAATTCGGCA CGAGGCCTCG	60
TGCCGCGCCG	TTTTTTTTT TTTTTTCAC AGGGGGGCAG TCGGGATTAT AATACACTGT	120
AGCAGTTGGC	TGGGGAAAAG TCTATCAAAT TCCATGACCA ATTGGACTTT TCTCCCACCT	180
GTAATATAAA	TAAAATATGT ACTGTTTCAT ACTGAATTTT TTCAATGCAT TGGGGTTCAA	240
CATAAAAGGC	ACAAATAAAT AAAAATATCA TTAAATAAAC GGAAATTACA ATTTCAAGTT	300
	TTGTATCTCA CTGTTTGGTT ACTTTTTCCA ATTTAATTTG ACAGACTTAG	360
TAATAGCACA	CAACTGTCCT ACCCTCGAG	389
(2) INFORMA	ATION FOR SEQ ID NO:1055:	
(5) 111101112	1210 FOR OBY ID NO. 1055:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 213 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1055:	
GAATTCGGCT	AAAGGGTCTA CGAGGTCAGC AAGGACGCCC AAGGAGACTC AGTCATGAAA	60
GGTGAACTGC	TCCTGTTTTC CAGTGTGATT GTCCTGCTCC AGGTGGTATG CAGCTGCCCG	120
	ACTGTCAGTC ATCTACAAAT TTTGTAGACT GCAGCCAGCA GGGTCTGGCC	180
GAAATCCCTT	CCCATTCCCC TCCGTCGCTC GAG	213
(2) INFORMA	ATION FOR SEQ ID NO:1056:	
(i)	SEQUENCE CHARACTERISTICS:	
,-,	(A) LENGTH: 173 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
		•
(11)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1056:	
GAATTCGGCC	TTCATGGCCT AGCGATTCCA GGTTTTAAAT AGTTTGTAAA TTTTCAGTTT	60
CTACACACTT	TATCATCCAC TCGTGATTTT TTAATTAAAG CGTTTTAATT CCTTTCTCTG	120
TTCAGCTGTT	GATGCTGAGA TCCATATTTA GTTTTATAAG CTTCCCCCTC GAG	173
(2) INFORM	ATION FOR SEQ ID NO:1057:	
(1)	SEQUENCE CHARACTERISTICS:	
(1)	(A) LENGTH: 555 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(11)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1057:	
GGTCATACTC	TCTCATCCAG ACTGGAGTGC ATGGAGTGCA GTGGCACCAT CTCGGCTCAC	60
TGCAACCCCT	GCCTCCCAGG TTTAAGCAAT TCCCCTGCCT CAGCCTCCCG AGTAGCTGAG	120
ATTACAGGCA	CATGCCACCA TGCCTGGCTA ATTTTTGTAT TTTTAGTAGA GACGGGGTTT	180
CACCATGTTG	GCCAGGCTGG TCTCGAACTC CTGACCTCAA GTGATCTGCT CACCTCAGCC	240
TCCCAAAGTG	CTGGGATCAC AGGTGTGAGC CACTGCACCC GGCCTAGTTT CCATTTTCT	300
	ACTICTATIC ACTICATIAN AC ACTATIANTETE ATTENDED A TRANSPORTED A	200

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CTTAGTTCTT TGAACATATT TATAAGAGCT ATTTTTAAGT ATTTGTCAGT TGAATCTAAC ATCTTTTGGG GCCATTTTCT ATTGACTGCT TTTTTCTTGA TGATGAGTCG CATTTTCTT TTTGCCTATC TAGTAATTTT TAAATTATAT ACTGTACCTT GTGGATGTAT GGTAGAGACT CTGGGGTCTC. TCGAG	420 480 540 555
(2) INFORMATION FOR SEQ ID NO:1058:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 324 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:	
GAATTCGGCC TTCATGGCCT AGAATGTTAG AAGGTGCCTG CCGAGGCGGG ACAGAGTGTT CGCTCGCGCT GGAGAAGGCT CTGCTCAGCC CTGAGAGTCC CTTCCTGCCC CACCGATACT GGCACTTTAA CAAGGAAGCT GACCGCACAG TGTCCAGACG AATTGGCCCC CAGAAGATGG GGAGTTCTGT CCTGCCCTTC TGTGTCTGCG TGACCTCACC CAGCCTAGGA GGGAGGTGCA TTCAGGGTAG ATTTGCCTCT CATTCAAAGT TCTGGGGCTT TGGGTGGAAA ACAGCCAGCT TTGGCGCTGC TGGGGAGACT CGAG	60 120 180 240 300 324
(2) INFORMATION FOR SEQ ID NO:1059:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 219 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:	
GAATTCGGCC TTCATGGCCT ACTTGATGCT GCAAAGAACA AGATGCGAGT GAAGATCAGC TATCTAATGA TTGCCCTGAC GGTGGTAGGA TGCATCTTCA TGGTTATTGA GGGCAAGAAG GCTGCCCAAA GACACGAGAC TTTAACAAGC TTGAACTTAG AAAAGAAAGC TCGTCTGAAA GAGGAAGCAG CTATGAAGGC CAAAACAGAG CAGCTCGAG	60 120 180 219
(2) INFORMATION FOR SEQ ID NO:1060:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:	
GAATTCGGGC CTTCATGGCC TAGTATTTAT AGCCAAGGAA ACAGGGCTAT GAGTTTGTAC TGTAGGCAGC AGTAGGAGG GGGAATTGGA AGCAGGGGGG AGGGCTCTGC AGTAGTTCAG TTGATGCATA CATAAGGCCT GAATTAGGGA ATTAGGAGAG TGATCATAGG TGTGGAAAGG AGGGGAGGGC TTCCAGGCAC ATTTGGTGTA AAATGGATAC AACTTGGTAA CCTGTACATT GCTACCTTTG CACATTTGGT TTCCCCTGTC TCAAAGGCTC CCTCTTCTCG AG	60 120 180 240 292

- (2) INFORMATION FOR SEQ ID NO:1061:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 386 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

GAATTCGGCC	TTCATGGCCT	AAAGAAAACA	AACAAACAAA	GAGAAAACCC	ATGAGCATTT	60
TAATTCTGAC	TTTTTTACTT	TTCTCCCTAC	ATTTAGAATA	CTGTGGCACT	TTCTGTTATC	120
CAAATGTGTC	TCAGTCTCCA	TATTTAAGGA	CTGTGGGTGA	AAAGCTTCTA	CCTGGAATTG	180
AAGTGCTTTG	GACAGGTCCC	AAAGTTGTTT	CTAAAGAAAT	TCCAGTAGAG	TCCATCGAAG	240
AGGTTTCTAA	GATTATTAAG	AGAGCTCCAG	TAATCTGGGA	TAACATTCAT	GCTAATGATT	300
ATGATCAGAA	GAGACTGTTT	CTGGGCCCGT	ACAAAGGAAG	ATCCACAGAA	CTCATCCCAC	360
GGTTAAAAGG	AGTCCTCACT	CTCGAG				386

- (2) INFORMATION FOR SEQ ID NO:1062:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

GAATTCGGCC	TTCATGGCCT	ACATGAAGCT	GAATTACTCT	CATCTTATAT	CTCTCTGCAG	60
TGGCATATCC	TGATGGTGAT	TTCCTCTTTT	TGTGCCTCAG	TTTCACCCCC	TATGGAATGG	120
GGATAAACAC	TTGCGGCTGG	GCATGGTGGC	ATGTGCCTGT	AGTCCCAGCA	CTTTGGGAGG	180
CTGAAGTGGG	AAGATTGCTT	GAGGCCAGGA	ATTTGAGACC	AGCCTGGGCA	ACATAGTGAG	240
ACACTCTCTC	TACAAAAAA	AAAAAGAAAA	AAAAAATCAG	ATGTGGTTGG	TGCATGCTAC	300
TGAGGCGAAA	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1063:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 289 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (2) INFORMATION FOR SEQ ID NO:1064:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 288 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

GAATTCGGCC	TTCATGGCCT	ACAGAGCTGA	GAAATAATTC	CCTTGTGTGT	TTATAAGTAA	60
GAGTTAAATC	CCTCCCATTG	TAATGTAGCA	CCAGATCGAA	GTAAACAGAC	TATGATTTCA	120
GTGCTAGACA	CAGCCTTAAG	GCAGAAGAAA	TTACACTGTC	ATGCAAAGGA	TATGTAGCTG	180
CTGCTATTTT	GGTGCTTGAA	TTCTTCGTTG	TCACATAGTT	GAAGGCAATC	CAGATGAGGA	240
AGAGTGTTAA	CCAACAAAAA	GAGAAAATTC	CCTGCACATG	GTCTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:1065:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 495 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

GAATTCCCAT TAATGAGCAG TCTTCAGTAT TAAAACCACT GTCTTGTCAC CTCATTTTGC 1	.20 .80
	.80
ATTACTGTCT TCCGTGGATG TTTCAGTTAC AACTGTAATG TTATTTATAG AACAACATTA 1	
ATCCATTAAA GCTAACCTAT TTTTCAATAT TTATGATAAT CTATGTACAT ATATTGTCTG 2	240
TCCATATGTA TTTGTAAATA GGTTGTATAT AATGTCAGGT TTGGGTCTTG GGTTCAAGTG	00
TATATATTCC TGTAAGTTTC TTAACTGCAT TTTGATGAAT TCACATTATG TAACTATAAG	60
AATTGTCCCA AAAGTACCTG TACAGAAAAT TGAATATTGA AAAATTGACA AATTGTGTAC 4	20
AAACACTAAA AAAAACTTGT TTAAATTGTA TTTGCAATAA ACAACATCAA ATTTTTTCAT 4	80
GAAATCTGCC TCGAG	95

- (2) INFORMATION FOR SEQ ID NO:1066:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 507 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

GAATTCGGCC	TTCATGGCCT	AAAGATTATA	AAGGAAAGGG	GGGTAGTTAA	GATTTAGAAT	60
TCAAGTTAAA	TTTCAGAAAT	TGGGGCAGTC	AGGCATTTGT	ATCTTTTAGG	GCAACAAGTA	120
AAACATGTAG	AGTGCTTGCT	ATCCCACTTC	ATAAAGCTTT	TACCCAATCT	TATTTCTAAA	180
CCTCTGTGCA	TTCTTAGTGT	CTTCTCATTC	TGAAACAGAA	AATAAGGAAA	AACATTTAAC	240
TTAGTTTTCT	AAAATCAGAT	AATCCTAAAC	AAAAATGTTA	GTCAGGGTCA	CTAAAAAGTA	300
TTGCACATTT	ATATAAATAC	AGTCCTTTTA	AAATTTGACT	TTTAAAAAAC	AAAAGACTTT	360
GTACGATATT	GTGTTTTTAT	TGCGTTTGCA	ATATTTTTAT	AGTAGCCTTT	ATGAACTCAG	420
TATAAGTGCA	AGTTGTTTGA	AAAGGTGTTT	TTATTAGTGC	ACAATAGAAT	TGTGAGGTTT	480
TCAATAGATG	TCATGAGATT	CCTCGAG				507

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- (2) INFORMATION FOR SEQ ID NO:1067:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

GAATTCGGCC	TTCATGGCCT	ACTTATTTT	TTCTTTTAAA	CAAATAAGCA	CACATTCTTT	60
TTAAATAAAG	TTTCTCTTCC	CCAACCTAAA	AGTAGTAATG	CTAGAATTTG	AGCATAGCAG	120
AAAAATATTT	AGGAAAATTA	AATCCCAAAC	AAGAGAGACC	ATCTTGGACT	GTGCTCACTC	180
GGGTGGAAAG	TCGACCCAGG	TGCCTGTGTG	CTTGACAGAG	GCGTGGCTGC	ATCCGCGTAG	240
CTGACCTTCA	GATGGACTGG	AGTTAGCACA	TTTGTAGTCA	TTTTTCCAAC	CATTCTTTCG	300
TATCTGAGGT	ACGTTTTTGA	CCTGTTTTAG	TATGTCACTC	GCGATCTTGA	AGCACACTCT	360
TTCATTTACT	TAAATATTTC	CTGAGCACTC	GAG			393

- (2) INFORMATION FOR SEQ ID NO:1068:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 290 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

GAATTCGGCC	TTCATGGCCT	AAGGTAATGT	GTCAGTGGAT	GGAAAAGTTT	AGAAAAGATC	60
TGTGTAGGTT	CTGGAGCAAC	GTTTTCCCAG	TATTCTTTCA	GTTTTTGAAC	ATCATGGTGG	120
TTGGAATTAC	AGGAGCAGCT	GTGGTAATAA	CCATCTTAAA	GGTGTTTTTC	CCAGTTTCTG	180
AATACAAAGG	AATTCTTCAG	TTGGATAAAG	TGGACGTCAT	ACCTGTGACA	GCTATCAACT	240
TATATCCAGA	TGGTCCAGAG	AAAAGAGCTG	AAAACCTTGA	TACACTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:1069:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 319 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

GAATTCGGCC	TTCATGGCCT	ACTCGACTCA	TATTTTTATC	ATACATTTCA	AAGTCAGTTG	60
CTGATGTTA	TCCCATTTCA	ATGTGGGGCA	GACTCTCGGG	GTAATTTCAA	AAAGATGTCT	120
CAAACATGTT	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	180
TGTGGAGACA	GGGTCTCACT	CTATTGCCCA	GGCTGGAGTG	CAGTGGTGCC	ATCATGGCTC	240
ACTGCAGTCT	CGACCTCCCA	GACTTAAGCA	ATCCTTCCCA	AATAGCTGGG	ACTCCAGGGG	300
CACCCCACTA	CAACTCGAG					319

(2) INFORMATION FOR SEQ ID NO:1070:

PCT/US98/06955 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 392 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070: GAATTCGGCC TTCATGGCCT ACTTCTAAAT GGCAAACAGT TGTCTTGAAG GCACTGTCTT TTTCTACCTA GATGTTGGGT GGAAAAAAA AAAAAAAGC TGCCTTTTAT ATAGAAGTTC TTGGGAATAT TTCTCATATA GTGAGATGAA CAGAATGCAA AAGTTTTCTT CCTGCAGGAT 180 CTCCCAAAAT CCTTCTTGGC TTGAATTTTT CTTCTCACTT TTTCTTTTGA AAAGCTTTGT 240 TCCTTTTGCA CCTTGGAAAA ATAAGTCTTG TTTGTCCTGA CAGCAGAGTG CAAGCATCTA 300 TTGCATCAAA ATTCCCAAGT GGAATAGAAA ACCAATGGTC CTTTTCTGAA TTTCGTTAGC 360 AGTAGCAACA AACATTTCAT TATAACCTCG AG 392 (2) INFORMATION FOR SEQ ID NO:1071: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 421 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071: GAATTCGGCC TTCATGGCCT ACACAATGGG AATCCAAGGA GGGTCTGTCC TGTTCGGGCT 60 GCTGCTCGTC CTGGCTGTCT TCTGCCATTC AGGTCATAGC CTGCAGTGCT ACAACTGTCC 120 TAACCCAACT GCTGACTGCA AAACAGCCGT CAATTGTTCA TCTGATTTTG ATGCGTGTCT 180 CATTACCAAA GCTGGGTTAC AAGTGTATAA CAAGTGTTGG AAGTTTGAGC ATTGCAATTT 240 CAACGACGTC ACAACCCGCT TGAGGGAAAA TGAGCTAACG TACTACTGCT GCAAGAAGGA 300 CCTGTGTAAC TTTAACGAAC AGCTTGAAAA TGGTGGGACA TCCTTATCAG AGAAAACAGT 360 TCTTCTGCTG GTGACTCCAT TTCTGGCAGC AGCCTGGAGC CTTCATCCCT ATACGCTCGA 420 421 (2) INFORMATION FOR SEQ ID NO:1072: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 335 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA

60

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

(	BAATTCGGCC	TTCATGGCCT	AATCGGTCAC	TGATAGTATG	TATTTCTTTA	GTAAGAATGT	60
C	<b>TTAAAATTA</b>	CAATGATCTT	TTAAAAAGAT	GATGCAGTTC	TGTATTTATT	GTGCTGTGTC	120
7	GGTCCTAAG	TGGAGCCAAT	TAAACAAGTT	TCATATGTAT	TTTTCCACTC	TTGAATCTCA	
(	ACACTGTAC	TTTGAAAATT	TCCTTCCATC	CTGAATAACC	AATACAAGIG	GCCATATATA	180
7	TGCCTCCTT	ATCCTTGAGA	TTTCACTACC	TOTAL TOTAL	AMIAGAAGAG	TAATTGTTAA	240
z	ATCTGTGAA	ACAATAAAA	GTGGATCCCC	TITAIGITAA	AAGTTGTGTA	TAATTGTTAA	300
•	- CIGIOAA	VOUV! WWWW	GIGGATCCCC	TCGAG			335

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 362 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073: GAATTCGGCC TTCATGGCCT ACAAAAATAG GCACAGTTTC AGATGCTTCA GCATATGAGG 60 CATGGATACT TCAATCATTT GCAAAGGGTT CTGCTCAGTA GACTGAATGG AAAAGATGGT 120 CATTGCTCTT TAATGTAATT TTGCAGCTCT CATCAAAGAA AATATCTCCA TGAAATTTAT 180 TGGTAACTGT TTATCTTTGA TCAGTGCAAA CTGAAGTCAA ATATACAAGG TAAACACACA 240 TAAAGATAAG TTCACACATT TCTGTGAATT TTCTAAATGT ACACACTTCT GCAAATTCTC 300 TAAATTCACA AATAACAAAT TTGCATGCAT GCAAGCATAT GTGCACATGT GCACACCTCG 360 AG 362 (2) INFORMATION FOR SEQ ID NO:1074: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 612 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEO ID NO:1074: GAATTCGGCC TTCATGGCCT ACCCAGGTGA TCAATGTTTT CAATGCGATC AGTAATAACC ATGTGCTCAT GAATCAGATA GGACTGAGGC AAATAGGTTC CAGCCTTGAT GTTAATAAGT 120 AACTCCAGTA GGTTTCTGGG TGGCATAACA ATGGAAGTGT TCAGAGGGAT CACATAGCAC 180 TTATCCAGGT TAAGATCTAA ATAGGCTGTA AGTTTCTTGT TAAAGTCATG AACAATGTTG 240 GCAGGATCAC TATCTGCAAA CTCTGGGACA GGCACACTGA TAAATTCAAC TTCTCTTCTT 300 CAAAGATTTT AATATTTTCT TCAATTGTCT GGTAGAGAGC AGCTGGGGCA TCTGCAGAGG 360 GCTCATTTAA GATGACATCA TCTTTGATGT ACTTTATTCC ACAGTAGTAC ACGTCATCTG GTTGAAGTGC AAAATATTTG TACAAGTATG CTCCTCCTAG AATAACACCT GCAAGCATAA 480 ATGCTAGTCC AAAGCACATG CACCACCACC ACCCGGCTAA TTTTTGTACT TTTAGTAGAG 540 ATGAGATTTC ACCCTGTTGG CCAAGATGGT CTTGAACTCC TGACCTCAAG TGATCCGCCC 600 ACACCACTCG AG 612 (2) INFORMATION FOR SEQ ID NO:1075: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 252 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075: GAATTCGGCC TTCATGGCCT AAGTTTGTGG TCCTCTGAGA ATTCTCTGAA GGAGGAAATG 60 GGTTGACCTA TTTGGTTGCT ATGAAGTAAA AACAATCTTG TTTTCATTTT TTAGTGAACA 120

180

240

252

TCTGGGTTGC ATTTATTATT TCACATTCTG GAGATTCTGT AAAACCACAA TTTGATAATA

TGAGGGTTCA TCAAAGCGGT AATTATTGAG CTATTTTTAT AGTTGATTCA AGAATTAGGG

nga ngaw<del>a</del> ngayang ga

TGGCGACTCG AG

# (2) INFORMATION FOR SEQ ID NO:1076:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 151 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

AATTCTAGA	CCTGCCTCGA	GTGTGATACC	AGCAGCTATG	AACCAAACEG	M3 MM3 3 MM3 -	
مەس لا شاملىشاران	TTCTCTCTTTTC		NOCAGCIAIG	MAGCAMACTG	TATTAACCAA	60
ICITITIALI	TICIGIGITE	TGATGCATGA	CTTTCATGGC	CTTGTCAACC	CTACACACCC	100
GCCCCTCCC	ATAGCTAGCG	AACCTCTCCA	~		CINGAGACCC	120
	······································	AUCO I C I COM	G			151
	ICITITATT	TOTTTATT TTCTGTGTTC	TCTTTTATT TTCTGTGTTC TGATGCATGA	AATTCTAGA CCTGCCTCGA GTGTGATACC AGCAGCTATG TCTTTTATT TTCTGTGTTC TGATGCATGA CTTTCATGGC GCCCCTCCC ATAGCTAGCG AACGTCTCGA G	TOTTATT TICTGTGTTC TGATGCATGA CTTTCATGGC CTTGTCAACC	AATTCTAGA CCTGCCTCGA GTGTGATACC AGCAGCTATG AAGCAAACTG TATTAACCAA TCTTTTATT TTCTGTGTTC TGATGCATGA CTTTCATGGC CTTGTCAACC CTAGAGACCC GCCCCTCCC ATAGCTAGCG AACGTCTCGA G

- (2) INFORMATION FOR SEQ ID NO:1077:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 542 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

GAATTCGGCC	TTCATGGCCT	AGGAAGTAGT	CTABBBBBBBB			
CATCTCAAAA	TTCATGGCCT	HOUMBINGI	CIMMMMATI	AACAGTTATG	GTTTTAATAG	60
GATCIGAAAG	ACAATCTTTA	AAGAAATGGG	AGAAATTGGG	GGTATCAGTG	ስ እ <i>ርር</i> ሞአጥአርር	100
AACCTCTCTT	TGTACATAAA	TATCCTCATC	M3.00m3.03		MCCIAIACC	120
201 201	TGTACATAAA	INIGGIGATO	TAGCTAGATA	TAAAAATCAG	TGTCTTACTG	180
GCACCATTTA	CAGTTTAGAA	AACAATCTTT	ΤΤΌΤΤΑΔΑΔΑ	TCCCCATCTC	h Time on a more	
TTAGGAGCTA	רידייביים אינייביים	The management		IGCCCATCIG	ATTICIATT	240
	CTTGGATTTG	TATGTATTT	TTCTACGTGA	AAATATATGT	ACTCTTCACT	300
TTTGTTCCAG	TACTATAATT	GCTCATGCAC	TOTOTOTO	CTTTTCACAAC	1	
<b>ልጥልሮል እርጥም</b> ር	ATCABACATO		1011101000	CITIGAGAAC	ATTCAGTGAA	360
NINCHACIIC	ATCAAAGATT	TGCTCAAAGG	AGAAGAATCG	CATGAGTGTG	AAAAGTAGAT	420
GCTCGTAGCC	AGAACAGAAA	AGGTTACACA	TCATCATCA	101010	- SELIGINGAL	440
CTTCCTCCCC	C1=10.0.0.0.0.	MOOTINGACA	TGATCATGGC	ACAGAAGATA	GGAGGTTTGA	480
CITOGIGGG	CATAATGTTT	ATTATCCTTT	TTGAAATAAC	AGGGACCAGC	ACCACTOTOC	E40
AG				HOOGNECAGE	AGCACICICG	540
						542

- (2) INFORMATION FOR SEQ ID NO:1078:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 574 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

GAATTCGGCC	TTCATGGCCT	AGGTTGCCAT	TACTTGTGAT	GCCTCTGAAT	GTGGAGGCTG	
ACTCTCCCGT	CTCTCTGTCC	CTCCTACCCC	100000000	occicionni	GIGGAGGCIG	60
TTCC3 CTCCC	222222	CICCIACCCC	MCGGGGGGG	AGCAAAAGCC	ATCCTGGGCC	120
TICONCIGGG	CCAIGICITE	AGGAAGATTC	CTGAAGAGGA	GGGCCCCAAA	Th COMO COMM	180
TATAGGTTCC	CAGAGTGCCC	TAGAACATTC	TTACATACAT	A W/W/W/W/WARA	CAAGTAGGAC	
ፐርርልርርጥታልጥ	TTTCTCCAND	10000000	TINGNINCNI	ATTTTTAAA	CAAGTAGGAC	240
-carcerini	TITCICCAAT	AGTCCCCAAG	CAGTACAGGT	CACTTGAAGA	CATAAACATT	300
CITCITGGTT	GAGGGATCCA	CGCCCTTGTT	TCAGAAATGA	CACCACACAA	GGCTGTGAGC	
TCCAGGAGCA	TGCGTTGGGA	TOTOGGAMO	10000000	CACCACAGAA	GGCTGTGAGC	360
Thancome	TOCOT TOGGA	TGTCCGGATG	ACCGGGGTTT	AAAGGTTTTC	CTATTCTCGA	420
IAAAGCCTGT	GCGCACTGTA	CGGGGAGTGG	GGGTGAAGCG	TGTTCTCTAC	ATACCCAACA	480

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CACGGGCGCA TGAAGTCTGG GTGCTGTGCT CGAG

(2) INFORMATION FOR SEQ ID NO:1079:

CAGCCGCCTA AGTCACAAAG TCAGTGGTCG GCCGCTTCGA CCAACATGTG GTGAGCATTC

540

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 284 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:
GAATTCGGCC TTCATGGCCT AGGGGCCAGG CGGCCGCCG GAGTCTGGTA TCCTGAGCTT CGTGAGTTGA GCGCTGCTGC TCCGCGGTGG AGTCACCGCA CCGCTCCCGG GATCATGGTG TTCTACTTCA CCAGCAGCAG CGTTAATTCA TCTGCCTACA CTATTTACAT GGGAAAAGAT AAATATGAAA ATGAAGATCT GATCAAGCAT GGCTGGCCTG AAGATATCTG GGAGAGAATA TAGAAGACAT CCCAAAGGAA GTGCTGATGG ACTGTGCGCT CGAG  (2) INFORMATION FOR SEQ ID NO:1080:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 359 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:
GTGAACACCA GAAAATACCC TGCAATTCAG CAGAACCAAA ATCCATACCT GCCCTTTCAA TGGAAACACA GAAACTTGGT TCAGTTTTGT CTCCAGAATC GCCAAAACCT ACTCCTCTTA 12 CTCCCCTGGA GCCTCAGAAA CCTGGCTCTG TTGTTTCTCA TGAGCTACAG ACACCTCTTC 18 CTTNTCCTGA GCCTTCAAAA CCTGCCTCTG TTTCTTCTCC TGAACCTCCA AAATCAGTCC 24 CTGTTTGTGA GTCTCAGAAA CTTGCCCCTG TTCCTTCTCC AGAACCACAG AAACCTGCCC 30 ATGTATCTCC TGAGTCAGTA AAGGNTACTA TTNGTAATCC CAAACCCCAG ATTCTCGAG 35
(2) INFORMATION FOR SEQ ID NO:1081:
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 474 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:
GCCCGGCAGA TGGGAAACGC ATCATATTCT GATTCCTACC TGGAAGGAAT TTTGTTGAAA GGGGTTTTCA CCTGTGAGCC TTGGTCTGTC TCGGTAGGGT GGTCAACTTC AGTGGACTGT 12 GGTTGGTTTC AGAGCGCCTG GCTGAGGAGT TCCACTGAGG GGAGCACTGG AGCAGCCCTT 18 TGGCAGAGGC TGAGGAGGGA GATGGACCAG CCCACGCCTG GCACCTGGCT CCATGGCATA AGGAAAGGGA GATGCTGGCC TCTGTGCTCC TGCTGTCTTT TCCTGTTTCT GTTTGCGTTT 30 GACTTAGTAG CAACCGACAG AGTGGCAAGG GATTTGGTCT TCAGCAGTAG ACATCCTTCC ACCCCTGCCC TCAGCCAAGT CTCTTGCTGC CATGCCAATG CTATGTCCAC CCTTGCCCCT 42

> CGGCCCAAGA GTGTCCAGCG GTGGCCCACT TTTTCCTCCC ACCACAACCT CGAG 474 (2) INFORMATION FOR SEQ ID NO:1082: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 505 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082: GAATTCGGCC TTCATGGCCT AATGTGTGTG GCACAAAGAA GAAAGTGGAC TCTACACTGT 60 GTTAGTTAGG AAAACCAGAA ATTGGGCCAA ATTGCCTGTT TAGTGGGAGA GATANCTTTT 120 GAGAGCTGTG ATCCCGCTGG TGTGGCTGGC TCTGGGCAGA TATTTGTATC TGAAATGACT 180 CATGCTGTGG GACCCTTCCT GAGATCTAAC ACTTACAGTG GTTTGATCAG AAATTGCACC 240 ATGCTTGCCA AGCAACTTTT GGACTAAAAG TTGCTGCCCA CGTATATCAG GGGAAGAATA 300 TATATATATA TATATAGT ACCTATCTTA GCATCTGATT TGTATGACCA TTACTTCAAT GTAAAATAAT AAATTGGCTT TCCAGCTTAA ACTTCAATTT CTTGTATATT ATATGATCAT 420 GAGACAACCT CCCTGGGCTG ATCAACAGCA GGACGCTAAA AAGATTGAGT ATCTGAGTCA 480 GGAAGGTAGA GGGCCAAACC TCGAG 505 (2) INFORMATION FOR SEQ ID NO:1083: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 481 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083: GAATTCGGCC TTCATGGCCT ACTACTATTC AGAGACAACA GTGACACGGA CCTATGTGAT 60 GCTGGCCTTA GTGTGGGGAG GTGCCCTGGG CCTGGGGCTG CTGCCTGTGC TGGCCTGGAA 120 CTGCCTGGAT GGCCTGACCA CATGTGGCGT GGTTTATCCA CTCTCCAAGA ACCATCTGGT AGTTCTGGCC ATTGCCTTCT TCATGGTGTT TGGCATCATG CTGCAGCTCT ACGCCCAAAT 240 CTGCCGCATC GTCTGCCGCC ATGCCCAGCA GATTGCCCTT CAGCGGCACC TGCTGCCTGC 300 CTCCCACTAT GTGGCCACCC GCAAGGGCAT TGCCACACTG GCCGTGGTGC TTGGAGCCTT 360 TGCCGCCTGC TGGTTGCCCT TCACTGTCTA CTGCCTGCTG GGTGATGCCC ACTCTCCACC 420 TCTCTACACC TATCTTACCT TGCTCCCTGC CACCTACAAC TCCATGATCA ACCCTCTCGA 480 481 (2) INFORMATION FOR SEQ ID NO:1084: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 389 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084: GAATTCGGCC TTCATGGCCT ACCATTTTA TTAAACCCAA ATCCATGGAA AATATCATGG

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AAATGAATAA GCGTCTAACA GAAGAACAAG CCAGAAAAAC ATTTGAGAGA GCCATGAAAC TGGAACAGGA GTTTACTAGAA CATTTCACAG CTATTGTACA GGGGGATACG CTGGAAGACA TTTACAACCA AGTGAAACAG ATCATAGAAG AACAATCTGG TTCTTACACTC TGGGTTCCGG CAAAAGAAAA GCTATGAAAA CTCATGTTTC TCTGTTTCTC TTTTCACACA TTCCATTTTC TTTGGCATCT CTTTGCCCTT TCCTCTGGAG TCTTTCTTGA GTACTGATT CATGTTGAAT TGTATCCCAC ACATCATGGT CATCTCGAG	120 180 240 300 360 389
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 350 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:	
GCGATTGAAT TCTAGACCTG CCTCGAGACC GCCTACGAAT GGAAATCCAT AAGAATGAGG	60
CTTGGCTCTC TGAAGTCGAA GGCAAAACAG GTGGGAGAGG AGACAGAAGA CATAGCAGTG ACATAAATCA TCTTGTAACA CAGGGACGAG AAAGTCCTGA GGGAAGTTAC ACTGATGATG	120 · 180
CARACCAGGA AGTCCGTGGG CCACCCCAGC AGCATGGTCA CCACAATGAG TTTGATGATG	240
AATTTGAGGA TGATGATCCC TTGCCTGCTA TTGGACACTG CAAAGCTATC TACCCTTTTG	300
ATGGACATAA TGAAGGTACT CTAGCAATGA AAGAAGGTGA AGTACTCGAG	350
(2) INFORMATION FOR SEQ ID NO:1086:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 276 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:	
GCTCCACCAG CTACTGAGAA AATGGCCTGT AAAGATCCAG AAAAACCCAT GGAGGCCTGT	60
GCCTCAGCAC ATGTGCAACC CAAGCCTGCC CCTGAAGCCA GTAGCCTAGA GGAGCCCCAT	120
AGCCCAGAAA CAGGGGAGAA GGTAGTAGCA GGAGAGGTAA ACCCACCCAA TGGCCCTGTG	180
GGGGACCCAC TGAGCCTCTT GTTTGGGGAT GTGACATCCC TGAAAAGCTT TGATTCATTG ACAGGTTGTG GTGACATAAT AGCAGAACAA CTCGAG	240 276
	270
(2) INFORMATION FOR SEQ ID NO:1087:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 295 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:	
daga-na	
GCAGAGACTT AAAGGGTTAA TAAAAATTGT AAAGCCAGCA GAGATTCCAG AACTAAAAAA	60
GACTGAAACT CAGACTACAG GTGCAGAAAA CAAAGCTAAA AAGCTTACAT TGCCTCTATT	120
TGGTGCCATG AAAGGAGGAA GCAAATTCAA ATTAAAAACT GGAACAGTAG GGAAGTTACC	180

CCCCAAGCGT CCAGAACTCC CTCCAACTCT AATGAGAATG AAAGATGAGC CTGAAGTAGA

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs (B) TYPE: nucleic acid

240

295

(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:	
GAAATGAGGG TCCCTGAAGA AGCTCTTAAG CATGAGAAGT TTACCATTCA GCTTCAGTTG	60
TCCCAAAAAT CTTCAGAATC AGAATTATCC AAATCTGCAA GTGCCAAAAG CATAGATTCA	120
AAGGTAGCAG ACGCTGCTAC TGAAGTGCAG CACAAAACTA CTGAAGCACT GAAATCCGAG	180
GAAAAAGCCA TGGATATTTC TGCTATGCCC CGTGGTACTC CATTATATGG GCAGCCGTCA TGGTGGGGGG ATGATGAGGT GGATGAAAAA AGAGCTTTCA AGACAAATGG CAAACCTGAA	240
GAAAAAAACC ATGAAGCTGG AACATCAGGG TGCCTCGAG	300 339
(2) INFORMATION FOR SEQ ID NO:1089:	
(i) SEQUENCE CHARACTERISTICS:	
<ul><li>(A) LENGTH: 433 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:	
GAATTCGGCC TTCATGGCCT ACTCAAGAAT ACAGGTCTTA CTCGTATAGT CTTTGAACAA	60
TAGGCTGTGT GACTAAAAGA GAGACACAAT CAATTGCTTC CCAGTCAAGA AGCCAGAAAA	120
GCTTCAAAAC CTTTCCCCCT CCCTACTCCT TGCCACCGCA CCTAAAAAAA AGAGAAATCT	180
TTTAAGTGTT TAAAATCTGT AGGAGTCTTA TGAAGAAGCA GCTTTATGTG TATTCTTTAT GGCATAATAT TAATGCATGA AAATCTGTTG CTTTTTTAAA AATTGTGGCA AAATATACAT	240
AACATAAAAT TTATCATTTT AGCTATTTTT AATATACAAT TCACTAGCAT TAAGTATTAA	300
TACATTCACA GCACCATTGC AACCATGGCC ACCATCATCT CCAGAACTTG ATCTTCTTCA	360 420
ACGCCCACTC GAG	433
(2) INFORMATION FOR SEQ ID NO:1090:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 319 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:	
GACTGGGTCC ATGGGAGCAA GATTAGTGGC TGCTAAACTT GAACCGAAAA GCTTCAAACA	60
TACCCATATA GATAAACCAG ACTGCTCAGG GCCCCCCATG GACATAAGTA ACAAGGCTTC	120
TGGGGGAGATA AAAATTGCCT ATACTTACTC TGTTAGCTTC GAGGAAGATG ATAAGATCAG	180
ATGGGCGTCT AGATGGGACT ATATTCTGGA GTCTATGCCT CATACCCACA TTCAGTGGTT	240
441	

TAGCATTATG AATTCCCTGG TCATTGTTCT CTTCTTATCT GGAATGGTAG CTATGATTAT

GTTACGGACA CCACTCGAG	319
(2) INFORMATION FOR SEQ ID NO:1091:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 328 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:	
GTGCAAATTG AGCACATCAT TGAAAACATT GTTGCTGTCA CCAAAGGACT TTCAGAAAAA TTGCCAGAGA AGTGGGAGAG CGTGAAACTC CTGTTTGTGA AAACTGAGAA ATCGGCTGCA CTTCCCATCT TTTCCTCGTT TGTCAGCAAT TGGGATGAAG CCACCAAAAG ATCTTTGCTT AATAAGAAGA AAAAAGAGGC AAGGAGAAAA CGAAGAGAAA GAAATTTTGA AAAACAAAAG GAGAGGAAGA AGAAGAGGCA GCAGGCTAGG AAGACTGCAT CAGTTCTTAG TAAAGATGAT GTGGCACCTG AAAGCGGTGA TACTCGAG	120 180 240
(2) INFORMATION FOR SEQ ID NO:1092:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 109 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:	
GATCATGAAG TCCATCATCC CAGTGGTCAT GGCTGGCATC ATCGCCATCT ACGGCCTGGT GGTGGCAGTC CTCATCGCCA ACTCCCTGAA TGACGACATC AACCTCGAG	60 109
(2) INFORMATION FOR SEQ ID NO:1093:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 388 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:	
GAATTCGGCC TTCATGGCCT ACTGGAATTC ATAAGTCTAA ATGGTTCTAT GAGTCTAAAA TTAAAGTGTT AGCAGGGCTG GGCTTCCTTT GGAAGCTCTA GAGAATGATC TGTTTTCATA CCTTTTCCAG CTTGTATGAG CTGACTACAT TCCTTAGCTC ATGGCCCTGC TGCCCACAGC TTCAAATGAG ACAACACCAA GTTGAGTCCT CTTTAGATCA CATCAATTTA AATCTCCTAC TATTCATATT TCCTTGTGAC TCTCCTATGC ATCCTTCCTT CTCTTCAAAG GATCTTTGTG ATTATACTGG GCCCTCTGAA GAATCCATGA TAATCTTATC TCAAGGTGCT TAAGTTAATC ACATTTACAA GATCTCCTTT TCCTCGAG	120 180 240 300
(2) INFORMATION FOR SEO ID NO.1094.	

PCT/US98/06955 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 461 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094: GAATTCGGCC TTCATGGCCT AGGTGGCACA TGCCTGTGGT CCCAGTTACT CGGGAGGCTG 60 AGGTGGGAGG ATTGCTTGGG CCCGGGAGGT CAAGGCTGCA GTGAGCCGTG ATCTTGCCGC 120 TGTACTCCAG CCTGGTGATA GCGAGACCCT GTCTCAAAAA AATGCTTTTA GGGAAATTAA 180 TATGTCCTGT GCCTGTTTAA TCATTGAAAA CATTTTAATA TTTTCAGAGC CATAGAGGGC 240 AGTGAAAAAC AGAGTAGCAG AATTGATTAT ACCAGTACTA TTTATCCAAT GGCTAATACA 300 AATAAGACTC TCAGGGATAA TTCACACGTG CTTCCAAGAA CACTAGATGG CACCAATTAT 360 TTAGGATTCA GACTACCTCA GGGAACAGCT GTCTTCATTC AACAAATATT TATTAAATAA 420 TGAACAAAAC AAAAATATCT GTCATTGTGG AGCAGCTCGA G 461 (2) INFORMATION FOR SEQ ID NO:1095: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 317 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095: GAATTCGGCC TTCATGGCCT AAACCTATGC AGATGCCTGT GATGAGTTCC TGGATCCCAT 60 TATGAGCACA CTGATGTGTG ACCCTGTGGT GCTGCCATCT TCCAGAGTCA CTGTGGATAG 120 ATCCACCATT GCAAGACATT TGCTCAGTGA CCAAACAGAT CCCTTTAACC GTAGTCCCCT 180 CACCATGGAC CAGATCCGGC CAAACACAGA ACTAAAAGAA AAAATCCAAC GGTGGCTTGC 240 AGAGAGGAAA CAACAAAAGG AGCAACTTGA ATAGATACTG TGAACTAACC AAACCAAAAC 300 CAACCCCAGA TCTCGAG 317 (2) INFORMATION FOR SEQ ID NO:1096: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 360 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

GCTGCAGCCA ACGCGCAGCT	CCACTGGAAG	AGGATGGAGA	ACCTCAAGGA	GGAGGAAGAT	60
GACGACTCCT CCACAGCCTC	AGACAGCGAT	GTTCTCATCC	GGGACAACTA	CGAGCGGGCA	120
GAGAAGCGGC CCATCCTGTC	TGTGCAGAGA	CGTGGATCTC	CCAACCCGTT	TGAAATCACA	180
GACCGGGTGG AAATGGGACA	AATGGCCTCC	ATGTTCTTCA	ATAAAGTGGG	GGTCAACTTG	240
TTCTATTTCT GCATCATCGT	TTACCTGTAT	GGAGACCTCG	CCATCTATGC	TGCTGCCGTG	300
CCCTTCTCCC TCATGCAGGT	GACCTGCAGC	GCCACTGGCA	ATGACTCCTG	GCGGCTCGAG	360

(2) INFORMATION FOR SEQ ID NO:1097:

WO 98/45436	PCT/US98/06955	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 311 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	•	
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:		
GAATTCGGCC TTCATGGCCT AGTGAGCCAC CGCACGGGGC CTAACGATGA ATGTGACATC TGCAGGATCC CCAGCTAGTC AGCAGCATCT AGAGGGCTAG AGCTGACTGG GCCTTTTGCT AACTGTTTTC TGTCCCCTCT GTGCCGGGGT TTTGCGGGAC AGGCTGGTCT GTCGTGCCTT CAGCTCAGGG AATGTGGCTC GGCTGGACTG AGAGGCGTTA GGTGAGCCAG AGAAGGCCTC AGACACAGGG GCTCCCTCGA G	AACTCTGGCC 1 GTCACTGAGC 1 CCGAGCATAG 2 CTTAGAGAGG 3	60 20 80 40 00
(2) INFORMATION FOR SEQ ID NO:1098:		
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 436 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:		
GAATTCGGCC TTCATGGCCT ACCTGCAGCT CTACAATATA TTTTCAAACT GAGAACAAAG GATACCTGAA TGTCTTTCA CTTAATTATT TCTTTAGGGC CTAATGAAAA TCCATGGACA AGATCCTGTT TCATTTCAAG ATGTCAAGGA GACATGGTAA AACCAAAGGA TCCTTTGAAA ATCTCTCTTC AGGATTTAAT CAAGGAGACA CAGTAACCAC CATTCTAATC GATTTGAATG GCTTCTGGAC AGAGAGGCTC TTGTTGCAAA TGACAGTGAA AACTCTGCAG ACCTTGATGA CTGAAAGACT AGACTGTCTT ATATTATGAG ATACTTGAAT GCTGCATGTA AGCAAAAAAAC CTCGAG	CATACAGGAA 1 TGAAATCTTT 1 CAACAGTAAT 2 TTACGAGAAC 3 TACATGATCT 3 AAGCCTTTAA 4	60 .20 .80 .40 .60 .20
(2) INFORMATION FOR SEQ ID NO:1099:		
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 291 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:		
GAGAAGATGC AAGTGGACCA GGAGGAACCA CATGTTGAAG AGCAACAGCA GCAGAAAATA AGGCAGAGTC TGAAGAAATG GAGACCTCTC AAGCTGGATC AAGATGGACC TACCACCCCA AGCCAAGAAG GCAAAAGTGA AGACCAGTAC CCAATCGAGA ATCAGCTATT ATGGCAGATA GACAGAGAGA TGCTCAACTT	CAAGGATAAA 1 TGTGGACCTG 1	60 120 180 240

- (2) INFORMATION FOR SEQ ID NO:1100:
  - (i) SEQUENCE CHARACTERISTICS:

AATGAGGGTA AGATGATCAT GCAGGATAAA CTGGAGAAGG AGCGGCTCGA G

<ul><li>(A) LENGTH: 101 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:	
GAATTCGGCC TTCATGGCCT AGTCATTTTA TAGGTTAAAA AAAGGTCAAA TTGTGACAAT TTCATATGGT ACAATATAAA ATTATATTAA ATATACTCGA G	60 10
(2) INFORMATION FOR SEQ ID NO:1101:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 492 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:	
GAATTCGCCT TCATGGCCTA AGAAATACAT AGATCAAGTA AAACTCCAAC TACTGTAGCT GGAATTTGTA AACTAAGTTT GTAAGACCTC TTTTATTTCC TATGGAGTTA TTCTTTAATT TACAGTTTAT TCTGTAAGTT GGGAAGTAAA ATAGAGAAAA TAATAAATCT AGATGTTCTC AGTGTCTTAT TCAGGAACTT TTTATCCCTC CTCACTAAGG AATTCCCACT GTGACTTTAA AATAGAACTA AATTACTTGT GTGCATGTAT ATGTCTGTAT TTTTTACACA CATGCAAAAA TATACATTGG GGGCACGTGT GTGAGAGATA TGAATGTTGT CTTATATAAA AATAGATAAA GGTAACCGAA TGTATTGTAG AAACATGATT TATTTAGTTG AGGGTATTGG AGTTACTTTC TCATTGTCTC TGTTGTATAA ATACACCAAA TTAATCATTA TGTTATCTTA TGTTAAAAGG	60 120 180 240 300 360 420 480 492
(2) INFORMATION FOR SEQ ID NO:1102:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 343 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:	
GAATTCGGCC TTCATGGCCT AGGCCTGCGT TAATACTCTT AATTATAGAA ACAATCCTTA ATTAATAAAC AAGTCCTTTC ATTGGAAAAA GAACTAATAC ATTTTGTTCT CTCAGTCAAA ATTCTGTTTT TGTGGTTAGA GTAATAAAAT GGTAACACCT AGGGTCTGCC ACGATCATGG TTCTCACTCT GGATTCATTC CCTACCACAT CCTTATTTCC CTCCTCTTCC CCATTCCCTC ACTCACCCTC CTCCTTTCCT TCCCTCACTC ACCCTCCTCT TCCCCATTCC CTCACTCA	60 120 180 240 300 343
(2) INFORMATION FOR SEQ ID NO:1103:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 282 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GAATTCGGCC TTCATGGCCT AACCGGGCAA	AAAAAAAAA	AAATCTTAAA	AGCACTAACT	60
TACTATCAAA TCTCAAGAAA CAGAAGCAAT	TTCAAAAAAT	CAATACTATC	CTTTTGGTCA	120
GTAACACTTT CTTCATTCCT AATGTATGAG	AACAATAAGG	ACATTTTAGC	TCCTTTACTC	180
TTCCTTCATT TAGTGACTTC CACATTTCTC	TCACCATTTT	TCCAGCCTCT	GGGTGTGGTT	240
CTGATGAACC TTAAACTTGA AAGGCACAGG	CCAGAACTCG	AG		282

- (2) INFORMATION FOR SEQ ID NO:1104:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 205 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

GCGATTGAAT	TCTAGACCTG	TCTTACGCTT	CCCTTCCTAA	GCCTTTGTCT	ACTCTGCTTT	60
GTCTGCTTTT	ATGCTTCTCT	CTCTTTTGTC	TGAACTGGTC	TCTGTCCTCG	TCCATGCTTC	120
AAGTCCTAAT	TCAAATGCCA	CTGTCTTTAT	GAAGGGCTCC	CTGATTGTTC	CAACCAAAAT	180
AAGCTTTTAT	TCCTTTGAAC	TCGAG				205

- (2) INFORMATION FOR SEQ ID NO:1105:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 249 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

GAATTCGGAC	TTCATGGCCT	ACGTTTTTAT	TACAAATATT	ACATTAAACT	AAAGCTCACA	60
ACTGTTACTA	TGCATCAGGA	ATTAACAGTC	ATTTCTCATT	TGTGTTATTC	TCCTATTTGA	120
TCACATATAG	TGACTATCTC	TTTATGGGTT	AAATATCAGT	TTCTTGGCCA	GAATTCAAGA	180
TCTGCCCCTA	ACNAATCCTA	CTTCTCCCAG	TACCCTTACA	GCACTCCTAC	CCTACTAGTA	240
ACCCTCGAG						249

- (2) INFORMATION FOR SEQ ID NO:1106:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 237 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

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AATTCTAGAC CTGCCTCGAG ATTGTCTGCC AGTTTAATTC TTTAAAACTC AGTTTAGCTG TCCTTTTCTT TGGAACACTT TCCCTAATCT TCCCCACCAC CTGTTCATCA ACATATATAG AAGCACATTT ACTCTCTCAT TCTCTCTCTT TCTCTCTCCA AGTCTATGTT AGGTGTTTTA GCGTTTATCA TAGGTTTATG TTTACTTATC TCCCCACTAG TCTATGAAAT CCTCGAG	60 120 180
(2) INFORMATION FOR SEQ ID NO:1107:	237
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 313 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:	
GATTTATTAT AAAGCTGCAA AGAAGCTGTT GCACTCAGGA ATGAAAATTC TTAGCCAGGA AAGAATTCATGAAAATTCATGAAAAATTCATGAAAAATTCATGAAAAAATTCATGAAAAAAAA	60 120 180 240 300 313
(2) INFORMATION FOR SEQ ID NO:1108:	323
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 467 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:	
GCGAGAACAC CATCACCATG ACAACCAGTC ACCAGCCTCA GGACAGATAC AAAGCTGTCT GGCTTATCTT CTTCATGCTG GGTCTGGGAA CGCTGCTCC GTGGAATTTT TTCATGACGG CCACTCAGTA TTTCACAAAC CGCCTGGACA TGTCCCAGAA TGTGTCCTTG GTCACTGCTG AACTGAGCAA GGACGCCAG GCGTCAGCCG CCCCTGCAGC ACCCTTGCCT GAGCGGAACT CTCTCAGTGC CATCTTCAAC AATGTCATGA CCCTATGTGC CATGCTGCCC CTGCTGTTAT TCACCTACCT CAACTCCTTC CTGCATCAGA GGATCCCCCA GTCCGTACGG ATCCTGGGCA GCCTGGTGGC CATCCTGCTG GTGTTTCTGA TCACTGCCAT CCTGGTGAAG GTGCAGCTGG ATGCTCTGCC CTTCTTTGTC ATCACCATGA TCAAGATCGC GCTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:1109:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 74 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:	
GAATTGCGGA AACGGTCGTT CCACTCGCTC CAATGTGGCC CCCAGGCACC TACCTGATAG	60

- (2) INFORMATION FOR SEQ ID NO:1110:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 427 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

GAATTCGGCC TTCATGGC	CT AGGAATTTAG	GAACCAAGAT	ACTGGGGTGT	TATTGTTTCT	60
AAGCTCTTTC AGTGAACA	GA TCTAGGAAAT	ACATGTGTGT	CCTAATCCAT	GAATACACAC	120
ТААААТАТАА ТТАТТТСТ	GT ATCTATGTCA	AGCTAAACCT	AAGTTCACAT	TGAGGTTTCT	180
GACTTTAATA CAGTCCCA	CA AGGTTCGTTC	TAGCTTTCCT	TCCTTGCATA	CCTTTGACTT	240
TCCTCTCCAG CTGTGGGA	AA CTTGGCTCTC	TCCATCCACC	ACCCCTTCAC	TATTTGTTTA	300
ACCCTTGTAC ATATATAA	AG CAGCGTTGGA	ACTGTCAACC	TGTGTCCCAT	GAGAAACTTT	360
ACCCACTAGA GTACAGCG	TT TATGCAGTTC	TTTTTGTAGT	TTTTATAGAT	TATAGCCAAA	420
ACTCGAG					427

- (2) INFORMATION FOR SEQ ID NO:1111:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 372 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

GGTGAACCCG	AATCACCGAT	GGATGTGGAT	AATTCTAAAA	ATAGTTGTCA	AGACTCAGAA	60
GCAGATGAGG	AGACAAGTCC	AGGTTTTGAT	GAACAAGAAG	ATGGTAGTTC	CTCCCAAACA	120
GCAAATAAAC	CTTCAAGGTT	CCAAGCAAGA	GACGCTGACA	TTGAATTTAG	GAAACGGTAC	180
TCTACTAAGG	GCGGTGAAGT	TAGATTACAT	TTCCAATTTG	AAGGAGGAGA	GAGTCACACT	240
GGAATGAATG	ATTTAAATGC	TAAACTACCT	GGAAATATTT	CTAGCCTGAA	TGTAGAATGC	300
AGAAATTCTA	AGCAACATGG	AAAAAAGGAT	TCTAAAATCA	CAGATCATTT	CATGAGACAG	360
CCCAAACTCG	AG					372

- (2) INFORMATION FOR SEQ ID NO:1112:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 108 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

GAATTCTAGA CCTGCCTCGA GCTATACCTG TATCCAGTCT TGATGCACAC CAGGCTGGGC 60
ACTTTCCAGA AACTACCTCT AACCTCCAGG GTTCCCTCAT CACTCGAG 108

(2) INFORMATION FOR SEQ ID NO:1113:

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(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 382 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:	
GAATTCGGCC TTCATGAAGA TTGAGAAGAA GGAGGAAAAA AAGCCTGAAG ACATTAAGAA GGAAGAAAAA GACCAGGATG AGCTGAAACC CGGACCTACA AATCGGTCTA GAGTCACCAA ATCAGGAAGC AGAGGAATGG AGCGGACGGT CGTGATGGAT AAATCGAAAG GAGAGCCCGT CATTAGCGT AAAACCACAA GCAGGTCCAA AGAGAAAGC TCCAAGAGTC AGGATCGCAA GTCAGAAAGC AAAGAAAAGA	60 120 180 240 300 360 382
(2) INFORMATION FOR SEQ ID NO:1114:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 253 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:	
GAATTAGCAA AGGAAATCTC AGATTGCATT TCCAAAGATG GTTGCTAGCT GCTGCCGTTT CCTTTGCTAT TTCTGTCGAA TTAGCCGGCA AAATCAGAAG GCCATGTTTG AGCATCTGAG TTATCTTCTG GAGAATAGCA GTGTTGGCCT AGCCTCCCCG TCGATGAGGG GATCCACCCC GCTGGATGTG GCAGCTTCCT CTGTGATGGA CAACAATGAG TTAGCGCTGA GCTTAGAGGA ACCAGACCTC GAG	60 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:1115:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 76 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115;	
GAATTTTTT TTTTTTAAA GAAAGAAAAC TAGGGCGATG CAATGTCCAG ACAGAAGCCG GGGGCCGGGG CTCGAG	60 76
(2) INFORMATION FOR SEQ ID NO:1116:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 70 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
449	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:	
GAATTCGGCC TTCATGACGA CCGCGTCCAC CTCGCAGGTG CGCCAGAACT ACCACCAGGA CACCCTCGAG	- 60 70
(2) INFORMATION FOR SEQ ID NO:1117:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 526 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:	
GAAAATGAAA AGTTCTGTCT TTGATGAAGA CAAAACTTTT GTAGCAGAAA CATTGGAAAT GGGTGAGGTT GTTGAAAAGG ATACAACAGA ACTCATGGAA AAACTTGAGG TAACCAAGCG AGAGAAATTA GAGCTGTCAC AGAGACTGTC TGATCTTTCT GAACAATTGA AACAGAAACA TGGTGAGATT AGTTTCTAA ATGAAGAAGT TAAATCTTTA AAGCAAGAGA AAGAACAAGT TCATTGAGA TGTAGAGAGC TAGAAATCAT TATTAACCAC AACAGGGCAG AAAATGTACA GCTCATGATAA ACTCAAGTAA GCTCTTTATT AGATGGAGTT GTGACTATGA CAAGCAGGGG TGCTGAAGGA TCAGTTTCTA AAGTAAATAA AAGTTTTGGT GAAGAATCAA AAATAATGGT GGAAGATAAA GTTTCTTTTG AAAATATGAC TGTTGGAGAA GAAAGTAAGC AAGAACAGTT GATTTTGGAT CACTTACCAT CTGTAACAAA GGAATCTTCA CTCGAG	60 120 180 240 300 360 420 480 526
(2) INFORMATION FOR SEQ ID NO:1118:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 190 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:	
CGATTGAATT CTAGACCTGC CTCGAGCCGA CCTACTCCAC AGCTGTCCTG ACTGTGTAAG CGAGATGATG ATTAGTGATC AGACGAAAGG ATTCCTGTCA TTGGTAACCC TCTCAAAGTA TTTGGAAAAC AGTTCAATTT TCATCTATTT CAGAAGCACG CCGTGGTGTC TATTGAGGCT CACCCTCGAG	60 120 180 190
(2) INFORMATION FOR SEQ ID NO:1119:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 331 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:	

120

GAATTCGGCC TTCATGGCCT ACCATCCTGC ACTCAACCAA TCATCTGATG CTGACTCAGA AGCTCTGTTT GGAGTACCTA ATGATAAGAA TTTACTGTGG GCTTATGCTG TTATCGGTAC

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TTACATGTTC	TTAGTTTCTG	TCD TOTOTOTOTO	TTOMOROWO	mm	GCTCAAAGCA	
ACAAAAACCA	1010011010	101111111	TIGICIGITI	TTAAAGAATA	GCTCAAAGCA	180
MUMMAAGUA	AGAGCATCTG	CTGAGACATT	TCGAAGAGCA	AAATATCACA	ACGCCCTTCT	240
TTGTCTCCTT	TTTCTGTTCT	TCTTTTTTT	TCTTCCACCT	CACCOMANCAM	ATGGCTCTTA	
<b>TCTTTTCTCX</b>	TTTGCAACCA	2222	1011GGAGC1	GAGGTAACAT	ATGGCTCTTA	300
TOTTLICICA	TITIGCAACCA	CCCATCTCGA	G			221

- (2) INFORMATION FOR SEQ ID NO:1120:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

GAATTCGGCC	TTCATGGCCT	ACAGATTTGC	ATCTTTACAA	CCAGAAGCTC	AGGGAGAAGT	60
TGAAGGAGGA	GGAGAACACA	CTCCCCTTTCCT		44101210616	AGGGAGAAG I	60
10.1.00MGGA	GGAGAACACA	GIGGGTATGT	TCAGATTGCT	TTTGGGTACC	CTTGATCCAG	120
CCACATTGTC	TACCCTAGAT	CCCTCCTCAT	GGM3		CITORICUMO	120
	ICCCINONI	GGGIGCICAI	GGTACTTCTT	GGTGGCATTT	CAATAATAGG	180
TTGAGTTGTA	TACCGTCTGT	CTTTACACTA	CATTAMOSS	100101	TAAATAAGAA	100
		CITICACIA	CATTAIGAAA	AIGAGATTAT	TAAATAAGAA	240
TTTTGATGTA	GCTGATAAGC	TAGTAGAATT	GGCACATCAT	CCCMmmm + m +	CCCAGCCCTC	
CTCTCTCTC			GGCACATGAT	CCCTTTTATA	CCCAGCCCTC	300
CIGICIGGIG	TGCTTGAGGT	AATAATAACC	<b>CCTTTTTDTDC</b>	CCAAACCTCC	3.0	
			CCTTTIMIAC	CCMMMCCICG	AG	352

- (2) INFORMATION FOR SEQ ID NO:1121:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 484 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

GAATTCGGCC TTCATGGCCT ACCAATCTCT TTTACTGAGC A	3.03.3.000.00		
CTCTATAGTA CCACAATTEE GEORGE A	ACAATGTGGG	TAAAACTGCT	60
CTCTATAGTA GCAGAATTTT GTTTTTCCCC TTTCCTAGTT A	ACTGATGAAG	AGACAGCTTC	120
AGAIGCICIG GAGAGAACT CTCTATCCTC TCAAGACCCA C	CAGCAGCCCA	CCA CTA CTCT	180
CTCAGTAACG GAAGATTCTA GTACATCGGA GATTGACAAG G	7777777777	CONSTRUCTS	
TCAAGATCCT GACTTGACCA CCCAACGAAA	GAAGAGAAAG	AACAAACCAC	240
TCAAGATCCT GACTTGACCA CCGAAGCAAA TCCTCAGTAT T	TTAGGACTGG	CAAGAAAGAA	300
AAGTGGCATC CTGCTGCTCA CGCTGGTGTC CTTCCTCATT T	TTCATACTCT	TCATCATAGT	360
CCAGCTCTTC ATCATGAAGC TGAGGAAAGC ACATGTGATA T	TOCARCACAC	111101	
TTCAGAACAC ACACTAGAAA GTTACAGATC AAGGTCAAAT A	IGGAAGAGAG	AAAACGAAGT	420
CGAG	AATGAAGAAA	CATCATCGCT	480
CGAG			494

- (2) INFORMATION FOR SEQ ID NO:1122:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 247 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:
- GAATTCGGCC TTCATGGCCT ACTTATGTTT TTCTCATTTG TTGACCTAAA TGATCTTTAT

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CCAAACTATT CCAAAATCTG AATTTCTGGG TCCTTCTTC TTTAAAATAT TCTGTTCAAT ATTAAACAAA CAAACGTTTG AGAACATGAG TAACCTTTTG ACTTTATCCC GTATCTGTTT GCTAATGTTC TGTTCCATGT CTTTCTTGTC AGAACACACT GTTGCAGCAG CTAGGAGTGC ACTCGAG	120 180 240 247
(2) INFORMATION FOR SEQ ID NO:1123:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 276 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:	
GAATTCGGCC TTCATGGCCT AGGAGGAAGC TAATAAGAGA CTGTCAAGAT TGTATACCTT CTTGGTTTCT TTTAAGAATT TGTTGCCTTT CTACTATTAC AGCAAAGCAG CATTTTGTTA CTGACTGCCT AAAATCACTT AATCTCAGGT GAACGCATCA CTTGCCAAAC TGTTGGAATG CTATTTGTGT TTTGTTGCAC TGTTTTTTTC GTTTGTTTTTT TTGTTTATTT GGTTGGCTTT TTGGAGAGGG AAATTTGGAA ACGGGACACA CTCGAG	60 120 180 240 276
(2) INFORMATION FOR SEQ ID NO:1124:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 252 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:	
GAATTACTAG CAGAGATCAG TGCTATAAGG GAAAAGGAGA TTGATTTGAA AGAAACTGGA AAAAGAGACA TTCCCATGAT GGAGAAAGTA TCAGGAAAGA TGGCTGTTGT TGAAGAAATG GAGGCAGATT TGAAAGAAAC TGGAAAAGAA AATTTTAGAG AGAGAGGATC TGAAGAGATC TGTGTTACTG AGGAAAAGGT GGCAGAATTG AAACAAACTG GAAAAACAGA CATTTCTCCA AGGGCCCTCG AG	60 120 180 240 252
(2) INFORMATION FOR SEQ ID NO:1125:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:	
GAATTCGGCC TTCATGGCCT AAACAGAATA TTCTGAGGCT AAAAGAAAAT ACACCCCCGC AAAAATCAAT ATAACTATGA TTAAGTACAC AAAACATGCA GCCCATAAAA CATATTTCAC CTATGAAACT GAGACTGAGG AATTTAACAG TAAACAGTCA TTTGTTAAAG AAATATTTT ACAATTTATT GCCTATGTAT AAGGCAGCAG GCCTGTACTC TCTTGTATTT TCAATCTCTT CCCCTACTCT GGCTCTTCCT CAGCATATAA ATATGTTTCT ATCCCTACCT TATGGAAACC ATTCCCCATC CCTCGAG	60 120 180 240 300 317

- (2) INFORMATION FOR SEQ ID NO:1126:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 382 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

GAATTCGGCC	TTCATGGCCT	ACTTTGTAAC	TGTGAAATAC	TCTCCAGGAT	TTAAAAGGCT	60
	AGATAAAGAA					120
TTTACCCCAT	AAACGGCAAC	ACACTCACCT	CCATCCAAGA	CAGACTCAAG	GTGGAGGAAG	180
	TGCTTCCGGA					240
	TTTTCTACTG					300
	CAACCGGCAG		GGTTCTCTCT	GCTGGTGACC	ACCCACCCCA	360
CAACCACTCA	AGAAGCCACT	CG				382

- (2) INFORMATION FOR SEQ ID NO:1127:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 334 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

GAATTCGGCC TTCATGGCCT					60
TCTGAAGAAG CTCTGGTTGG	TCAGCTGCTG	CCTCACATCA	GCATGTTGTC	AGGATCTTGC	120
ATCAGTATTG AGCACCAGCC					180
AGACTCAGGA GTCGCAATTT					240
ACTGGGGTTG GTGAATTCTG					300
CAGCACTAAT CAGAATCTCA					334

- (2) INFORMATION FOR SEQ ID NO:1128:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 251 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

GAATTCGGCC TTCATGGCCT	AGTCTGTCCA	TCTGCTTTCT	CTGGACCTCC	TTCTCATACT	60
TTGAATTTTT TAAGTAGTTT	GTCCCTCATA	TGATTTTTTT	TCTATTCCTT	TTTCCCTTCC	120
TGTCCTTCCT TCACTCCTTT	CCCTCCCACC	TCCCTCCCTC	CCTTCCTCTC	TCCCTTCCTT	180
CCTTCCTTCC ATCCAACCAT	CCATCCATCC	ATCCATCCAT	CCATCCATCC	ATCCATCTAT	240
CCACTCTCGA G					251

(2) INFORMATION FOR SEQ ID NO:1129:

#### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

GAATTCGGCC	TTCATGGCCT	AATTTCATGT	NCCTTTGAGC	TATCTTTCCA	TTTTGTAGGA	60
ACACCGTCAC	AGGAGACAAT	TTCATGGACC	TTTGAGCTGT	CTTTCCATTT	TGTGGGAACG	120
CCGTCACAGG	AGACAATTTC	ATGTGCCTTT	GAGCTGTCTT	TCTATTTTGT	AGGAACGCTC	180
TCAGAGGGGA	CAATTTCATG	TGCCTTTGAG	CTGTCTTTCC	ATTTTGTAGG	AACACTCACA	240
GCAGTGCTTG	GGGTTCACTG	TTACCTAAAT	CCCATGATGG	GTGAGAAGAC	TGAATGGGAC	300
GTTTATTTTT	TGTGTTAAAA	AGCCCACGCA	AATAGAGTTT	AAAATAGTCT	CAGTGAGCTG	360
GGCATTCTCG	AG					372

#### (2) INFORMATION FOR SEQ ID NO:1130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 275 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

GAATTCGGCC	TTCATGGCCT	AGTGCCTAGT	TACAAGGTTT	TATTACAGCA	GTATTTCTAA	60
ACATTTGGTT	AGTCTGTCTC	TGCTTTTCCC	ACCATAATTT	TCTAGCACTT	GTAGCTCACC	120
TTATCTCCCA	CTTCCCTTTT	TAAATAGAAA	ACAGGCTTGT	TCTGTTTTGA	CCAGGTATAA	180
CTCTTTGCTC	AGACTGTCTC	TAAAGCCCAG	AAAACTATTC	CTCTAGTGGT	CCAATGAAGT	240
GTTCCCCATT	GAAAGTTTGC	CTCATGTCAC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:1131:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 388 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

GAAAATTGAG	CCTATGTTGG	AGACACTGGA	GAATCTTTCC	TCTCGCCTGC	GTATGCCACC	60
ACTGATCCCT	GCTGAAGTAG	ACAAGATCAG	AGAGTGCATC	AGTGACAATA	AGAGTGCCAC	120
CGTGGAGCTA	GAAAAACTGC	AGCCATCCTT	TGAGGCCTTG	AAGCGCCGTG	GAGAGGAGCT	180
TATTGGACGA	TCTCAGGGAG	CAGACAAGGA	TCTGGCTGCA	AAAGAAATCC	AGGATAAATT	240
GGATCAAATG	GTATTCTTCT	GGGAGGACAT	CAAAGCTCGG	GCTGAAGAAC	GAGAAATCAA	300
ATTTCTTGAT	GTCCTTGAAT	TAGCAGAGAA	GTTCTGGTAT	GACATGGCAG	CTCTCCTGAC	360
CACCATCAAA	GACACCCCAG	GACTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:1132:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GAATTCGGCC TTCATGGCCT AAAGTTATAC CAGCTAAAGT GCAGTAGTGT CACTTTT	TTC 60
CTGTCAATAT ATAGAGACTT CTAAATCATA ATCATCCTTT TTTAAAAAAA AGAATTT	TAA 120
AAAAGATGGA TTTGACACAC TCACCATTTA ATCATTTCCA GCAAAATATA TGTTTGG	
AAATTATGTC AAATGGATGT AATATAGGGT TTGTTTGCTG CTTTTGATGG CTACGTT	TTG 240
GAGAGAGCAA TCTTGCTGTG AAACAGTGTG GACTCGAG	278

- (2) INFORMATION FOR SEQ ID NO:1133:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 368 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

GAATTCGGCC TTCATGGCCT	AATCATTATA	ATTTAGTTTG	AATTCTTAAA	ACCCCGTTAC	60
TAGAACTTAT GTTTAAATTT	ATAAATTAA	AATAGTTATA	AATTATAAAT	AAATTGAGAC	120
TGAGGCAGGA AAATCACTTG	AACCCAGGAG	GCAGAGGTTG	CACTGAGCCA	AGATCACGCC	180
ACTGCACTCC AGCCTGGGTG	ACAGTGAGAC	TCCATCTCAA	AAAAAAAAA	AAATTATATA	240
TAAATTCTGG TAAGTAAGTT	TGAAGAAAA	CCGATTCAAA	TAGTATATAT	TCAGCTTTAT	300
AAATTCTGTT AAGCATATTT	GAATGAGAAT	TTATTAAAAT	GGTTTATATT	AAGTCTACGG	360
TTCTCGAG					368

- (2) INFORMATION FOR SEQ ID NO:1134:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 441 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

CARTTCCCCC	mma.maa.aa					
GAATTCGGCC	TICATGGCCT	ACGTCTGATT	CTCTAAGTTC	ATTTCTTGGT	GGTGGAGGCT	60
CATTTCTTCT	GGAGTCACTG	AAATTTTTGG	GATATCTTTC	GAAGCTTGGA	TCTTCCCTTC	120
GTGCAGTAGG	TCGTGCTTTT	TTCCCCTCAC	TTTGACCAAC	AAAGCGATCC	CCCCTTTCAA	180
22020022202					cocciiican	100
AAGATGAAGA	CIGTACTGCT	GAACTCTCAG	GAAACCTGCC	CCTCTCTCGG	TGATCAAAGT	240
CATTAAATCT	GTTCTCTTCC	CCACACTACT	CCC3 MCC3 MC	GGG3 3 3 BGG=		
	0110101100	COMOMOTAGI	CGGATCCATG	GCCAAATCGT	GCATCTGTAT	300
CTAGAGACAA	CTTTTTATTC	TCGCTCCAGT	<b>AAGGATCATC</b>	TCGCCTATGA	TCTACATCAC	360
CTCCCCCTTT	CAACCAATTC					
0100000111	CHAGGAATIC	CITITITETT	GITCATAACG	AAGCTGCTGT	TGTTGCCTTC	420
TGAGTTCCTC	TCTTTCTCGA	G				444
		_				441

- (2) INFORMATION FOR SEQ ID NO:1135:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1135:	
	TCTAGACCTG CCTCGAGCAA GAAACGTTTT CTAAGTCAAA GGAATAAATC AAGACTGGGT GAGAGAGGG AAAAGAAATG ACGGAAGCAC TCGAG	60 115
(2) INFORMA	TION FOR SEQ ID NO:1136:	
· (i) s	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 253 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1136:	
GCTTCAGTTT GGGTGACGAT	TTTACTGAAG CTATGTTAGA AACGTCATGT AGAAACTCTT TAGATACTGA GCTGAAAATA AGCCAGGCAT GTCTTTGTTG CAGGAAAACG TAAGCACAAA ACAGATGTCA TGCTCACAGG TGACACTTTG AGCACCTCAT TGCAGTCTTC CAGGTACCTC CTACCTCCTT CGAAACAGAA GAAACGCCCC GTCGGGTACC GAG	60 120 180 240 253
(2) INFORMA	ATION FOR SEQ ID NO:1137:	
(i) :	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 339 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1137:	
CAGGACAGCG TGGCTCTTCA GGTCTTTTGG GTGACCCTGA	TCATGGACGA GGAGATCGTG TCCGAGAAGC AAGCCGAGGA GAGCCACCGG CCAACCTGCT CATCTTCATC CTGCTGCTCA CCCTCACCAT TCTCACAATC AGCACCGCCG GGCCCGCTTC CTGCACGAAA CCGGCCTGGC TATGATTTAT TGGGCCTTGT GCTTCGGTAT GGCATTCATG TTCCGAGTGA TGTAAATAAT GCTGTGAAGT GCAGTCAAGT CCAACTACCT TACTGGTAAA TGTTAGTGGA AGTATATGCT GAAAGGAGAG ATACTCGAG	60 120 180 240 300 335
(2) INFORMA	ATION FOR SEQ ID NO:1138:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 363 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

CAAMMOOOOO .						
GAATTCGGCC 1	TTCATGGCCT	AATTCAGAGG	TGGTGGGACC	TTGGCTATGA	TTCTGTTCAA	60
GCCCCCTAAT	TTTACAGATT	TTATGGAATT	GAGCAACAGA	CAAGATGATT	TTGCCTAGGT	120
TCATAAACAG (						
						180
TCTTGATGTT (	CTGTCTTCAT	TCATCATCCA	GCCTTTCCTA	GGAGTGTCAG	AGATAGACCC	240
AGGTAGAAGT (	GGGCTGCCCA	TGGGGGGGCTT	AGCACAACAG	ΔΔΔΤΤΤΔΤΤΟ	ተተመቀው y ርብረውው	300
						300
CTGGAGGCCA (	GACATCTAAA	ATAAAGGTGT	TGATGGGGTC	ATTCTTCCTC	TTGAGGGCTC	360
GAG						2.52
						363

# (2) INFORMATION FOR SEQ ID NO:1139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 367 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GAATTCGGCC	TTCATGGCCT	ACTTGTAGAA	TATTGAGCAA	TTTGTGTGAA	GTGGGGAAGA	60
TGAAAGAAGT	CAGAATTTGA	AACGGAAGAA	TGAAGAAAAG	АААТААААТ	GAAGTTAAGA	120
TAAGAAGTAA	TCTGGAATCA	GAAAGCACTA	CGCTAAGAAT	CCCGTTCTGC	TTCCAGAAGT	180
GGAAGTGCTC	ACGGATCGGG	GAAATCTGCA	AGGCATACCC	CTGCAAGGTC	TCGCTCCAAG	240
GAAGATTCCA	GGCGTTCCAG	ATCAAAGTCC	AGGTCCCGAT	CTGAATCTAG	GTCTAGATCC	300
AGAAGAAGCT	CCCGAAGGCA	TTATACCCGG	TCACGGTCTC	GCTCCCGCTC	CCAAGGACGA	360
TCTCGAG					CGBIOONCON	
						367

# (2) INFORMATION FOR SEQ ID NO:1140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 389 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

GAATTCGGCC	TTCATGGCCT	ACACCCTCAC	CACCCAAGGG	GTCATCATCT	CTGGCCACCA	60
					AGGCCACAGC	120
					ATAAGCTGAC	180
GAAGGTAGCC	AGACTTCCGG	AGGACTGACC	ATCTCTCACT	GTCCTCCCCA	CCTTCTTCCT	240
CACTCACACA	TTTTTTGTAC	ATCTGGGCCC	TTAGTTTTTA	TTCTGTTTAT	TATATGTCTC	300
TGTCTCTCTC	TATTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTGTGG	360
	CCACCCCCAG				0.01010100	389
						309

# (2) INFORMATION FOR SEQ ID NO:1141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 311 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

GAATTCGGCC	TTCATGGCCT	AGCAGCACTA	ATCTTGATGG	GACAGAAAAT	TTCAAATGAA	60
GAGCTTTCCC	TCTTTTTTC	TTCCTTGGGG	GCATGCCAGC	TTGTGCTTCT	ATGTCAGTAG	. 120
CCTTGTAGTT	GCCATTCCTG	GCCCAGACAC	TTGCATGCAG	TTTGGTTTGT	CCTCCACCAC	180
TTTGATCATG	TTGCCCATGG	TCTAGACACC	TCCGTGTCCT	TGTTATCATG	GCATATAGTC	240
TGTATGCCTC	TGCTGGATTT	ATAAGCGGCC	CCATAATAGC	CTTCCTTTCT	GGTTACCCCC	300
TTGATCTCGA	G					311

### (2) INFORMATION FOR SEQ ID NO:1142:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

GAATTCGGCC	TTCATGGCCT	AAAAGATCAG	ATTTTGTCAT	TTAAGACACA	TATTTTACAT	60
TCAAAAATGT	AAAGTCAGGG	TGTGTCTTAA	AATCCATTGG	TGTTTTAATC	ATGCTTAAAC	120
ATGTGACTGC	TGTTGGCCAG	GATACAGTTG	TGGTGGTGTC	GTCAGTATCT	GAGCACATGT	180
GAACTTNGCC	ATGACTATTC	ATATTGTCTT	CTCTTAAACT	GAATTATGTC	CATGGTTGCC	240
AACATGTACT	GTCCATAGTT	GCCACCATGT	ATTTAGGTTG	TCATTTAAAA	TGTCCTCAAA	300
AAGATTTCAC	CATGATTCTC	CATCAAAATA	GAAAGCTATT	TTGTATGAAG	AAGAACTCAG	360
ACCAGAAAAG	TCTGATAAAA	ATAATCTCTT	AAATAAGTCT	ACATTAGGTC	TTTCAATTTG	420
TATAAAATGT	AAATTTTGAA	TTATAAGAAA	ACAATTTGTT	ATACTGTAAT	TGGTAGCATT	480
TTTTCTTAGT	AGTGTACAAA	ATAATGTGTA	CCTTACATTC	AAATCTCGAG		530

### (2) INFORMATION FOR SEQ ID NO:1143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 615 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

GAATTCGGCC	NNCATGGCCN	ACCTATGTNA	NGNATTTCNN	CTCCATTINC	CCNAGGGTTC	60
TTTCCTGTTC	TTAGAAATGT	TTTGTGATTT	TGCTTCAGAC	ACAGTTTGTC	TACTTCTNGT	120
AAGCATTGTT	CTTAGATNGC	TGGCTTTATA	TCTATCACTC	CCTTGCTCAT	CTGCCCATCC	180
ATCTATCCAT	CCATCCATCC	ATCCATCCAT	CATCCCTCCA	TCCACTTGCT	CATCTGCCCA	240
TCCATCCATC	CATCTATCCA	TTCATCCAGT	CCATTCACCA	CCCACCATCT	ATTATCCATC	300
CATCCATCCA	TCCATCCATC	CATTCATCCA	CTCACCCATT	CATCCATCAT	CCATCCACTC	360
ANCCATCCAT	TCATTCAGTC	ACCCTTCATC	CATTCACTCA	CCCATCCTTC	CATCCACTCA	420
TCCAATCACC	CATCCATCCA	TACATCCACT	CATCCATTCA	CCATCCATAC	ATCCACTCAT	480
CCATTCATCC	ATCCATCCAC	CCACCCAGAC	GTCCGTCCAT	CNATCCATCC	ATCCATNCAT	540
CCTTCTATNN	NNTCTGCCAA	CAATCCANAC	ACNTGTCCNT	CNATCCCTTC	CAACCACTCA	600
CCCAGCACAC	TCGAG					615

#### (2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

<ul><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:	
GAATTCGGCC AAAGAGGCCT AACCGCGGCC GCTACTTCGG CCTCTTTGGC CCTCGAG	5
(2) INFORMATION FOR SEQ ID NO:1145:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 227 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:	
GAATTCGGCC TTCATGGCCT AGGTTTTCTT TTATTTAAAA GATCATTCAC AAAATACCAT ATCCATAGAT TTACTTTCTG TCATATAGCT GAATGTGTTA AGTGTTTGGA ATTCCATTCT TACATTTAAA GGTCAACTGG ATTGCCCAGC AGTTTAGATG CATGTGTTTT GTTCTTATC TTATCCACAT TGAAGATGTA AGTATTGAAT TCTAGACCTG CCTCGAG	60 120 180 227
(2) INFORMATION FOR SEQ ID NO:1146:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 447 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:	
CTCGAGTATC TCCTCCTTTC TGATATCCAG TTTAGGTGGT CCAATTTTC CATCTCGGCA TACAGCAAAT TCTTCTGACT TTGCATAGGC AGATTCTTT TGTCCAACCC TGGCTTTAAC TCTGACCCAA AGAGAATTTG ATGGATCACC AACATGATCA GAAATATTAC AATAATGATG AGAAATATTG ATGCAGGCAT CAATCCATTC TGAATTCTTA ACACCATAGT TCTTTACCTC TACGGTAAAA ACAGGGACCT GTGGCATGAT CTGGTACTCC CAATATACGA TAGGGTTCAT GTTATAGGAT TCAATTGTAA CATTAGTTGG TGTAGGCACT GAGGACGGCC CCAGATCCGC GGTGCCCATC TCAGCCCTGC TCACACCCTG CATGACAAGG GGTAGGAGAA AGAGGAGAGC CATGCTGCTA CCGACGGTCG CTGGCTC	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:1147:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 271 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:1147:	

GGGTCTGATT CTGCTTTATG TAGCTGTGTG	TTTGCCATCT CAGGTCCAGG TTTCTCCCGG ACTTCGAAGA GCTCATTATC TTCAGCTCCT TCTGCAGAGT CTTCCGGAGC TCCAGCATCC GCTGCTGCAT GTCTTATTTT TCTCCAGAAG TTGCTGCTCC AAGTCCTGTT TCTCCTTCTG AGATCCATGG CCCCAACCTC ACCATTTGGT GTTCTTCCTG CAGTTGGAAG GGGTCCTGCA TGGCCCTCGA G	60 120 180 240 271
(2) INFORM	ATION FOR SEQ ID NO:1148:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 298 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: CDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1148:	
AATAGAATAT AAAATTAAAA GACAGGGTTT	GGGAGTGTGC GAATAGGTGT GGGTGACAGA CATCAAGTAC TTAACAGGGT CACAAGGCAA GTGGAGGCAG GGCGAGATCA CAGGACCACA GGACCAAGGC TTGCTAATGA AGTTTTGGGC ACCATTGTCA TTGATAACAT CTTATCAGGA GAGAGCAACC GGTCTGACCA AAATTTATTA GGCGGGAATT TCCTCCTCCT GGAGCCGCTAT GGGAGACTGG AGTTTATTTC ATCTCTGCCT GCCTCGAG	60 120 180 240 298
(2) INFORMA	ATION FOR SEQ ID NO:1149:	
	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 332 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1149:	•
CTCCCCCAGC CCAGAAGTTG GAGTGTGTCC AGAGTGGGGA	TTCATGGCCT ACGGCATTTC AGCGTCAAGT GCACTTAGCG GGGTACCCGG CCCCACACCC GTCCTGGGTC TCAGGGTGGT TCCAGCTTCT CCTTGGGCAG GAGTCCCATC CCCCANNGNA NATTTTTTTT TTTTTTTTT TGTGATCAGG AACGTAGCCC CCTGGCCTGT GCAAGCCCTG ACTCCCTCAT GGTGCCTCGG GCATATTGGG CTGGGGTAAG CACTAGACCC AAGTAGACTG GACACAAAGG GGCCCTGGCG CCACCCCTCG AG	60 120 180 240 300 332
(2) INFORMA	ATION FOR SEQ ID NO:1150:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 400 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1150:	
CTCACTCACA	GAAACTCACT TCACGTCTCT TTCCTTGTAG AGCATCATGC TTATTTCTGG TCTTTGTCTC GGGAGTTCTC TGCCGAGCCA TTGCCCCCTA CAGCAGAGAG TGCACTAGTG CTGAAGGAGC CAGCCCCAGA CCACGCATTT TGCCACGAGTT	60 120

CTTGTCCCAG AGCGGCAGGC GTTGTGTGCA GAGAACGCCC CTCCCACGCA GCACAGAGAA	24
CGCGGGGTGG GTGTGTGGCT CCGGGCCTGT GGGGCTTAGG CTGCCTGAAC CACCGCCGAC	30
TGGCACCATG ACTCGGCATT CCTGGAAGTG CCTTACCAAG TTGTTGTTGTTGTTTTTTTTTAAGA GACGGCCTTG CTCTATCATC CAGGCTCGAG	36
TITITIAAGA GACGGGCIIG CICIAICAIC CAGGCTCGAG	40
(2) INFORMATION FOR SEQ ID NO:1151:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 329 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:	
GAATTCGGCC TTCATGGCCT ACCCAGACAA ATACCAAGTT TATTTCACAA ACACTAGGAA	6
GATGGGTTGA GGGTGGAGGT GGGGGACACA GGTGCGCAGC TGCACAGAGT CAGCAGCACC	12
AGCCTGCTCC CCGCACTGAG GACTCGGCCT GGANTGCAGT GCCTCCAAAT CAACACGCAG	18
CAAGAGGGGA GTGCAGGGAG GGCCCTGAAC ACCAAGCCTC TGAAAGGCTA AGGGACACAG	24
CTCCAGCTGT CCCAGGAAAA CCAGCAATAA ATAAAAGTGA GGCACGGCCC CACCCACACA	30
TATCATCTAG TCACCCATCT TCACTCTGG	32:
(2) INFORMATION FOR SEQ ID NO:1152:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 313 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:	
<b>2</b>	
GAATTCGGCC TTCATGGCCT ACCCATAGCC ATGAGCATGA CTGGCTGCCA GCTCTTAGTC	60
ACCAAATGCC ATTCTCCGCT GAAAGAAGCA AGGGCTTTTC AGAGAATAGA CTGAGCACAA	120
AATGACAAT GGTAATGGAG TAGAACACCT TGACTTTTAA AAGTCCACGA GTCCACAGTG	180
ATGCCTAAGG GAAGTAGGGA GGAAAGCTCT TCTTTACAAC ATCTTCCAGC TAACAGATGG	240
AAAGGAATG ACAAAATGAA AAATCACCAT ATTGCAACTC TCAATAAAGT AACTGATTCA	300
GCATATCTC GAG	313
(2) INFORMATION FOR SEQ ID NO:1153:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 324 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:	
GGCTCCTCG CCAAGGAACT CGTGGCAGAA GAGGGCAGCA GTTGGCAGTA GCTGCCGATG	60
CIGTCCCCA GCTCCACCAT TCCTCCCTGT GGCTGTGCCG TGCTCGTGGT TTCACTGTCC	120
FIGTGTCCAT GTGTCTGCCC TTCAGGAGCT CGCAGCTGGT GTGCTTGGCG GTCCCAGGCC	180
GTGTAGTGT CTCTCCCCTG CTGCGGGCGC CCCCACCCCG ATTCCTCTCC CCAGAAGCGG	240

ATAAAGAAAC AGCCTCTACT CGAG

TGGGATGGGC CCCCATGAAC TGCAGCAGCA TGCTGAGGTG TCCATGTTGT CTGCCTTTGT

300

(2) INFORMATION FOR SEQ ID NO:1154:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 327 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:	
GCGAGTTCAG CGGAGAAAAG AAAAAGCAAC GTTTAATTCT AGAAGGCCTC CTGTCCCTGC CTGCTCTGGG TGCTCATGGA ATCAGCTGCT GCCCTGCACT TCTCCCGGCC AGCCTCCTC CTCCTCCTCC TCCTCAGCCT GTGTGCACTG GTCTCAGCCC AGTTTATTGT CGTGGGGCCC ACTGATCCCA TCTTGGCCAC GGTTGGAGAA AACACTACGT TACGCTGCCA TCTGTCACCT GAGAAAAATG CTGAGGACAT GGAGGTGCGG TGGTTCCGGT CTCAGTTCTC CCCCGCAGTG TTTGTGTATA AAGGTGGCGC ACTCGAG  (2) INFORMATION FOR SEQ ID NO:1155:	60 120 180 240 300 327
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 504 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:	
GAATTCGGCC TTCATGGCCT ACGAGCCCTT TGCCTCAGT AGTCCCACCT TTCTGGACTG AACTGATATT CACCTTACAC AAATGGATTG ATGTCTCATG TCTCCCTAAA ATGTACAAAA CCAAGCTGTG CCCCACCACC TTGGGCACAT GTCATCAGAC CTTCTGAGGC TGTGTCACGG GTGCACGTCC TCAACCTTGG CAAAATAAAC TTTCTAAGTT ATCTGAGACC TGTCTCAGAT TTTTGGGGTT CACACCACAT ATGTCTGAAT ACTGTCTTTT CCTATCTCTG GCTCCATCCC ACATTGTAAG GGGCCTTGCA CACACAAATG TGGACATTCC AGCCTGCACA CCTAAGCATC GCCTCCACTC CCACCCTTCC AGCGGATGGG TGTGAAAACT GGCAGTGTTG TTCATCTTCA AGATGATGTA TACAGGAAAG TGGTCCAGGC AGATCCTGTG AGCAGGCTTG GGCCCACTTG GGAAGAGTAA CCCCAGGATCT CGAG	60 120 180 240 300 360 420 480 504
(2) INFORMATION FOR SEQ ID NO:1156:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 686 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:	
GNNNNNNNN NNNNNNNNN TTCCCCCTTN TNNCATGTTT TGTTCCTTTN TCCTTGTTTN TTTTTTCGGC AAAATATTTC AAGNTATACC CAGGCAACAT NAANTCCAGT TCGGATTTTA ATTAGTCGAG TATGCAGCGT CTTTTCATTT TTATTACTCA AAAAAGTTTC ATTTTTTTAT	60 120 180

TTAGCTTTCT GACTCTGTGC TTGTGCCTTC AACACTTTCA CAACGATTTT CTGCTCCTCG	240
ATAAGGAAAG CACGCTTGAT CCTGTCACGA ACACATTTAG CACACATGGA ACCACCATAG	300
GCCCTGCTGA CATGTTTCTT TGTTTTGGAC AATCTCATAA GAACTTTAGG TCTTACAGCA	360
CGAACCCCTC GAAGTCTGCC TGGGCACACA CCACATGCAG ATTTTGGTGC TTTCCCAACC	420
TTCTTGGTAT AAAGGTAAAC AATTCTATTA CCAGGGGTTC GGGACAGCCT AGTTTTGTTA	480
GAGGCTGTAT TGTAGGAAAG CCTACGTCGG TATGTCAAAC GCTGGACCAT TCTGAGTGCC	540
TGCAGACAAC CAAGGGTGAC TATAATGACA GCGTGCAAGT TGTGGACTGT GGACTAAGTC	600
TGAATGATAC TGCTTTTGAG AAAATGATCA TTTCAGAATT AGTGCACAAC AACTTACGGG GCAGCAGCAA GACTCACAAC CTCGAG	660
GENGLAGEAN GACTEACAAC CTCGAG	686
(2) INFORMATION FOR SEQ ID NO:1157:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 274 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:	
CCA A THURSDOOM COMMON A A A A A A A A A A A A A A A A A A A	
GCAATTIGCT TITTTAAAAA TACATTITCA TACACTAAGT TITCTGTTAG CCTAAGTAAT	60
TATATTTCTA ATTAACTTCA AAGTAATTGA TAGGTGGCAA AGGATATCAA TCAAAACCAG	120
TCCAAGTAAA AAATGTACAC TAATTTAATA ACAATATTAT TCTATATTAC TTTTTTTT	180
GCTCACTGCA ACCTCCACGC CCCCCAGACT CGAG	240
	274
(2) INFORMATION FOR SEQ ID NO:1158:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 196 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:	
GAAGATGGAC AACCGGGATG TTGCAGGAAA GGCTAACCGG TGGTTTGGGG TTGCTCCCCC	
TAAATCTGGA AAAATGAACA TGAACATCCT TCACCAGGAA GAGCTCATCG CTCAGAAGAA	60
ACGGGAAATT GAAGCCAAAA TGGAACAGAA AGCCAAGCAG AATCAGGTGG CCAGCCCTCA	120 180
GTCCCCACAT CTCGAG	196
(2) INFORMATION FOR SEQ ID NO:1159:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 141 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:	
GAATTCGGCC TTCATGGCCT AGAGGTGAAA TACAGAAAGC CTTTTTTCT TGATCTTTTC	60
CCGAGATTCA AATCTCCAAT TCCCATTTGG GGGCAAGTTT TTTTCTTCAC CTTCAATATG	120

AGAATTCAGC GAACCCTCGA G

(2) INFORMATION FOR SEQ ID NO:1160:

<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 355 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:	
GAATTCGGCC TTCATGGCCT AGTAATATAT ATAATTTATA AGTAAATATA AATTAGGGAG GTGTACTCAA CATTTTCATA GAATACATAG TCAAAAATGG TTTGCAACCT CTGCCTAACA AAAATAAAAC ACCCTACATC TTTGGTTCAA GATTGTCACC CCCAACAGTT GTGTGAAATG IGGGGCAGGA ATTATCACTA TTTTCCTTTG GAAATTAAGG TTCCAAAGAT AATGAGACCA GAGCCAAAGG TCAGAGTCCA CTGTCTTCTC TCTGAGGCCT CAATGTGAAG ACCTGAACTG IGGCAGCAGA TAATTCTGGA GACCTGTTAA TCAGCTGTAT GCACCACAAC TCGAG	60 120 180 240 300 355
(2) INFORMATION FOR SEQ ID NO:1161:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 257 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:	
GTATTTCATC ATATAATTT CTTCGAATTG GGAATTTAGG CAGTATGTTA TGGGATTTTTTTTTT	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:1162:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 220 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:	
GAATTCGGCC TTCATGGCCT ACTGTTTCCT TGCCCTTTTC ACCGTCTGGT GGTTCCCTGC AGCCCTTGGC TTGTGGCCCT CTCATCCATC TTCCGAGCCT AGCACTCCAG TCTCTGCTTC TGTCATCACA TCGCCTTCTC TTGAGAAAGA TCCCAGGCTG GTATTTAAAT TGCCTGTTGG CAGGAACTTT GCCTGTCTTC CCCTACCCCC ACAGCTCGAG	60 120 180 220
(2) INFORMATION FOR SEQ ID NO:1163:	
(i) SEQUENCE CHARACTERISTICS:	
464	

(A) LENGTH: 405 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) Topologi. Timeat	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:	
GAATTCGGCC TTCATGGCCT AATCACTTGA GGTCAGGAGT TCATGACCAG CCTGGCCAAC	
ATGTTGAAAC CCCATCTCTA CTAAAAATAC AAAAATTAGC TGGGCATGGT GGGGGGCACC TGTAGTCCCA GCTGCTAGGG AGGCTGAGAC AGGAGAATCA CTTGAACCTG AAAGGTGGAG	120 180
GTTGCAGTGA GCGGAGATCG TGCCACTGCA GTCCAGCCTG GGTGACAGGG CAAGACTCCG	240
TCTCCAAAAA AAAATTAAAA ATAGAAATAC ATTTTAAAAC CCAGATACTT GTAGCATATA	300
TAAGGGACAA TTGCAGTTTG GAAGGTACTT CCACATGTAT TATATAATTT TATTTTTTAA	360
AATGAATCTC ATTTGGTTGT CATGAAATTT GGCAAGCTTC TCGAG	405
(2) INFORMATION FOR SEQ ID NO:1164:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 259 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
154 555 556 556 556 556 556 556 556 556 5	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:	
GAATTCGGCC TTCATGGCCT AGCAGAAGCG AGAGGAGGAG GAGAAGAAAG CGGAGTTCGA	60
GCGGCAGCGA AAAATTCGAC AGCAAGAAAT AGAAGAAAAA CTCATCGAGG AAGAAACAGC	120
ACGAAGAGTA GAAGAATTGG TAGCAAAAAG GGTGGAGGAA GAACTGGAGA AAAGGAAGGA	180
TGAAATTGAA CGAGAAGTTC TCCGAAGGGT GGAGGAAGCC AAACGCATCA TGGAAAAGCA GTTGCTCGAA GAACTCGAG	240 259
orrection directions	259
(2) INFORMATION FOR SEQ ID NO:1165:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 114 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(a) anough magning	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:	
21.00000	
GAATTCGGCC TTCATGGCCT AAATTTCAGC AATACAGCTC TCACATACAT AAATTATAAA ATAATTTTAT TTAAGGTGAT GAAATTTATA AGCAGGTTCA AAAATATAAT AAAA	60 114
(2) INFORMATION FOR SEQ ID NO:1166:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 316 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

GAATTCGGCC	TTCATGGCCT	AGTCAGCAAC	ACCCAACACT	GTCTGTTTTC	CATTTGTTGG	60
TTTTAATCAT	AAAATTGTCA	AGTGATTCGT	GTTTGTACTT	TATTTTTTTG	TGCCTTCTGA	120
AAGGATCTAA	AACAAAAATA	TTTTGCCTTT	TTTTCCCCAC	GTGTATCTGA	ACATTAAGCA	180
GATTGGCTCA	GACACAATGA	AAAGGATAAT	CCAATGTACG	TGCTGGTGCA	CTCTGCTAGT	240
TGTTATCTCT	GTAGGGCTCA	GGAAGCTGGA	AGGAGGAAGG	GAGGGTAAGT	GGCCTGGTGA	300
GTGGAGGTGG	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1167:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 300 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

GAATTCGGCC	TTCATGGCCT	AGGTACCAAT	AATTTCTTCA	CTTCTTCAAC	TGCTCTCTTC	60
AATTTGATTT	CTGCTCTGTT	CTGAGCATCT	TCCACAGTGA	TTAGTACATG	TAAATCTTCA	120
TTTAGATGCT	CCCAATTGGG	CTTGCCTCTA	TTTTGCTCCT	CCTTTTTTTT	ATCCCTCATT	180
GAGCCTTTGC	CTCGGACCAT	GATTTTACAT	CCGGTTTCTG	CTTCAAGTTG	TTTGGCTGTA	240
AGTCCTCTAG	GTCCAAGGAT	TCTCCCAACA	AAATTAAACT	TCGTCCAGCA	GCCGCTCGAG	300

- (2) INFORMATION FOR SEQ ID NO:1168:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 229 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

GAATTCGGCC	TTCATGGCCT	ACCTTCACAG	AAAAATGCAT	AGCTGGATGC	TGCAGACTCT	60
AGCGTTTGCT	GTAACATCTC	TCGTCCTTTC	GTGTGCAGAA	ACCATCGATT	ATTATGGGGA	120
AATCTGTGAC	AATGCATGTC	CTTGTGAGGA	AAAGGACGGC	ATTTTAACTG	TGAGCTGTGA	180
AAACCGGGGG	ATCATCAGTC	TCTCTGAAAT	TAGCCCCCCC	GATCTCGAG		229

- (2) INFORMATION FOR SEQ ID NO:1169:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 348 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

GAATTCGGCC TTCATGGCCT AGTGCTGGGA GCGCAGCCGG CGGGCGAGGC TGCCTGGAAC

GTGGAGCTGC TGGAGCTGTC CGGCTGACCT GGAAAGTTCT TTGGCCTCTA GGCTTTACCT

120

GGAGGCCTCT TCCTTCAGCT CCTTGTTTTT CCGCACCTCC TCGGCGTGCT TGTCCTTCTC TTGCAGCCGT TCCAACATGG CGGCGAGGTG GGCCTCCCTG TTCTCCTTGT TGGATTCCAT CTTCTGGGCC AGTTTTTCCT TAGCCATCTT GATGAAGTTG TTGTTTTCCT CAATGGCCTT TTGGATCACC TCTCTCTCAT GTTCCCGGAA TTCTAGACCT GCCTCGAG	180 240 300 348
(2) INFORMATION FOR SEQ ID NO:1170:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 81 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:	
GGCTTTTTCC AAATTGCTCT GGCTACCATA TAGAAAATTG ACTGAAGGAG GGCCAAGATG GAAACAGAGA GGACGCTCGA G	60 81
(2) INFORMATION FOR SEQ ID NO:1171:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 418 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:	
GAATTCTGAG GGACTAACTA CGACCATGAG ATTGGCAGTG ATTTGCTTTT GCCTATTTGG CATTGCCTCC TCCCTCCCGG TGAAAGTGAC TGATTCTGGC AGCTCAGAGG AGAAGAAGCT TTACAGCCTG CACCCAGATC CTATAGCCAC ATGGCTGGTG CCTGACCCAT CTCAGAAGCA GAATCTCCTT GCGCCACAGA ATGCTGTGTC CTCTGAAGAA AAGGATGACT TTAAGCAAGA AACTCTTCCA AGCAATTCCA ATGAAAGCCA TGACCACATG GACGACGATG ATGACGATGA TGATGACGAT GGAGACCATG CAGAGAACGA GGATTCTGTG GACTCGGATG AATCTGACGA ATCTCACCAT TCCGATGAGT CTGATGAGAC CTTCACTGCT AGTACACAAG CAGTCGAG  (2) INFORMATION FOR SEQ ID NO:1172:	60 120 180 240 300 360 418
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 431 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:	
GAAAACAGCA CTGCATGTCT TTGGCAAGCC ACAAGTTTCA TAGATACAGC TGTGCTCACT GCAGAAAGCC TTTTCATAAG ATAGAAACAT TGTACCGACA TTGCCAAGAT GAGCATGACA ATGAGATAAA GATTAAAATAC TTCTGTGGGC TTTGTGATCT TATCTTTAAT GTGGAAGAAG CATTTTTGAG TCATTATAGAG GAGCACCACA GCATAGATTA TGTATTTGTG TCAGAAAAAAA CTGAAACTTC AATTAAAACC GAAGATGATT TTCCAGTAAT AGAGACCAGT AACCAGTTAA CTTGTGGTTG CCGTGAGAGT TACATCTGTA AAGGCAAAAC TGTGGTTTCG CTGCAGTTTA TGTTCGGCAA	60 120 180 240 300 360 420

431

CAGCACTCGA G

(2) INFORMATION FOR SEQ ID NO:1173:

(i) SEQUENCE CHARACTERISTICS:

<ul><li>(A) LENGTH: 319 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:	
GAATTCGGCC TTCATGGCCT ACCCCTTAAA GGAAAGAATG GCTGCTCTAG AAGAAAAGAA	60 120 180 240 300 319
(2) INFORMATION FOR SEQ ID NO:1174:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 171 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:	
GAATTCGGCC TTCATGGCCT ACTTAATATA TTTGTGAGAT AATTATTGAG ACATTTTATT AATATTTTAT TTAGTCTTAG AATTTCAGAG AAAAGTGAAC CTAGAGAGGT ACTTCTCCTG GTTCAAACTG TGAACATGAA AATTCTGAAT TTAAGTAACT GGATCCTCGA G	60 120 171
(2) INFORMATION FOR SEQ ID NO:1175:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 366 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:	1
GAATTCGGCC TTCATGGCCT AAGGAAACAA AAAGCTAAGG GCAAAATGTA CAAACTTAGA AGAATTGGAA GATAGAAACA AGATAGAAAA TGAAAATATT GTCAAGAGTT TCAGATAGAA AATGAAAAAC AAGCTAAGAC AAGTATTGGA GAAGTATAGA AGATAGAAAA ATATAAAGCC AAAAATTGGA TAAAATAGCA CTGAAAAAAT GAGGAAATTA TTGGTAACCA ATTTATTTTA AAAGCCCATC AATTTAATTT	60 120 180 240 300 360 366
(2) INFORMATION FOR SEQ ID NO:1176:	
160	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:	
GAATTCGGCC TTCAGGCCTA CAAGAATTTT ATGCCATCCA AGAGTATTAG CACAAATAAA	60
TAAAGGCAAT TTGTAAATTT TTTCCCTGAA AATCTAAAAA ACAAGAAAAC TATCTCTTCA	120
GGGTGATTAT AATTAGGTCT ATGAGACTCT CAAGGTCCCT TTAGTGATTC AGAATCTATA	180
GTTGGAAATA CTTATTTTAA AATGTTCAGG CAGTTGCTCG AG	222
(2) INFORMATION FOR SEQ ID NO:1177:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 367 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:	
GAATTGTCCA CAGCCTGTCA TGCCGCACAA CTGTCCACGC TCGGTTCTCT CGGATATCAC	60
AGTACACTAC AAATGGCTTC AGGGGGCCAC TGCCATCAGG ATCAATGGTG AAGTTTCCAG	120
AAGITTTCCC ACTGAGCCGA TAAGCCTCAC AGGATTCCTT ATACAAAGGT GTGTGGCAGG	180
TCTCTCCCTT GTAGCCCGTC AGTTCGCAGT AGCAAATGAA GTCATCCCAA GACTGGTAGC	240
AGCGTCCATC ATGCTCACAC ATGTTAGGGC TGCACCTATC AGTGATGCCA CATGTATCAA	300
AGAGGACCTC AGCATAGAAT CCAAGCCGCC GGCCCTCCAC CAGAGTCAGG TTGACCAGTT	360
GACCGAG	367
(2) INFORMATION FOR SEQ ID NO:1178:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 367 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:	
GAATTTAGAA CGGGTACAAA AGGACCTAAG CCAAACACAG TGTCAAATGA AGGAAATGGA	60
ACAAAAGTAT CAAAATGAAC AAGTTAAAGT GAATAAATAC ATTGGAAAGC AGGAGTCTGT	120
AGAGGAGAGA TTGTCTCAAC TACAAAGTGA GAATATGTTG CTTCGACAAC AACTGGATGA	180
TGCCCACAAC AAGGCTGACA ATAAAGAGAA GACAGTGATT AATATCCAAG ACCAGTTTCA	240
TGCTATTGTG CAAAAACTTC AAGCTGAGAG TGAAAAGCAA AGTCTTCTGC TAGAAGAAAG	300
AAATAAGGAG TTAATCAGTG AATGTAATCA CTTAAAAGAA AGACAGTATC AATATGAAAA TCTCGAG	360
	367
(2) INFORMATION FOR SEQ ID NO:1179:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 247 base pairs	

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:	
GAAACCGAAA GTGGAAATGT ACTCTGGGAG TGATGATGAT GATGATTTTA ACAAACTTCC TAAAAAAGCT AAAGGGAAAG CTCAAAAATC AAATAAGAAG TGGGATGGGT CAGAGGAGGA TGAGGATAAC AGTAAAAAAA TTAAAGAGCG TTCAAGAATA AATTCTTCTG GTGAAAGTGG TGATGAATCA GATGAATTTT TGCAATCTAG AAAAGGACAG AAAAAAAATC AGAAAAACAA GCTCGAG	60 120 180 240 247
(2) INFORMATION FOR SEQ ID NO:1180:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 149 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:	
GAATTCGGCC TTCATGGCCT ACGAGTTCTT CATGCTTGTT GTTGAGATTT GAGATGTTTA TTGGTAACAT TGTCTTTTTT CCATCCTTTT TTTTCTTTCC TAACCTGGTT TCTTCCAGTG CAACTGCAGA TAGAAGACCT GACCTCGAG	60 120 149
(2) INFORMATION FOR SEQ ID NO:1181:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 251 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:	
GAATTCGGCC TTCATGGCCT AGAAAATTAA ACTGTTTTT AAACCAGGTG TTCACTTTC ATTGATTTTT GCATAGTACT TGGTGAACCC TATTGATTTT TAGATTCAGG TAATTTTTCA GTGTGAAAGA GTTTTCTGT TATATCTTCA CTGTGATATC CATTCCATTC	60 120 180 240 251
(2) INFORMATION FOR SEQ ID NO:1182:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 176 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:	

TITACIGGAT	CCTGCCTAGA GTGCTCTGTG TATGCGGATG ATTTAGAATT GTCAGTTTATTTAT AAAGATCTGG CCTGTTCCTG CGTCTGCGGA GCGCATCTATAACC TTAGCTAGAG TGTCGCCTTG TGGGTTCCCT CTCG	CCCTTC 120
(2) INFORMA	ATION FOR SEQ ID NO:1183:	
	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 410 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1183:	
AGGAGATGGT A CATTACGGGC 1 TTTGTTCAGG 1 GTGTGGACCT 1	TTCTTGACGG GTTCTCGGGG GTTCCTGTTG TATAAAGGCC TTCA CAAGTGAAAG GGGCATTTAC CTCGTGACAA GTGGATTATA GGAG AGGTCAGAGT GTGCTTAGAA GTCATGCCCA GTGTTCTCAT CAAT TGCCCTTCCA TCAGCCATTC TACCTTTCTT CCTGCTAACA ATAT TATCAGGCCA CTTAATATGT TCAGGGAAA ACTGGTTCCA GCCC TGATTACATC AAACTAATCA TGGTGAGTCC ATTTTCCTTG CCAG. GGACATGTAT TTCACTTGTG AGTACACAAG ACGACTCGAG	AAAAAG 120 GCCAGA 180 CCCAAT 240
(2) INFORMAT	TION FOR SEQ ID NO:1184:	
(i) S	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 286 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1184:	·
GGATTCCACA A NACAGAAGCC T NAAGGGAAAT A	AGTACCAAGG AAGAAGCAGC TAAGATGGAA AAGGAATATG GAAGGAATGATA ACTCCAAACCC AGGAGGAAAG ACAGATGAAC CCAAATTTGGAAG CCATCAGAAA AAATATTGAA TGGTTGAAGA AACACAAAAGAAGAATT ATGACCTTTC AAAGATGAGA GACTTCATCA ATAAAGTGGAGAAAG GCATCCTTGA CAAGGAAGGG CTCGAG	AGGAAA 120
(2) INFORMAT	TION FOR SEQ ID NO:1185:	
(i) S	GEQUENCE CHARACTERISTICS:  (A) LENGTH: 417 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) 1	MOLECULE TYPE: cDNA	
(xi) :	SEQUENCE DESCRIPTION: SEQ ID NO:1185:	
CCCIACAAG A	CTAGACCTG CCTCACCTTA CCCCAGGACT CCGCTATGAC ACCGCACACAGATCT CTCGTCAGCC CCAAAGCCTG TGGCTGCAGC CACGCTGAAGAGGG CCTCACCTTA CCCCAGGACT CCGCTATGAC ACCGCACACAGATCT CTCGTCAGCC CCAAAGCCTG TGGCTGCAGC CACGC	ATTGTG 120

TCCCAGCAGG CTGAAGAGGG CCTCACCTTA CCCCAGGACT CCGCTATGAC ACCGCCTCTG CCCCTACAAG ACACAGATCT CTCGTCAGCC CCAAAGCCTG TGGCTGCAGC CACGCTTGTG TCCCAGCAGG CTGAAGAGGG CCTCACCTTA CCCCAGGACT CCGCTATGAC ACTCGAG	300 360 417
(2) INFORMATION FOR SEQ ID NO:1186:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 260 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:	
GGAAGGGGCT TTTACAACTT CCTTTTGTTT CCAGGCGTTA GTATCTCTGC TTGGTATAAG ATACCAGTAT TCCTAGGAAA GGCCTTGAAA AGAGGGACAG ATACAAGCCT CTTCTGAAAA ATCTATGCTT TTCTTACCTC TACCAAGTAA TAGCAAACAT GAAAATGGTA AAGATCTTTA CAACATTTGT CTCTGTACAT ATAAAACGTT TAAACACATG CGCAAAGATG GAGCAAAATA TCATAGAAAA TAATCTCGAG	60 120 180 240 260
(2) INFORMATION FOR SEQ ID NO:1187:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 337 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:	
GAATTCGGCC TTCATGGCCT ACAAGGAAAT GCCCAAGGAA AAACGTGAGC TTCAGTTTCG GCGAAAGGTC TTAGCAGTCA CAGACTCACC TGCCAGGAAG GGCAAGGACT CTCCCTCTAA GCAGAGCCCT GGGGAGTCCA CGAAGAAGCA GGATGGCCTA GTCCAGATTG CACCAAACCT GACTGTGATC CAGTTCATTA AAGTCTTCCC CAGGGTGCTC CTGCAGACCC TACGCCACCC CATCTTCCTG CTGGTGGTCC TGCCCAGGT ATGCTTGTCA TCCATGGCTG CGGGCATGGC CACCTTCCTG CCCAAGTTCC TGGAGCGCCA GCTCGAG	60 120 180 240 300 337
(2) INFORMATION FOR SEQ ID NO:1188:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 537 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:	
GAATTGGCCT TCATGGCCTA CGAGGCGTCA CTGATCTTAA CGAGACTTCC AAATCGTCTC AGCAGGGGCT CCAGACTTCC CCAGCAGGCG GCAGGTTTCC TGTCATGCTT TCGCCTTCCT TCTCATATAC ACCAGTGCTA GAGTTCATCA TGTGTCAAAA TTGTATCTTG CTTCTTGTTT TCAAGATGAT CTAATAGTTG TCTTATCTCA GCATCATACT CCACCCATTC TGGGACAATT CTGGCAGCAG CTTTTAGTTT GGATTCTTTT GTTTTTGGCAT TATTGCACAG ATCAATTGTT TTGGCCCTCC TTGGACTAAC CACATACAAA TATGAATCTG GCTGCAAGAA CAGGATATCC	60 120 180 240 300 360

AGGTAACTAG AGAGTGGGCA TTGATAAAAA TATCTGGTGG AGAAGCCTAG GATTTCAACT TTTTGTCAGA GGATTCCTGT TGGGACAGCT TTACCAGAAA AGAATAATAG CGGATATGTT CATCCAAACT AAGAACTTTC ATGCATCTTG CATTGTTACA TAGCCTGTGG ACTCGAG	420 480 537
(2) INFORMATION FOR SEQ ID NO:1189:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 65 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:	
GAATTCGGCC TTCGTGGCCT AATTGAATTC TAGACCTGCC TCGAGGATTC AATTAGGCCA TCGAG	60 65
(2) INFORMATION FOR SEQ ID NO:1190:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 398 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:	
GAATTCGGCT TCATGGCCTA ACTITATGTC ATAAAACTGA TTTAAATAAT CTTGAAATGG CCATTAAGGA AGATCAGATT GCAGATAACT TTCAAGGAAT ATCAGGTCCT AAAGAAGACA GCACAAGTAT AAAAGGTAAT TCAGACCAGG ATTCTTTCT TCATGAGAAT TCGTTACACC AAGAAGAGAG TCAAAAAGAA AATATGCCTT GTGGGGÁAAC AGCAGAATTT AAACAAAAGC AAAGGTATA CAAAGGAAAA CAAGGAAAGG AGCAAAATCA GGACTCACAG ACAGAGGCAG AAGAGCTACG CAAACTTTGG AAAACCCATA CTATGCAACA AACTAAACAG CAAAGGGAAA ATATTCAACA AGTGTCACAA AAAGAAGCTA AACTCGAG	60 120 180 240 300 360 398
(2) INFORMATION FOR SEQ ID NO:1191:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 231 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:	
GAATTCGGCC TTCATGGCCT AGCCATTGTT TATACATTAT TGCTGTCAGT ATTCACCAAG ATGGTGCTAT TACCTGTTGT GGGGCAATTT TCCTTGTCAT TTCTACATAT CTTGGAACAG CTTTTGTCCT TATATTTTCA AGAATGTTCT AAAGCAGACA GCCTTGGAGG AGAGACAGAT AGTGACTCCC TCCAGGGAAA AAGTCGGATT TGTGTGCTCC CCTGCCTCGA G	60 120 180 231
(2) INFORMATION FOR SEQ ID NO:1192:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:	
GAATTCGGCC TTCATGGCCT ACACTAACCG CAGCATGGCG GATCTGAAGC ACAGCAGCTT GCGGTACGAG CTCCGAGCAG ATCTGGAGGA AGAAAGAATG CGGCAGAAAA TAGCAGAAAG GACCTCAGAA GAAACAATAC GCATTTACTC TTTGAGACTG TTTTTGAACT GTATTGTTCT GGCTGTTTTA GGGGCATGCT TTTATGCAAT ATACGTAGCA ACTGTCTTCT CGCAAGAGCA CATGAAAAAAG GAAATCCTCG AG	60 120 180 240 262
(2) INFORMATION FOR SEQ ID NO:1193:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 381 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:	
GAATTCGGCC TTCATGGCCT AGAGGAAATT GCTAATGTAA CAGAGACATC AGATCCAGAA TTCCAACGAA CCTGAATGAG CCCTGGTGTG GAACAGCCGT GAGCCTGTCC ACGTTTTCT CCTGATCTCT GCTTTTCATT AGTAATGAAT TTCCACTCCT TCTCCCCTTT CATGACAAAT CAGTACAGTG AATGTAATTG CCACATCCAG CGATGCATCA TCTTCCCACT TTTCTAGGCT GCAGAGAAGG AAGCAGCCCT TGTGCAGCAA GAAGAAGAAA AGGCTGAACA ACGGAAAAGA GCTCGGGCTG AGAAGAAAGC GTTAAAAAAAG AAGAAAAAGA TCAGAGGCCC AGAGAAGCGC GGAGCAGATG ATGGACTCGA G	60 120 180 240 300 360 381
(2) INFORMATION FOR SEQ ID NO:1194:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 294 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:	
GCGATTGAAT TCTAGACCTG CCTCTCTTAC CCTTGGCTTA CTAATATATT CTTAGTGGCA TTTCATTTGG TGGTACTGGT GGCGCATTCA AACAGGACAC TTGTATCTGA GTGAGCAGCT GGAGCAGTAA GAATGACAAC ACTTGGTCTC TGCAGATTGG CTGGACCCAC CACTCTGGTG CTAGTGCTGG CTTGGTGGCT GAGGGAACAA GCAGGAAGTA GAAGAGGAAA TGAGATGTGG GTGGAGTGGG AAGAGAGGAC AGATTGGGGA GGGGAGGGAA AGTGCAAACT CGAG	60 120 180 240 294
(2) INFORMATION FOR SEQ ID NO:1195:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 262 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

G	CGATTGAAG	TCATTGCCAC	GCCTACTAGT	TTCCACTAAA	CCAAACMOAG	TTTGGTATGA	
Δ	TTACAATCC	CCAACCTTAC	ATTOMOSTICS	TIGCACIAAA	GGAAAG I CAG	TTTGGTATGA	60
		CCAACGITAC	ATTOTOTOC	GTTTTGTTTT	TTTTTTTAA	TCTCAATTTC	120
1	CTTACTTT	CTTATTCCCC	CTATGCTGAT	GCCAATCAGT	TTCTTTTGGG	AAAGTTTTAA	180
C	AGATCGGTT	TTATGTTTTG	AAGTACAGCA	Δατατττικτ	COTOTOTOTO	AAATACAAAA	
C	CCAGAAACC	CAGGAGCTCG	NC.	MOTATTICAL	CCICICITIA	AAATACAAAA	240
_		CHOOMOCICG	MG				262

- (2) INFORMATION FOR SEQ ID NO:1196:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 266 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

GAATTCGGCT	TCATGGCCTA	GACCGTCTCA	AAGAAAACAC	ስጥስጥስ <i>ር</i> ምምም	TGCTCAGATT	
ATTCTTAAAT	THE PROPERTY OF THE PROPERTY O	COURT COMMON OF CO.		MINIMOCITI	IGC I CAGATI	60
	TITACCICAL	TTACTTTATC	AATTGCTCTT	TCTCTATTTA	TGTGTATCAG	120
ATTATTGTTA	AATGTTACCT	TATTTGCCTT	ATCAATTGCT	СТСТТТАТОТ	ATGTTTGTGT	
GTACTGTTGC	ACATCCAAAT	CCACACAAA		CICITIAIGI	AIGTITGIGT	180
0776707700	VCVIQCWWVI	GCACACAAAT	ATATGTTTCT	GAATTTTTTG	AGAGTAGATT	240
GCATACATTA	TGGGACCTGC	CTCGAG				
						266

- (2) INFORMATION FOR SEQ ID NO:1197:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 232 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

GAATTCGGCC	TTCATGGCCT	AAGAAACACT	TTTAAAAATC	TTTTC > CT > CT	TATTTTGTAC	
ΔΤΑΩΑΤΑΑΩΑ	TACTORIA	000000000	TITOMANAIC	TITCACTAGT	TATTTTGTAC	60
TINONIANOA	INGITGATIC	CCAGCTTTTA	TCTGTAAAGT	TGTCATAATT	GGAATTAACT	120
TCGGTGATTC	TGTTGTATAA	AACATTGTTA	TATTTTACC	TOTOTOCOCA	TTTTAGGCAA	120
ACAAGAAAAT	ATTACACTCA	TCCNATTOO		TOTOTOCOGA	TTTTAGGCAA	180
	AT TAGAGTGA	TGCAATTGGC	TTTGTTCCAG	GGGATGCTCG	AG	232

- (2) INFORMATION FOR SEQ ID NO:1198:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 302 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

ATTGTGCAAC GGCCAGCTGT GGCAATGCCC	ACTAAGTGGA GCCAACTTTA GCACCTTGCT AATGAATCTG GGTCCTGAGA ACTGCTGCTC TTTGTTTTAC TTGAGAGTAA AATTCTGCTG CATTCTCTTA CTTGACTGGG GTAGCTGAAG CTGTTGTAGC TATGATCTTT CCATTTCAGT ATATATCCC CTTTGTCCTC TTTCACTGC TGCAGTGCTT AGTGCACCTT	120 180 240
AG	AGTTGGAGTT GACTCAAGGT ATTTTGATCT TCATGACCCA CCAAGGCTCG	300 300
(2) INFORMA	ATION FOR SEQ ID NO:1199:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 231 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1199:	
CCTTCCAGAA ATTTTACAAT	CTGGCCAGGA CTCTCTTATT AGGTTTGACA TTTCAAGAGT TTAGAAATTA TTCACAGGTA AAAGCCAGAC CTCTCCTTGG TGAAGATACA ATTCTTTACA AGTTAAGTAT ATTTTATCAG TCTATATTGG CTGTTTAGTT GACAAACCGT TGACAGTCCA GATGTGGTCA CTCATGCCTC TAATCCTCGA G	60 120 180 231
(2) INFORMA	ATION FOR SEQ ID NO:1200:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 235 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: CDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1200:	
GGTAAAGGTG AAAATCCAAG	CCTGACCCAG CCCCCATGGC TTCAGAAGAG CTACAGAAAG ATCTAGAAGA TTGCTGGAAA AGGCTACTAG GAAAAGAGTA CGTGATGCCC TTACAGCTGA ATTGAGACAG AAATCAAGAA CAAGATGCAA CAGAAATCAC AGAAGAAAGC GATAATGAAA AACCAGCTGC TGTGGTTGCT CCCATCACTC TCGAG	60 120 180 239
(2) INFORMA	ATION FOR SEQ ID NO:1201:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 119 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1201:	
GAATGAGAGG CTAGCCTTCA	TCAGAGTATT CCATTGCACA CGCACCCTGG GGCTGACAGA CTTGTGCCCC TGCATGCCCA AGCACTGGCA GCTTTGCAGC CCCTGCCCCA CGACTCGAG	6
(2) TNEODMA	ATION FOR CEO ID NO. 1202	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

GATTGAATTC TAGACCTGC	TCGAGATTCT	TTGAGCACTT	TCCCCCATCC	CCAGGGCCAC	60
AGATCCCCTT CCTTACTTG	TGGGGGGAGG	TCTGGAGCAC	CTCGCCAATG	CCCTTCCCCC	120
ATCCGGCTGG GTCCTTCCA	TTATTTATTT	GTGTATTTAT	TTATTTATCT	ATTTATTATT	180
CTATTTAATC TCTTGGCCT	C ACCCAGGGAC	CGTCTGGCTT	CCCCAGCTGG	ACTGGGAGGT	240
CAGGAAGCCA GGCAAGGAG	A GGGACAGCAC	AGGCCACAGA	GGGCTGCCCC	CACCACACAC	300
ACCCCCGCGT CTCGGGAGA	ACCCACCCTC	TTCAGAGCCT	GCACTCGCTA	AGGAAGGGGA	360
CTCGAG					366

- (2) INFORMATION FOR SEQ ID NO:1203:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 342 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

GGTGAGATGG AAAAGGAGTT	TCCTGAGCTT	ATCCGAAGTG	TTGGTTTACT	TACGGTAGCT	60
GCTGACTCTA TCTCTACCAA	TGGCAGTGAA	GCAGTTACTG	AGGAGGTATC	TCAAGTATCT	120
CTCTCAGTAG ACGACAAAGG	TGGATGTGAG	GAAGACAATG	CTTCTGCAGT	CCANCACCAN	180
CCAGGCTTAA CACTGGGGGT	GTCATCATCT	TCAGGAGAAG	CTCTGACAAA	TOTOTON	240
CCCTCCTCTG AGACTGTGCA	GCAAGAATCC	ACTTCCTCCT	CCCATCATCA	TOCIOTICAA	
CAGCAGCCTG TTCCTTGTGA	AAATCCAACC	CCCLLANGE	CCCATCATGA	I GCAAAGAAT	300
alocalocato freefrench	MATGCAMCC	CCCAAACTCG	AG		342

- (2) INFORMATION FOR SEQ ID NO:1204:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 645 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

CAATTCCCCCT	TO MOO O O O O		_			
GAMIICGGCI	ICATGGCCTA	CGTCTTTCTA	ACTATCTATG	GGGTGGAGCT	GTTCCTGAAG	60
GTTGCCGGCC	TGGGCCCTGT	GGAGTACTTG	TCTTCCGGAT	GGAACTTGTT	TCACTTCTCC	120
GTGACAGTGT	TOCOUTTOUT	CCCACTCCTC	CCCCTTCCCCC	TCAACATGGA	TOACTICICC	
		GOGACIGCIG	GCGCTGGCCC	TCAACATGGA	GCCCTTCTAT	180
TTCATCGTGG	TCCTGCGCCC	CCTCCAGCTG	CTGAGGTTGT	TTAAGTTGAA	GGAGCGCTAC	240
CGCAACGTGC	TGGACACCAT	GTTCGAGCTG	CTGCCCCGGA	TGGCCAGCCT	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	
CTCCTCSTCT	mmma cma cm c		CIOCCCCGGA	TOOCCAGCCI	GGGCCTCACC	300
CIGCICATCI	TTTACTACTC	CTTCGCCATC	GTGGGCATGG	AGTTCTTCTG	CGGGATCGTC	360
TTCCCCAACT	GCTGCAACAC	GAGTACAGTG	GCAGATGCCT	ACCGCTGGCG	Chaccaches	,-
CTCCCCAACA	COLCOOMOOM	0010010		ACCOCTOOCG	CAACCACACC	420
GTGGGCAACA	GGACCGTGGT	GGAGGAAGGC	TACTATTATC	TCAATAATTT	TGACAACATC	480
CTCAACAGCT	TTGTGACCCT	GTTTGAGCTC	ACACTTCTCA	ACA ACTOCOTA	CAMCAMOAMO	
CARCCCCTCA	COTOMONONO	~~~	manufatur.	VCHACIOGIA	CATCATCATG	540
GAAGGCGTCA	CCICICAGAC	CTCCCACTGG	AGCCGCCTCT	ACTTCATGAC	CTTTTACATT	600
GTGACCATGG	TGGTGATGAC	GATCATTGTC	CCCTTTATCC	TCCAC		545
				· CONG		645

- (2) INFORMATION FOR SEQ ID NO:1205:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 336 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

GAATTCGGCC	TTCATGGCCT	ACAGTACACA	AGTGCTAGCC	CTAGCAGCTC	GCGATGTGCT	60
TCAGCAGAGC	AGACGCTGCG	GATAACTACC	CTTTTGGAAC	ATGTCAACAG	AGGAAACTTT	120
TTCCTCACTT	CCATCCCCCG	AATTTGATTG	GGAACAAGTT	TGTCCCTCTT	AGGGGATCAC	180
CCCACAGAGG	GCCTGGGTGT	TATTTTTCAG	ATGGATATGG	CTTGGCATAC	GACTTATCTA	240
AGATCCCAAC	CAGTATAAAA	<b>GGATATACTT</b>	TGGGAGCCAG	AACAGCTGTG	AGGTTTAAGC	300
CAATACAGAA	GGAAATGACA	CCTCATGCAG	GCAGGT			336

- (2) INFORMATION FOR SEQ ID NO:1206:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 309 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

GGAAAATCTG	AACAAACAAC	CGAATAAGCA	GTGGAAGAAA	TCACAAACAT	CTACAAATCC	60
AAAAGCTGCT	CTCAAGTCTA	AGATAGTTGC	TGAATTTCGA	TCTCAGGCCC	TAATTGAAGA	120
GCTGTTGCTA	TACAAGCGCT	CAGAAGATCA	GATAGAACTG	AAGGAAAAGC	AGTTGTCAAC	180
TATGAGGGTG	GATGTGTGCA	GCACAGAAAC	TCTCAAATGC	TTAAAAGATA	AAACAGGTGG	240
GAAGAAGTTC	TCCAAAGAAT	TTGAAGAGGC	AAGCTCCAAG	CTGGAAGAAT	TTGTGAATGG	300
ATCACTCGA						309

- (2) INFORMATION FOR SEQ ID NO:1207:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 341 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

GAATTCGGCC	TTCATGGCCT	ACAGCTTTTG	AGCGGAAACC	TGAAAGAAGG	TTTGCAGTAT	60
CTTCAGAGTC	TGAATTTTGA	GCGGATAGTG	ATGAGCCAGC	TAAATCCCCT	GAAGATTTGC	120
CTGCCCTCAG	TGGTTAACTT	TTTTGCTGCA	ATCACAAATA	AGTACCAGCT	CGTCTTCTGC	180
TACACCATCA	TTGAGAGGAA	CAATCGCCAG	ATGCTGCCAG	TCATTAGGAG	TACCGCTGGA	240
GGAGACTCAG	TGCAGATCTG	CACAAACCCC	CTGGACACCT	TCTTCCCCTT	TGATCCCTGT	300
GTGCTGAAGA	GGTAGGTACT	TTTAAACGTT	GACATCTCGA	G		341

(2) INFORMATION FOR SEQ ID NO:1208:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 588 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

GAATTCGGCC	TTCATGGCCT	ANCGAGCGGC	AGGTGTGCAC	AGAGGTNCTC	CACTTTGTNT	60
TCTGAACTCG	CGGTCAGGAT	GGTTTTCTCT	GTCAGGCAGT	GTGGCCATGT	TGGCAGAACT	120
GAAGAAGTTT	TACTGACGTT	CAAGATATTC	CTTGTCATCA	TTTGTCTTCA	TGTCNTNCTG	180
		TACTGATAAT				240
TCTGTTGTCA	GTTTTGCCCC	CTCCTCCAAT	GGTACTCCAG	AGGTTGAAAC	AACAAGCCTC	300
AATGATGTTA	CTTTAAGCTT	ACTCCCTTCA	AACGAAACAG	AAAAAACTAA	AATCACTATA	360
GTAAAAACCT	TCAATGCATC	AGGCGTCAAA	CCCCAGAGAA	ATATCTGCAA	TTTGTCATCT	420
ATTTGCAATG	ACTCAGCATT	TTTTAGAGGT	GAGATCATGT	TTCAATATGA	TAAAGAAAGC	480
		TATAACGAAT			GTCTCTAAGT	540
GAATTAAAAC	GCTCAGAGCT	CAACAAAACC	CTGCAAACCC	TACTCGAG		588

- (2) INFORMATION FOR SEQ ID NO:1209:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 418 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

CAATTCCCCC TTCATCC	CCT ACAACCAMAC				
GAATTCGGCC TTCATGG	CCI ACAAGGATAG	AATTCATTCC	ACCTATATGT	ACTTAGCAGG	60
GAGTATTGGT TTAACAG	CTT TGTCTGCCAT	AGCAATCAGC	AGAACGCCTG	TTCTCATGAA	120
CTTCATGATG AGAGGCT	CTT GGGTGACAAT	TGGTGTGACC	TTTGCAGCCA	TGGTTGGAGC	180
TGGAATGCTG GTACGAT	CAA TACCATATGA	CCAGAGCCCA	GGCCCAAAGC	ATCTTGCTTG	240
GTTGCTACAT TCTGGTG	TGA TGGGTGCAGT	GGTGGCTCCT	CTGACAATAT	TAGGGGGTCC	300
TCTTCTCATC AGAGCTG	CAT GGTACACAGC	TGGCATTGTG	GGAGGCCTCT	CCACTGTGGC	360
CATGTGTGCG CCCAGTG	AAA AGTTTCTGAA	CATGGGTGCA	CCCCAGGGAG	TGCTCGAG	418

- (2) INFORMATION FOR SEQ ID NO:1210:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 379 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

GAATTCGGCC	TTCATGGCCT	AGGTTGCAAC	TGCCACGCAG	CAACTGCCAC	GCAGAAAAAG	60
GAGGGGTTGA	AAAGGGAGTA	GCTTCTGATA	TTCAGAAGCT	ATTGGAAGAG	ATGCTCAAAG	120
AAGAAAAAAT	TACCATAATC	CAATAAAGAA	GAAGACCTGA	GATCCAGGAA	GCAGATGATC	
TGAACTGCAG	AGAAAGTTCA	GGAAAGTTCC	CTCATTCATG	ATGATGGGAA	ATAACAGTAA	240
ATTCTGTACA	GCAGTCTTGG	ACAACAACCA	ATCTAAACTG	GCACAGTGCA	GAGGCAATCA	300
ACAGAGAACA	TAATATTGAT	AGAATGCCTG	ACGCTTTTGA	TTGTATTCAC	AGGAAACATA	360

379

AACAATTGGA AAACTCGAG

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 380 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211: GAATTCGGCC TTCATGGCCT AGAAACAGGG TATTATTTAT CCTCTTAGCA TATGTTTTGT 60 AATGATTCTG TTACATCAGA GCTTCTGTTG ATGAGTGCCA CTAAAGTGAG ATTGTTGATG 120 AGGATTGGCC TTATTTTTT GTGGTTCTAT TCAATACTTG CCACAGCATT TATTTTCTAA AACATTTCTA CGGTCTATAC TTATCAGTGT CTGATCACAT GCAGGCACTG GTCAAGGTGG 240 AGCATGGTCG AGGCGTTCTT ACTGATACAA ACTCGTGCCT TCTCTTGGAC ACAAGGAGCC 300 CATGTTCTGG TTAACTCTGT GTTCATTTAT TTCACTTGTC ATGCATCGCC TCTATCTTCT 360 CCCTTTATTG CGTCCTCGAG 380 (2) INFORMATION FOR SEQ. ID NO:1212: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 430 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212: GAATTCGGCC TTCATGGCCT AGTGAAGGGT ATTGGTGGTG TTTTTTCCCC TTTACCTCTC 60 ATTTGGGCAT TTTAAAATAG GAGGCCAACT TCATTTACTC CTGTTTAGTA AATCTAAATG AGTGTAGGTT TTAAATTAGA TTTTTTCCCA AAACCCTTCA GAAGGTCTAG TATTAGGGCA 180 GTTGATAAGT AAGTGGAAGC ACCTTGGGCA GGACCCAGTG ACCTGTCCTT TTACTTATTA 240 CAGCACCTGC ACGGGAAGCA GATCTGGAGG ATGAAATTTA ACCTGTTACA GTGTGTGTAT 300 GTTTTAGGGT GTGTGTTTTC CGAATACTGT GGGGAGTTCC CTTTTTCCTT CTCCCATGAT 360 GGATTCTTTT GTCTTTCTAG AGATACCATA GGAGGATATC TGGATTTTTC ACCTAAGGCA 420 **GTGTCTCGAG** 430 (2) INFORMATION FOR SEQ ID NO:1213: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 437 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213: CTCGAGTCTC TCCTGTTAAT CTCCTATTTA TAAAAGGATC ATGAGGCTGC CAAGTGCTAA 60 120 CCCTACAACC TAATAATGTG ATGTGTTTTG GAACACAGAC ATTAGAACTT CATGAAGTTT 180 TAACTGTTGA TTCTTTCCCA AGCATCATCA AGTTATGATT TAGGCAATGT ATGATTGAAA 480

TGCATTCATT CATCACGCAT AGGCACAATC ACAGAAATAT TGCACAAAAT ATGTCCCTGA CTGAAACTGA GAGGTACAAA AACGTATTTC ACTCTTCGTA AAGAAGTTTG TGAGGAAATA CAACTCTGCG ATCGTATAGA CATGTTTCCT GATAATACAC TGACATTCAC AAACAGTAGG CCATGAAGGC CGAATTC	300 360 420
CCATGAAGGC CGAATTC	437
(2) INFORMATION FOR SEQ ID NO:1214:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 295 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:	
GAATTCGGCC TTCATGGCCT AAAAAGAAAT GATGTTTTCT CTCCAACAGT GTGTTTTTAT TTCTTTCATC TACCTGTCCA GTAATCATTT TAAAAAAGAA AATAGCATTA GTTACTGCCT GTGTGATGTG GCCCCGGCTT ATCTGCACTC TCCCTCCTGT TTACTGTTCC AGCCACCTCA GCTTTTTCTC TGTTCCTCTA GCATGGCAAG CTTATTCCTG CCTCATGACT CTTTCGCATG GTGTTTTCAG ATTTTCTCTG TAGCACTCTG CACGCATTGT CCACCTAAAC TCGAG	60 120 180 240 295
(2) INFORMATION FOR SEQ ID NO:1215:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 265 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:	
GACCTGCCGC GAGTGTTGTT GATAGCTTGC TCAAGATCAC ACAGCTAGTA GGTAGTGAGG CTAGGATTTA GACTTAAGTA GTTGGTTGTA GAGTCCACGT GTTTAACCAT TACACTACTT TGATAACAAT ATCATTATTA TTATTATCTT TTTTTTTTT	60 120 180 240 265
(2) INFORMATION FOR SEQ ID NO:1216:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 344 base pairs  (B) TYPE: nucleic acid  (C) STRANDENNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:	
GAATTCGGCC TTCATGGCCT AAAAGAAGGA GCGCGAGAGA AAAAAGCGAG ATGAAGAAAA AGCGAAACTG CGGAAGCTGA AAGAAAAGA AGAGTTAGAA ACAGGTAAAA AGGATCAGAG TAAACAAAAG GAATCTCAAA GGAAATTTGA AGAAGAAACT GTAAAATCCA AAGTGACTGT TGATACTGGA GTAATTCCTG CCTCTGAAGA GAAAGCAGAG ACTCCCACAG CTGCAGAAGA TGACAATGAA GGAAGAAAAA AGGAACAAAA AAGAAAGGAA AAGAAAGGAAGA AAAAGGAAGA AAAAGGAAGA AAAAGGAAAAA AAGGAAGAA	60 120 180 240 300 344

- (2) INFORMATION FOR SEQ ID NO:1217:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 371 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

GAATTCGGCC	TTCATGGCCT	AGCCATTATT	AAGACCTGTG	ACAAAAACTA	TAGACATGAT	60
GCAGTGAAGA	TTCTGAAACT	CAAGCCTGTG	CTGCAGAGAA	GTCTCACTCA	CCCTCCTACC	120
			GGTTTGCCCA			180
TTTGCCAAGA	CATCTGTTGC	TGCTTCTCTA	TACCACACAC	CCTCTGACTC	CAAGGAAATT	240
			AGACCTCCTG			300
CCACGACTGC	TGAAGAGGAT	GGGCATTGAG	GTCAAAGGAG	GAATATTCCT	TTGGGATCCA	360
CAACCCTCGA	G					371

- (2) INFORMATION FOR SEQ ID NO:1218:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 349 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

	CTCCCGCGCG					60
TGGTGACACC	TTAGCCACTG	GAGACAAAGC	AGAAGTTACT	GAGATGCCTA	ATAGTGATTC	120
TTTACCTGAG						180
AGCTGACCCC	AGAGGGGAGG	GGCATGAAAA	TGCAGCTGTG	CAGGGTGCAG	GGGCTGCCGC	240
CATTGGGCCC					TCAATGGAGA	300
CGTGACTGAG	GATACACTTG	CTGAATGTAT	TGATTCCTGG	AGCCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:1219:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 392 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

GAATTCTAGA	CCTGCCTCTC	CTGTCACTTC	CTTGTGTTTT	CTCTGTGACC	GGCCTCTGTT	60
CCCACCACCC	TTTTGGAACT	GCTGTCCTGA	TGGTCACCAG	TGCTTTCCTA	ATAGCCAAAT	120
TCAGTGGCCT	GTCCTCAAGC	TCCCCCGAAT	TCTTTGGCCA	CACAGATCAA	CCTCTAAGTC	180
CTGGGAACTC	CCTCCTTTGT	GATTTTGAGG	CGCTGTGTGC	TGCAGGCTCT	GCTTTTCCCT	240
CCCATCACCC	CATGGTTCTT	CCTTCTCCTC	TGACCCCTCC	CTCTTCCATT	TCTCCCACAG	300
CTCTGTCCAC	AGCCACAATG	TCCATAGGAG	CCTGCCACAC	CCTTTATCCA	ACTGCAGCCT	360
CAACCCACCT	GCAAAGGACC	CCTGAACTCG	AG			392

- (2) INFORMATION FOR SEQ ID NO:1220:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 598 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

GCAAGCTACT	TCTTCAACAG	CTGTATCTGC	TTCAAACCCC	ACTGCCTCTC	OMMO3 3 003 0	
MOO1		CIGINICIGC	1 1 CAAAGCCG	ACTGCCTCTC	CTTCAAGCAT	60
TGCAGCAAAC	AATTGTACTG	TGAATACGTC	ATCAATTGCA	ACGTCTTCAA	TGAAGGGTCT	120
TACGACTACA	GGAAACTCGT	CTCTTAATAG	САСАТСТААС	ACTAAAGTAT	CACCACTOCC	
Th Ch h h ma ma			CHARCIANC	ACIMMOIMI	CAGCAGIGCC	180
TACAAATATG	GCTGCCAAGA	AAAACATCTA	CCCCCAAAAT	AAATTTTGTT	GGTGGTAATA	240
AGCTGCAGTC	NACAGGAAAT	AAAGCAGGAG	ACCTTAAAAG	GGACCCGAAT	CTCTTNAAAC	300
TIN NECCOMMEN	3 mmm om a om -			OOMCCCOAMI	GIGIIAAAAG	300
TAATCCTGTC	ATTTCTGCTG	TGCAGATTCC	TGAAGTAAAG	CAAGACACAG	TGTCAGAACC	360
AGTCACACCT	GCATCTCTTG	CTGCTTTACA	CACTCATCTC	CAGCCAGTGG	CCCATCATTA	420
mamaaaaaa			G.IOTOMIGIG	CUGCCUGIGG	GCCAIGALIA	420
IGIGGAAGAG	GTACGAAATG	ATGAAGGAAA	AGTAATTCGG	TTCCATTGTA	AATTATGCGA	480
GTGCAGCTTT	AATCATCCCA	ATCOTARCOA	C a mc ca a comma	AAAGGGCGAA		
	MITOMICCCA	ATOCIANGGA	GAIGCACTTA	AAAGGGCGAA	GACACAGACT	540
TCAATATAAA	AAAAAAGTAA	ATCCAGATTT	GCAAGTAGAA	GTAAAGCCAA	TACTCGAG	598
				GINERIOCCUM	INCICONO	598

- (2) INFORMATION FOR SEQ ID NO:1221:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 338 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

CARTTCCCCC	THORMOODO					
GAATTCGGCC	TICATGGCCT	AGAGGAGTCC	TGTCAGTTCG	TTCTCTGCTG	TGTCCCCAAG	60
ACCATGAATC	ATCCCTCCCA	TOTAGEN				••
carronarre	A100C10GCA	I G I WG I WGGC	ATTTAATAAT	ATATGTTCAA	CAAGTATTTG	120
GCAGTCTTGG	AGGGCAGAAA	ACCACCTCCC	CAACAMMOON			
	HOUGHAN	AGGAGG1GGG	GAAGATTITI	AAATAACATT	TTTTAAAAAG	180
TCACATTGTC	CTACAATACC	CATTTTTTTT	CCATATTTAC	CARATTORCO	GTTTTTTCT	
		O.I.I.I.I.C.I.I	GCATATITAG	GAAAT IGAGG	GITTITTCI	240
AAAACATGCG	GACATATGGG	AAATAGGATG	CAACATTTCC	מדים מדים מדים מ	CAGACACAGT	300
MICI COMMO			42.411100	ACIMIGITI	CHOHCHCHOI	300
TAGAGGTTTC	CAAGAGATTT	TGCGCTGGGT	CACTCGAG			338

- (2) INFORMATION FOR SEQ ID NO:1222:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 335 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

COTOCA CHOO CAMBOO CAMB					
GCTCGAGTGA CATGGAAACT	GAGGTCTTAG	AGACACGTGT	AATGGAGAGG	AGAGGAATGG	60
ACACOMORGO ORMOGRASIO					
AGACCTGTGC GATGGAAACC	AGAGGGATGG	AAGCAAGGGG	CATGGATGCA	AGAGGATTGG	120
AGATGAGGGG CCCTCTCCCC	1 COMMON 2 CO. C				
AGATGAGGG CCCTGTCCCC	AGTTCAAGAG	GCCCTATGAC	TGGTGGAATT	CAGGGTCCTG	180
CTCCCATTAL TATACCCC	~				100
GTCCCATTAA TATAGGGGCA	GGTGGCCCTC	CTCAGGGACC	CAGACAGGTC	<b>ሮሮልርርር እ</b> ምሞም	240
C1000000000 011				CCAGGCATTI	240
CAGGGGTGGG GAATCCTGGA	GCTGGTATGC	AGGGTACAGG	ሮልጥልሮአልሮርአ	ACACCCATCC	300
			CATACAMOOM	MCMOGCHIGC	300

(A) LENGTH: 534 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

335

AGGGAGCAGG CATACAAGGA GGAAAAATGC TCGAG

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1223:

(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1223:	
GAGTCCCAGC TGGCAGAGTC TCGTGACTAA AAAGTGACCA TGTGTGTGGA TGCAAGGAAA CAACTCATTA CTTATAATAC (2) INFORMA	TTCATGGCCT AGGTACAGAC TGAACCCAGG AACCCGGGTA TCTGCGTCCT GCCCACCAGG ACTGGGGCCT CCTCACATCT ACTCTGAGGA CAGAATCTAT TTCCTTTTTG TTTGGGATGC TGGGTTTGAG AACATGCCGG GAACCAAGAG TCCAATTTTG AGCGCTTGAG GACCAAGTGG AAAGAAACTC AAGCAGATTT ATGTCTGGTT ATGCCCTTGA GCCCCTGCAG AAGCAAACAA TAATTTTGTG CAAATACATT TGTATTCCAG ATCTCACAGA ATTTCCTACA CAAAGAAATT ATGGACATTG CACCCTAAAA ATTAACAAGG AAAGAAAGGTA CCAGGAGCAA ACAGGAACAG AAACAATATT GCAAATATTT CAGATGCAAA GTGTATCCGA AACTGTCCCT ACTGTGTCTA AAGAAATGAA AGGCAATCCT CGAG  ATION FOR SEQ ID NO:1224:  SEQUENCE CHARACTERISTICS:  (A) LENGTH: 354 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	60 120 180 240 300 360 420 480 534
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1224:	
GAAGAAGAAC GAAATCGCTC GAGAAATCAT GCACGACCAC (2) INFORMA (i) (ii)	CCCACAGGGA TCAGGAATGG TATGATGCTG AAATTGCCAG AAAACTGCAA TTTTGGCTAC CCAGGTGGAC ATGAGAGCCG CTCAAGTAGC TCAAGATGAA GACTTCTAAT GGCTGAAGAA AAGAAAGCTT ACAAAAAAGC CAAGGAGCGG CTTTGGACAA AAGAAAGCAA GACCCCGAGT GGAAGCCAAA AACAGCTAAA CCAAGTCAAA AGAGAGTGAT GAACCTCACC ATTCTAAGAA TGAAAGGCCA CACCACCTAT CATGACAGAT GGTGAAGATG CGGATTCTCT CGAG ATION FOR SEQ ID NO:1225:  SEQUENCE CHARACTERISTICS:  (A) LENGTH: 488 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  MOLECULE TYPE: cDNA  SEQUENCE DESCRIPTION: SEQ ID NO:1225:	60 120 180 240 300 354
GAATAAAGCG TGGCTCACCT	AAAACAAAAC ACACTTATGG TAACCCATTC TGTTGAGGAG TCCAAAACTC CCTCATTGCC TTTAACTGGT TCTGTGGCAG TGAGATCATC ATCCTTATGC AGTGTCTCTC TCTCTCTCCC GTTTTCTCTC TCCCTCTCTT ATCCCCTTGA TTCTCATCTT CTCTTTAGAT TATGTGGTAG CTATCCTCAA GAGCTCATAG	60 120 180 240

TGCCTGCCTG	GATCACTGAC	AAAGAACTGG	AAAGTGTATC	AAGTTTCAGG	TCCTGGAAGC	300
GCATCCCTGC	CGTCATCTAC	AGGCACCAGA	GCAATGGAGC	TGTCATTGCC	CGCTGTGGAC	360
AGCCAGAGGT	TAGCTGGTGG	GGCTGGCGAA	ATGCAGATCA	TCACCATCTC	GTACAGTCAG	
TAGCCAAAGC	TTGTCCCTCT	CACTCCCCAT	CCACAGAIGA	CARCATCIG	ACTAGGAAAC	420
GACTCGAG	1101000101	GACICCCGAI	CGAGTGGCAG	CAAGCTGTCA	ACTAGGAAAC	480
GACICGAG						488

- (2) INFORMATION FOR SEQ ID NO:1226:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 328 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

GATCCCCACC AAAACAGGAA	AAGAAGTGCT	CTCGTGCAGG	GCTTGTTCAC	AGTGAGCCTG	60
GCTGGCTCCT CATGATCTCT	GAGTTTAAAA	TGTGCCAGCA	GATGATTTTA	ACCATCCCAT	120
CAAAAATTGT TGTCTGGATC	AGTTTCGAGC	TAGCGTTTCC	TTCCACACCC	CATHORNOOM	
TTTTTGACAA AAGTTGGGTC	GGCCAGGTGC	ACTCCCTCAT.	A COMPORTOR DO	CATTCTTCCT	180
GGCCTCCCAA AGTGCGGGGA	TTCTACCCAT	Chagaran	ACTIGIGATO	CACCTGCCTT	240
TTAAAAGAG AATTACAAAG	TICIAGGCAI	GAGCCACCAC	ACCCTGCCAG	AAAAATGGAT	300
TIANAAGAG AATTACAAAG	TACTCGAG			•	328

- (2) INFORMATION FOR SEQ ID NO:1227:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 527 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

GAATTCGGCC TTC	ATGGCCT AAAATTTTT	TTTATAAAAA /	ATAATGATAG	TTAGAGAACT	60
GTTTATATGA GGA	TCAGACA TTGTTTCAGO	ACTGGATCTC	CTCTGTCCCC	TCTCTTGCTA	120
CAGCATACAG CCC	'AGAGACA CACATGTAA!	AGTAGATGAT	CTCTGTAAAC	TTCAGCTGCA	180
TTTCTGTATG TGT	'AGGATTG TCCTANTAT(	AGATATCCTT	TGAGAAAGAG	TTGGAGAGGC	240
ATGGAAGGAA GCA	TATTCCT GACCTCCCC	CTTTTTAGCT	AAAGATACAA	ATTCAGAGCT	300
GTTTGAAAAG GGC	TTAGAAT AATATTAAT	T AAACATATTC	TATAATACAA	AGAGAAGTAC	360
TTTTTTAAAA TAC	ATTTATT TTTCTTTCT	TTTTAGCAGG	CATTTCTGAC	AGAAAATCTT	420
TAGGGCCAAT TAG	AGTTTCT TTCTGACTT	TAATTGCCCT	CTGCCTTTTG	GGAAAGTGTT	480
GAAAAAAGCT CTG	GAAAAAA ATATGCTGG	CAAGGTCGCA	ACTCGAG		527

- (2) INFORMATION FOR SEQ ID NO:1228:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 278 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

GAATTCGGCC	TTCATGGCCT	AAGAAAACAG	CCTAGAATTA	AACCTCCAAG	ATGAGTGTGA	60
GATGAAGCCT	TTCCACCTAT	CCCAACAAGG	TTTAAAAAAA	ATAAAAACTA	GAATGGGGCT	120
ACTACACAAC	AGCCCTTTGC	CCCACCCAAG	GCTCATTCCC	TAGAGGCAAG	TGTACGAGTT	180
TATTTCTCCT	TGAAATTATT	TCCATATCTC	CAAATAGTGT	TTATACCACT	CAAGGCAGAG	240
ATAGCAATTT	GCCTACCCAG	TATACATTTC	CCCTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:1229:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 603 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

GAATTCGGCC TTCATGGCCT	AGCCACCTTG	AAGCTCTCAA	ATATCACTGT	TGTGAATACA	60
GAGAGGGAAA ACCAACTGTA	ACGTGCCACC	CAAATTTTTT	CAGATTAATA	CATCATTCAT	120
CAGACTTCAT TCGTGATCTC	GAAGAGTGAC	ATCAGTCTTC	CTTGGAATAT	GAAGAGAATT	180
TCTTTGGTTC TTCTTTTGCA	TTTCTATTTG	ATTTATTTTA	TTTTATTTTA	TTTTATGTTT	240
TTTGGTACAG AAAGCTCATT	ACTAGTCCTG	TCCAGCAACG	TGCCTCTCCT	GGCCCTAGAG	300
TTCTTGGAAA TAGCCCAGGC	CAAAGAGAAG	GCCTTTCTCC	CCATGGTCAG	CCACACGTTC	360
CACATGCGCA CAGAGGAGTC	TGATGCCTCA	CAGGAGGGCG	ATGACCTACC	CAAGTCCTCA	420
GCAAACACCA GCCATCCCAA	GCAGGATGAC	AGCCCCAAGT	CCTCAGAAGA	AACCATCCAG	480
CCCAAGGAGG GTGACATCCC	CAAGGCCCCA	GAAGAAACCA	TCCAATCCAA	GAAGGAGGAC	540
CTCCCCAAGT CCTCGGAAAA	AGCCATCCAG	CCCAAAGAGA	GTAACATCCC	CAGAGCCCTC	600
GAG					603

- (2) INFORMATION FOR SEQ ID NO:1230:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 362 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

GAATTCGGCC TTCATGGCCT	ACCGGGCAGT	TAGGCCCAAG	CGCCGGGTTC	AGGCCTCCAA	60
AAACCCCCTG AAAATGCTGG	CGGCAAGAGA	AGATCTCCTT	CAGGAATACA	CTGAGCAGAG	120
ATTAAACGTT GCCTTCATGG	AGTCAAAGCG	GATGAAAGTA	GAAAAGATGT	CTTCCAACTC	180
CAACTTCTCA GAAGTCACCC	TGGCGGGTTT	AGCCAGTAAA	GAAAACTTCA	GCAACGTCAG	240
CCTGCGGAGC GTCAACCTGA	CGGAACAGAA	CTCTAACAAC	AGCGCCGTGC	CCTACAAGAG	300
GCTGATGCTG TTGCAGATTA	AAGGAAGAAG	ACATGTGCAG	ACCAGGGTGG	TGGAACCTCG	360
AG					362

- (2) INFORMATION FOR SEQ ID NO:1231:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 468 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

${\tt GAATTCGGCC}$	TTCATGGCCT	AGTCCCTGTT	CAATTTCTCT	CAGCCTCAAT	ATCTTTTACT	60
TTAAACTAGG	TAGGGTTACC	AGTTCAATGA	TCTGCTCATT	AAATACTTAC	TATACCTTAG	120
${\tt GTACTATATG}$	AGAAGCTAGG	AAAAGAGTGA	TGAAAAAGAC	ACACCTAGAG	AGGGCATTGG	180
ATTATTAAAT	CAGCAGCTAC	TGTAAAGGTA	TTTAAGTTCT	GTGACAGGCA	GCATTCTGGG	240
TATCACAGGA	ACATCTTACA	AGAATTTCTA	ACTTCAGGAG	GAGGGTTCAG	AGAATTAGCC	300
AGGCCAGGGG	TGAGAGTGTT	CTTCCCGGAA	GAGGGAACAA	TGAAGACCCA	GGAGGAGATA	360
CAGAGTATCT	CGCTGTATTT	AAAATAACCA	GAAATAGATT	TATATATTTA	GTACAGAGGC	420
TGAGGGGAAG	AGAAGTGAGT	GTGAGAAGAT	CAAAAGGAGA	AGCTCGAG		468

## (2) INFORMATION FOR SEQ ID NO:1232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

GAATTCGGCC	TTCATGGCCT	ACAATCATCT	CAAACAGTTC	CGGGTTGCTG	CCCTTTTGGC	60
TTTCCTAGGT	GCTACAGTAG	CAGGCTGTTT	TCCCCTTTTC	CATAGAGGGG	AATATTCTGC	120
ATCACCCCTT	TGTTTGCCAT	TTCCTACAGG	TGAAACGCCA	TCATTAGGAT	TCACTGTAAC	180
GTTAGTGCTA	TTAAACTCAC	TAGCATTTTT	ATTAATGGCC	GTTATCTACA	CTAAGCTATA	240
CTGCAACTTG	GAAAAAGAGG	ACCTCTCAGA	AAACTCACAA	TCTAGCATGA	TTAAGCATGT	300
CGCTTGGCTA	ATCTTCACCA	ATTGCATCTT	TTTCTGCCCT	GTGGCGTTTT	TTTCATTTGC	360
ACCATTGATC	ACTGCAATCT	CTATCAGCCC	CCCACTCGAG			400

## (2) INFORMATION FOR SEQ ID NO:1233:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 418 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

GAATTCGGCC TTCATGGC	T AGGATATAGA	CCAAACCCAA	ATCCTGTTGG	ACAAGGGATT	60
AGACCACCTA TGGCTGGA	TG CAACAGTTCG	GTAGGCGGCA	TGAGTATGTC	GCCAAACCAA	120
GGCTTACAGA TGCCGAGC	AG CAGGGCCTAT	GGCTTGGCAG	ACCCTAGCAC	CACAGGGCAG	180
ATGAGTGGAG CTAGGTAT	GG GGGTTCCAGT	AACATAGCTT	CATTGACCCC	TGGGCCAGGC	240
ATGCAATCAC CATCTTCC	TA CCAGAACAAC	AACTATGGGC	TCAACATGAG	TAGCCCCCCA	300
CATGGGAGTC CTGGTCTT	GC CCCAAACCAG	CAGAATATCA	TGATTTCTCC	TCGTAATCGT	360
GGGAGTCCAA AGATAGCC	TC ACATCAGTTT	TCTCCTGTTG	CAGGI GCGCA	CTCTCGAG	418

## (2) INFORMATION FOR SEQ ID NO:1234:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

GAATTCGGCC	TTCATGGCCT	ACGCCTCTTT	AACACATGGG	CCTTTGTGTG	GACACCATCT	60
TTCCCTGAAA	CCTGTCTGCA	TCTTTTCTGT	CCCTTCTAAC	CATCCAGTTT	GTTCTTCCCC	120
AAGATGGGCT	GCCACAAGTT	GCCATTTCCT	GACTGGTGCA	TGGTTCCAGA	CAGCTCGCGG	180
GCAGACACAG	GGAAGGAATC	TTATCTCGTT	TTTGTTTTTT	TGTTGTTGTT	TTTGTTTTTT	240
TCTTTTTTGT	TGTGGTTGTT	GCTGTTGTTT	TGAAACGGAG	TCTCACTCTG	TTGCCAAGGC	300
TGGAGTGCAG	TGGCGCAATC	TCGAG				325

- (2) INFORMATION FOR SEQ ID NO:1235:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

GAATTCGGCC	TTTATGGCCT	ААААААААА	AAAGAAAGAA	AGAAAATGTT	GGATATAGTA	60
GGTCTGAGCT	TTATGGAGAA	${\bf AGAAGGTTTG}$	AAGTAGCTTC	TGGGATATGG	AAAAAGAACT	120
TATGAGAGAA	ACAGACTTCT	GGGAATCCTT	CAAGGACTAG	AAGAGAACAT	AGATTATGAA	180
AGAATGAGTC	ATTGATCAGT	${\tt GTAGTTGTAG}$	ATTAGAATAG	TTGGACAGTT	AGGATTTGCT	240
AGGCAGAAGA	ATGGAGGAAG	TCACGGCCTA	GGGAGTTAAC	AGTGTTAGGA	GCAAGAGAGG	300
TTTTAACTAA	TGAGCCATGG	AGTTTAAGCA	GAGACAATAG	AGAATAAAGT	AAAATAGGAA	360
GAAAAATTTA	AAAAGAAAGT	AGAAAAGTCC	TCGAG			395

- (2) INFORMATION FOR SEQ ID NO:1236:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 565 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

GAATTCGGCC TTCATGGCCT	ACACAATTCC	AAAGAAGGTG	GTGTGCCACT	TCAGTGGGAA	60
GGCCTATGCC GACGAGGAGC	GGTGGGACCT	TGACAGCTGC	ACCCACTGCT	ACTGCCTGCA	120
GGGCCAGACC CTCTGCTCGA	CCGTCAGCTG	CCCCCCTCTG	CCCTGTGTTG	AGCCCATCAA	180
CGTGGAAGGA AGTTGCTGCC	CAATGTGTCC	AGAAATGTAT	GTCCCAGAAC	CAACCAATAT	240
ACCCATTGAG AAGACAAACC	ATCGAGGAGA	GGTTGACCTG	GAGGTTCCCC	TGTGGCCCAC	300
GCCTAGTGAA AATGATATCG	TCCATCTCCC	TAGAGATATG	GGTCACCTCC	AGGTAGATTA	360
CAGAGATAAC AGGCTGCACC	CAAGTGAAGA	TTCTTCACTG	GACTCCATTG	CCTCAGTTGT	420
GGTTCCCATA ATTATATGCC	TCTCTATTAT	AATAGCATTC	CTATTCATCA	ATCAGAAGAA	480
ACAGTGGATA CCACTGCTTT	GCTGGTATCG	AACACCAACT	AAGCCTTCTT	CCTTAAATAA	540
TCAGCTAGTA TCTGTGACGC	TCGAG				565

- (2) INFORMATION FOR SEQ ID NO:1237:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 298 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

GAATTCGGCC	TTCATGGCCT	ACACTGAGAA	CCACATCCCT	ለጥጥጥ አጥር <b>አ</b> አጥ	TCATTCATAA	
COMMONOCON	0000000	TICHCT CAGAA	CONONIGOCI	ATTIATGAAT	ICATICATAA	60
CITIGIGGAA	GTTTTAGATG	AGTATTTCAG	CCGAGTGAGT	GAATTAGATG	TATCCTTTTT	120
CAATACTGTT	TTCCACAGTA	CTTGGCAAAT	GCACTCTCGT	CCTTATCACC	TAAGTACCAC	100
AACCCACCAA			0010101001	CCITATCAGG	IAAGIACCAC	180
MAGGCAGGAA	AACTATTCAG	CAGAGTCCAG	AGTGTTCATC	ACCAACAACT	ATGACAAGAC	240
AGCCAGAGGT	GTGTGTGTTC	TGCAGAACTC	CTCCCCAACT	TCGTCACCCA	ACCTCCA	000
				* CG * CMCCCW	AUL ILLIALI	298

- (2) INFORMATION FOR SEQ ID NO:1238:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 303 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

CTCGAGTGGG	GGGAGGGAGG	GGGAGGAGAG	AAGGGGAGGT	GGATGGGGGA	GGGGGACAGT	60
GGAGGAAGAG	GGAAGAGGGA	CARRENACO	100000000	COLLEGE	GGGGGACAGI	
CAACGGGGG	CONNONOGON	GAAAAIAAGG	AGAAAGAGAA	GGAAAGGCAG	AAGGGGAGGG	120
GAAGGGGAA	GGGGAAGAAC	AAGGGGAATG	GGAAGAGAAT	GAAGAGGAAG	AGAAGAGGAA	180
GAGTAGGAGG	AGAAATAACA	AAAGGCACCA	GGTTGGAAAG	CAACAATTA	AAATATATTT	
ATTTCCAAAC	CACATTATOO	Maria concern	COTTOONANO	OANGANIIIA	MAMIMIMITI	240
	GACATTATCC	TATAGTGAAA	AATCCTTAAA	AGTTAGGCCA	TGAAGCCGAA	300
TTC						303

- (2) INFORMATION FOR SEQ ID NO:1239:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 315 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

GAATTCGGCT	TCATGGCCTA	CTCTTCTCTG	AGACAGAAAA	CTAGCGAACC	CCAGGGGAAG	60
GTGCCGTGTG	GAGAGCACTT	TCGGATTCGG	CAGAATCTAC	CAGAGCACAC	CCAAGGCTGG	120
CTTGGGAGCA	AATGGCTCTG	GCTTCTTTTT	GTTGTTGTGC	CGTTTGTGAT	ACTGCAGTGT	180
CAAAGAGACA	GTGAGAAGAA	TAAGGAGCAG	AGTCCTCCTG	GCCTTCGAGG	CGGCCAACTT	240
CACTCTCCAT	TAAAGAAAAA	AAGAAATGCT	TCCCCCAACA	AAGACTGTGC	ATTCAATACC	300
TTAATGGAAC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:1240:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 553 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

GAATTCGGCC TTCATGGCCT AAAATGACCT TGGTAAGAAT GGGTTTTTAC AATAAATGAA 60 TTTTTAATTC CAAGATGTTT TTTCATTGAA ATTACTGCCC CAGTTGCATT AAAAGTGTGG 120 CTGTGCAAAG CTTCCTTCTA CCAGGCTTCA TGTGCAGGAC CTTGGTTTTT GTTGCCTTGG CAATTCCAAA AGCAGGTGTT GAAAGAGAAG AAGACAGGAA AAAGAAGATG GGAGAAAAAT 240 TTTCCAAATC AGAGTTCTCA GTCCAAGGAC TTATTCTTGG GGGTTCAAAA ATTCTAACAG 300 TATTTTAAA TTGCCTCTAT TTCGATGGTT ACTTGATTAA ACTGTTCTAA CATTTCTAAA 360 AATAAAAATT TGCAATGATA ACTTTTATAT CAGACTTTAC CTCTGTTTCC CAAATTGGAA 420 TCTTTAGGAA TATTTTTTTG AGATCACTTT TTTCCTTTTT TTCTTTAACA AAGATTGGGA ACCGCTCTTA GGAACAGACA AATGGATTTC CATATTTCTT AAAGCGTTGA AGTAAATCTC 540 TGCCACCCTC GAG 553

- (2) INFORMATION FOR SEQ ID NO:1241:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 437 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

GAATTCGGCC	TTCATGGCCT	ACTCTTCTCA	AGGCTTTGAA	ATCTCCCCTT	GCACTGAGAT	60
TAGTCGTCAG	ATCTCTCCCC	GTCTCCCTCC	CAACTTATAC	GACCTGATTT	CCTTAGGACG	120
GAACCGCAGG	CACCTGCGCC	GGGCGTCTTA	CTCCCGCTGC	TTGTTCTGTC	CCCTCCCTCG	180
GACCAAACAG	TGCTCATGCT	TCAGGACCTT	GTTTGTCGAA	GATGTTGGTT	TCCCTTTCTC	240
TGTTATTTAT	ATAAAAATAA	TTTATCAAAA	GGATATTTTA	AAAAAGCTAG	TCTGTCTTGA	300
<b>AACTTGTTTA</b>	CCTTAAAATT	ATCAGAATCT	CAGTGTTTGA	AAGTACTGAA	GCACAAACAT	360
ATATCATCTC	TGTACCATTC	TGTACTAAAG	CACTTGAGTC	TAATAAATAA	AGAAATCAGC	420
ACCCCTAGGC	CATGAAG					437

- (2) INFORMATION FOR SEQ ID NO:1242:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 523 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

GAATTCGGCC TTCATGG	CCT ACAAAAATAT (	GTCTTTTGAA	AACCNAGTCA	AGTACCTAGA	60
GATGAAAACC ACAAATG	GAGA AACTGTTACA (	GGAATTAGAT	ACACTTCAAC	AACAATTGGA	120
TTCACAGAAC ATGAAAA	AAG AGAGCCTGGA A	AGCAGAAATA	GCTCACTCCC	AGGTGAAACA	180
GGAGGCGGTA TTGCTGC	CATG AAAAACTTTA 1	TGAGTTGGAG	TCCCATCGAG	ATCAAATGAT	. 240
TGCAGAAGAC AAAAGCA	ATAG GATCTCCAAT (	GGAAGAGAGA	GAGAAATTAC	TTAAGCAGAT	300
TAAAGATGAT AATCAGG	GAAA TAGCCAGCAT (	GGAAAGACAG	TTAACAGATA	CAAAAGAAAA	360
GATAAATCAG TTTATTG	GAAG AAATTAGACA	ACTTGACATG	GATTTAGAGG	AACACCAAGG	420
TGAAATGAAC CAGAAAT	TACA AGGAGCTAAA (	GAAAAGGGAG	GAACATATGG	ACACTTTTAT	480
TGAGACTTTT GAGGAAA	ACAA AGAATCAGGA A	ACCAAAACTC	GAG		523

(2) INFORMATION FOR SEQ ID NO:1243:

(A) LENGTH: 352 base pairs

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243: GAATTCGGCC TTCATGGCCT AACTGATTAC AGGGAAAGAC AAAAAGCAAA AGGTGATTGA 60 AACATAGTTC TAAATAACAA GAAGGGAAGT TTTCTTAAAC TGATCATCTG TCTTATTGTC 120 ATGACAAAGG GTAAAATTTT ATTTCAGTC CTTTAGTGCT TTTTAATAAT TCACCATACA 180 TATTTTACTT ATATCCCATT AACTGTGGGA CTTAGCACAG TTTACATTTT CAGTCATGTG 240 AATATAATTA TCTGTATTCC CTGTTGGACT GATGGGGGAA ATTGGATCAT TATATAATTT 300 AAAAGACACC TCCCCAGGCA CCCATTGTGT TCTTAGGAAG TCAGTGCTCG AG 352 (2) INFORMATION FOR SEQ ID NO:1244: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 306 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244: GAATTCGGCT TCATGGCCTA ATTCAGCTTT ATCGTTCCCT CTGGCAGTTC AGTTGTTGGC CCAGATTTAT TAAGGTTCGA CAGAAAGCAA CTGAAATCTC CCTTAGAAAT AAAGTTCCTG 120 GTGTGAAGAA AAAAAAGATC CATAAAAAGT CTCATCCTTA GGACAGCAAC TTTTATAATG 180 CACAGCTGAT CTGAATAGCT CTCTGGATTG TGGCCTTGGA CAACAGTTCA GACTGCATTA 240 TTGAGTATGA ACCTTGAGCT TTCTGAGTCT CTTCTTTTTG CTCTTTTACT AGCAGACCCT 300 CTCGAG 306 (2) INFORMATION FOR SEQ ID NO:1245: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 591 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245: GAATTCGGCC TTCATGGCCT AGGGTTTGGG GGTTCTGAGA TGTTACTCTC ACTGAAGTCT 60 GTGTGGGAGG CGGATTACTA AACAAGAAAT TGCTAATTAA TCTCCAGATG GCAAGGAATG GATAAAGCAC TGTTCCCAAC AAGGTCCAAA TGTCTCCGCT GGAAGAGTGT ACAATGGATG 180 CAGTTGGTCT TCCTGCTGGC AACAGTACCA CCGAAGCGCT TGGGGCAAGT TCCAAATCCA 240 GTAACTTCTT TTTATAATCT TCTTTGGTAA ATTCCCTCCT GGGAAACATG GTTGCTAACG 300 AAAAATTACC GTAAGTGTTG CCAACAGTCT GTGCAGCAAA CTGCCTTGCC TCTTCTAGAG 360 GAGCATCAGA AGGGAACTGA TTTGTAAAGG AAGAACCATC AGGAAGACGG AATTGAATTC 420 TTGCAACAGT GCTTCTTTCT CTTGCATAAG ATTCCCTCTT GACTTCCATT TCTGCCTGTT 480 TTGCTAGCAA GGCAGCAGCT TTGGCAGCCT CTACTTCTTC CTTTGTCTTT GCAAAACGAG 540 CAGCTCTCTC TGCACGGTCC AATGCAATCT GCTGTTTTAT ACGTTCTCGA G

- (2) INFORMATION FOR SEQ ID NO:1246:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 593 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

GAATTCGGCC	TTCATGGCCT	ACTTCGGGGA	AGAAACCTTC	ACCAGAGTGG	AGCAGTTCAG	60
ACCATGGAAC	CTCTGATCCA	AGCAGCCCAG	CTCCTGCAAT	TAAAGAAGAA	AACCCAGGAG	120
GACGCAGAGG	CTATCTGCTC	CCTGTGTACC	TCCCTCAGCA	CCCAGCAGAT	TGTCAAAATT	180
TTAAACCTTT	ATACTCCCCT	GAATGAATTT	GAAGAACGGG	TAACAGTGGC	CTTTATACGA	240
ACAATCCAGG	CACAACTACA	AGAGCGGAAT	GACCCTCAGC	AACTGCTATT	AGATGCCAAG	300
CACATGTTTC	CTGTTTTGTT	TCCATTTAAT	CCATCTTCTC	TAACCATGGA	CTCAATCCAC	360
ATCCCAGCGT	GTCTCAATCT	GGAATTCCTC	AATGAAGTCT	GAAGATGCAT	GTTTCCAGCA	420
TTAGTTTGAT	TCCCAATGTG	AGCAAGAAGG	AAGTATATAC	AGTAAAGTAA	ATTCAAGGAT	480
CTGTTAAATC	TGGTAAAAGT	AGATCAAATC	AGAGATTGAC	AGCCTGTGGA	GGGTGCTGAA	540
CTATACAGAA	TTAGACACAA	CTATGTCATT	ATTTTTTGTA	CCAACTACTC	GAG	593

- (2) INFORMATION FOR SEQ ID NO:1247:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 599 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

•	GAATTCGGCC	AAAGAGGCCT	AAACTCAGAA	TGGTGCTACT	TGAAGACTCT	GGATCTGCTG	60
	ACTTCAGAAG	ACATTTTGTC	AACCTGAGTC	CCTTCACCAT	TACTGTGGTC	TTACTTCTCA	120
	GTGCCTGTTT	TGTCACCAGT	TCTCTTGGAG	GAACAGACAA	GGAGCTGAGG	CTAGTGGATG	180
	GTGAAAACAA	GTGTAGCGGG	${\bf AGAGTGGAAG}$	TGAAAGTCCA	NGAGGAGTGG	GGAACGGTGT	240
	GTAATAATGG	CTGGAGCATG	GAAGCGGTCT	CTGTGATTTG	TAACCAGCTG	GGATGTCCAA	300
	CTGCTATCAA	AGCCCCTGGA	TGGGCTAATT	CCAGTGCAGG	TTCTGGACGC	ATTTGGATGG	360
	ATCATGTTTC	TTGTCGTGGG	AATGAGTCAG	CTCTTTGGGA	TTGCAAACAT	GATGGATGGG	420
	GAAAGCATTA	TTGCAATCAC	AATGAAGATG	CTGGCGTGAC	ATGTTCTGAT	GGATCAGATC	480
	TGGAGCTAAG	ACTTAGAGGT	GGAGGCAGCC	GCTGTGCTGG	GACAGTTGAG	GTGGAGATTC	540
	AGAGACTGTT	AGGGAAGGTG	TGTGACAGAG	GCTGGGGACT	GAAAGAAGCT	GAACTCGAG	599

- (2) INFORMATION FOR SEQ ID NO:1248:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 418 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

GAATTCGGCC AAAGAGGCCT AACCGAATGG ATTATCTGTG GGAGTAACAT CTCAGAAGAC

492

TATGAAGCTA	ATTCCTGCCT	CAAGACACAG	AGCTACACAA	AAGGTGGTTA	TTGGAGATCA	120
TGATGGGGTA	GTTATGTGCT	TTGGCATGAA	GAAAGGAGAA	GCAGCAGCAG	TGTTCAAGAC	180
TTTACCCGGG	CCGAAGATTG	CAAGGCTGGA	ACTGGGAGGG	GTTATCAACA	CACCTCAGGA	240
GAAAATTTTT	ATTGCTGCAG	CATCTGAGAT	TAGAGGCTTC	ACAAAAAGAG	GAAAACAGTT	300
CCTCTCCTTT	GAAACAAACC	TCACTGAAAG	CATTAAAGCT	ATGTATGTCT	TTTGTTCTCT	360
TTTGTATTTT	TACATACTTA	TTTATAATAT	TTTGGATAGA	TGTGAGGCAA	CCCTCGAG	418

- (2) INFORMATION FOR SEQ ID NO:1249:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 800 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

GAATTCGGCC	AAAGAGGCCT	AGCAGAGCAC	AGCATCCTCC	GGACCAGACT	CCTCTCACCC	
CACOTOCALGO	OMM OMO 2 O O O		nochicoico	GOACCAGAC I	CGTCTCAGGC	60
CAGTIGCAGC	CTTCTCAGCC	AAACGCCGAC	CAAGGAAAAC	TCACTACCAT	GAGAATTGCA	120
GTGATTTGCT	TTTGCCTCCT	AGGCATCACC	TGTGCCATAC	CAGTTAAACA	CCCTCTTCTCT	100
CC N N CONTOUR	ACCELLAGO	0.000000	TOTOCUMENC	CUOLIVANCA	GGCIGATICI	180
GGMAGIICIG	AGGAAAAGCA	GCTTTACAAC	AAATACCCAG	ATGCTGTGGC	CACATGGCTA	240
AACCCTGACC	CTTCTCAGAA	GCAGAATCTC	CTAGCCCCAC	AGACCCTTCC	N N C TIN N C T C C	300
*********	100100101			MUNCCCIICC	AMGIAAGICC	300
AACGAAAGCC	ATGACCACAT	GGATGATATG	GATGATGAAG	ATGATGATGA	CCATGTGGAC	360
AGCCAGGACT	CCATTGACTC	GAACGACTCT	GATGATGTAG	ATGACACTGA	TORMOTOROG	420
A CITICATICA TICA	COCOTOR COR			ATOMCACTOM	IGNICICACC	420
MGICIGAIGA	GICTCACCAT	TCTGATGAAT	CTGATGAACT	GGTCACTGAT	TTTCCCACGG	480
ACCTGCCAGC	AACCGAAGTT	TTCACTCCAG	TTCTCCCCAC	AGTAGACACA	TATCATCCC	540
Chccmchma	MOMO OFFICE		1101ccccac	MULHONCACA	TATGATGGCC	540
GAGGIGATAG	IGIGGITTAT	GGACTGAGGT	CAAAATCTAA	GAAGTTTCGC	AGACCTGACA	600
TCCAGTACCC	TGATGCTACA	GACGAGGACA	TCACCTCACA	CATGGAAAGC	Caccacommoa	
ATTOCHHOOATTA	C110000000		TURCUTURUS.	CATGGAAAGC	GAGGAGTTGA	660
AIGGIGCAIA	CAAGGCCATC	CCCGTTGCCC	AGGACCTGAA	CGCGCCTTCT	GATTGGGACA	720
GCCGTGGGAA	GGACAGTTAT	GAAACGAGTC	ACCTCCATCA	CCACACTCCT	Chargona	
CCCRCRRCCR	Cm1 comes-	CAPTICOMOTO	VOCTOONTON	CCAGAGIGCI	GAAACCCACA	780
GCCACAAGCA	GTACCTCGAG					800

- (2) INFORMATION FOR SEQ ID NO:1250:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 347 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

CAATTGCCAA	GGAAACAGGC	CTTGGCCTGA	AGGTACTAGG	AGGAATTAAC	CGGAATGAAG	60
GCCCATTGGT	ATATATTCAG	GAAATTATTC	CTGGAGGAGA	CTGTTATAAG	GATGGTCGTT	120
TGAAGCCAGG	AGATCAACTT	GTCTCAGTCA	ACAAGGAATC	TATGATTGGT	GTATCATTTG	180
AAGAAGCAAA	AAGCATAATT	ACCGGAGCCA	AGTTGAGTAC	TAGGTTAGAA	TCTGCTTGGG	240
AGATAGCATT	CATAAGACAA	AAATCCGACA	ACATTCAGCC	AGAAAATCTC	TCATGTACAT	
Ca compania ca	100000			MOMBRICIG	ICAIGIACAI	300
CACTTATAGA	AGCTTCAGGA	GAATATGGAC	CTCAAGCCTC	CCTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:1251:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 301 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

GAATTCGGCC	TTCATGGCCT	ACAGCCCTCT	TACTAGGCCA	GCACGCTTTC	GCTTTTGCAT	60
TTACAATCAC	ATACCCCATC	CCCTCCACTT	GAAAAAGAAT	TTTGTTTTTG	TCGTTATCCA	120
AAAATCTCAT	CTTAAATCAA	CCGTCTCGTC	TCCCTGTAGC	TTCATTACCA	TCTCAGAAGC	180
AGCAAAGGAG	CCAGCAAAAG	CTAAGGTACA	GAAAGTCGCT	TTGGAGGATG	ATGGTGAGTG	240
GTTATACTTA	ATAGAAGCTA	TCATTTATTA	AGCACCTAAT	GTGTGTCTGG	AGGGGCTCGA	300
G						301

- (2) INFORMATION FOR SEQ ID NO:1252:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 392 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

GAATTCGGCC TTCATGGCCT ATCCTGGGGG ACAGAGCTAG ACGACTCCGT TTCCACTCCC AGACTGCCAA CTCACAAAGT	ACTCCATCTC ATAAAATGCT	AAAAACGAAA ACGTTAGCTG	GTGCCTGGTC TTTTGAGGGT	GTCTTTCCAC AGATGCCCTT	60 120 180 240
AAAAAGACAC ATCAGGTGGC	CTTTGCTTGC	AAGAAATCAG	CCTTTGGAAC	CTGTGGAGAÂ	300
AAGTTAAATA CTGCGTACTG	TGCAAATGAA	GGGTGGGAGC	TATTGAAGGG	AAGAGATTCA	360
CCCTGAAAAC CCAAGAATGG	CCAAATCTCG	AG			392

- (2) INFORMATION FOR SEQ ID NO:1253:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 610 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

GATTCGGCCT	TCATGGCCTA	GCTGGTCTCT	GGTTGCAGGA	TCGAATCGCC	CCCAGCAGTA	60
TGTGTATATG	CATCAGATAA	GGTGAGGGAC	AACCTTCCTC	ACCCCCATAC	CTGGCCAGCC	120
TGTAATGGGG	AGGAGGCCTT	TCTGTGGTGT	GGTGGGGCTG	GAGATTGGGC	AGGGACAGAG	180
ACATACCTTC	TCTGGGAATC	TGAGAGAGAT	ACCTTGAATC	TAGGGGAAAG	GGATTAGGTT	240
TTGAAAATGT	TAGCCATTTT	GTAAAGAGAA	GTCCCTCACC	ATTTCCCTTC	CCATTAGTCC	300
TGGGAAATAG	ATTGGGTAGA	GGCTCAGAGC	CTGGCCCCTG	CTGCACTCCC	AGCTTGGAGC	360
TACTGGGTTG	TTGACAATGT	TTTGGGGTTT	CCAGGCCTTA	GCAAGAGAAA	GCCTCCCCAG	420
ATACCAGTCT	AGGGGTAGAT	GAAGGGGGCA	GGAGCCCTGA	AGGAAGGATT	TGGGGCCGGC	480
CATTCATTCA	TTCAGAAACA	CTTATCATCC	CTTATCAGAA	GCCCTGACCT	ATTGAGAGTC	540
AGGCACGTGC	TATTGAGAGT	CAGGCACGTG	CTCATATAAA	GATGAGTTTA	ACATGGATCT	600
CCCTCTCGAG		·				610

- (2) INFORMATION FOR SEQ ID NO:1254:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 328 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (b) Toronoor: Timea

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

GAATTCGGCC TTC	CATGGCCT AGAGGATTT	A CACATGGCAT	TCAGTGTTCT	CTATACATOT	60
GCCTACCTTT GTC	GAATTCAT CTGTTAACC	CTCTTCCTTT	GAGAGAGCAC	CGCCGATGGT	120
GGTTAACTCC TGT	TGTTTTCT CTCTCTCT	A CTGGTTATTC	TTGAATTAAG	CACAGACTCC	180
TCAGCTCGGT TGC	CTTTATCA TGAATAATG	T GTGTGACCTT	GCAGTTCTTC	CACAGTTCAG	240
CAAACAAGTG CTA	AGCTTCAC TGACCAAAA	A TTAAGGAAGG	AAAACACAGT	TTTTDADACC	300
ATCCATCTTT TAR	ACAGCCGA AACTCGAG				300

- (2) INFORMATION FOR SEQ ID NO:1255:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 488 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:
- GAATTCGGCC TTCATGGCCT ACTAAGAGAA CAATTAGAAT ATTGGAAGAT AAAGGGACAA 60 GTACTGAATT AGTTAAAGAA AATCAGAAAC TTAAGCAGCA TTTGGAAGAG GAAAAGCAGA 120 AAAAACACAG CTGTCTTAGT CAAAGGGAGA CTCTGTTGAC AGAAGCAAAG ATGCTAAAGA 180 GAGAACTGGA GAGAGAACGA CTAGTAACTA CGGCTTTAAG GGGGGAACTC CAGCAGTTAA 240 GTGGTAGTCA GTTACATGGC AAGTCAGATT CTCCCAATGT ATATACTGAA AAAAAGGAAA 300 TAGCAATCTT ACGGGAAAGA CTCACTGAGC TGGAACGGAA GCTAACCTTC GAACAGCAGC 360 GTTCTGATTT GTGGGAAAGA TTGTATGTTG AGGCAAAAGA TCAAAATGGA AAACAAGGAA 420 CAGATGGAAA AAAGAAAGGG GGCAGAGGAA GCCACAGGGC TAAAAATAAG TCAAAGGAAA 480 CACTCGAG 488
  - (2) INFORMATION FOR SEQ ID NO:1256:
    - (i) SEQUENCE CHARACTERISTICS:
      - (A) LENGTH: 316 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

GAATTCGGCC	TTCATGGCCT	AGATCCAGAC	ACGGCACTGC	AGCTTTCAGC	TGACTAGCTG	60
TGTGACTTGG	GCAAGCCCCT	TAATCTCTCT	GATCTCGGGC	TCCCTCCTCT	GTAAAATGGA	120
ATTAAGAATA	ACCTCATTGA	GGAGCTTCCT	GAGGAGGTAA	GGAAAGTGCC	TGGCACAGTG	180
CCAGGCTGCT	AAGAGATCAA	TAAATGTCCC	ATCCCCCAGC	CCCACCCCAG	TTCTTTCCAG	240
GAATTTGAGA	GACTCCTCCC	CCTGTGTTTG	AAAGTGGCAA	AGTCTGGCAC	ACTTGCCTCA	300
TAACACATAA	CTCCAC				ACTIGUETCA	300
IMCACAINA	CICGAG					316

- (2) INFORMATION FOR SEQ ID NO:1257:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:	
CANDERCOOK THEATHEREN ACCOUNT ACCOUNT ACCOUNT ACCOUNT ACCOUNT	
GAATTCGGCC TTCATGCCTA AGCTTCCTTC AGCAGCGCAG GCGGTGGTCC CTGAGGCCCG TGGAAGGAGT CAAACTTGCG GGAATTTTGC AGTTTATCTG CAGGGCTGTT GTTTCCAGCA	60
AGACCCAAAG CTAGAAAAGG AGGAGGAAGA AACTGACCCG ATCAGTGCCA GAAGTCATTG	120 180
TATTCAAAGA AGAATAAGCA AGAAAGAAAA GAAGGAAGGA AGAGAGGTAG ACAGATACAA	240
GATGAAATCC TGTCAAAAAA TGGAAGGAAA ACCAGAAAAT GAGAGTGAAC CAAAGCATGA	300
GGAAGAGCCA AAGCCTGAGG AAAAGCCAGA AGAGGAGGAG CTCGAG	346
(2) INFORMATION FOR SEQ ID NO:1258:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 346 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(II) NOBBOOK IIIE. CHA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:	
GAATTCGGCC TTCATGGCCT ACGGCACTTC AAAAATATAA ATCAAAGTCC ATGACTCTAA	60
AAATAACATA TGCATTGATA TGCTCGCCCC TTTGACCCTT CTCTCAAGAG AAATTCCCTG	120
CCAAGTAATC CACATACATA AGAAGTGTAA AAAGTCCCTA GATTAAAAGA GCATAAAACT	180
TCATTATGGA AACACAGTAG TCCCGGCTAT TTGGGAGGCT GAGACAGGAG GATCACGAGT	240
CCAGGAGTTT GAGGCTACAG TGAGCTATGA TCGCGCCATT GCACTCCAGC CTGGATGACA	300
GAGGAAATAT TAATTTTAGA GTAATCAGAG AAAGCCAGGT CTCGAG	346
(2) INFORMATION FOR SEQ ID NO:1259:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 341 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:	
GAATTCGGCC TTCATGGCCT ACCCCATTCA TGCAGGAATA AATCAAGTGA GCAGTTCCAG	60
ACTITIGCAT AATATITITA CTATGATGCT GTTTTATTAA TATTTTCTAA ATTTCAAAAC	120
AAAAAGTGAA TGTTTGAAAT TGCTGGGTCC CGATGTTGGT GGCTGTTGGA GTTTTGGACC ACTCGCTAGC AGTGATTGA AGATTATAAT TAGCTAAAAT CCAAAACAAA AAACCAACAA	180
CAAAAATTGT ATGGTGCGGA ACATGCACCT TGACAATGGT ACTAACTTGT TATTCTATAG	240 300
AACACGTTAG AATAGATCTA TTTTTGCCAG AGCTTCTCGA G	341
(2) INFORMATION FOR SEQ ID NO:1260:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 416 base pairs	
(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:	
GAATTCGGCC TTCATGGCCT AAAGATAAGG TGGCTGTAAA TGCGTGGATT TATACCTGAG TTCTCTCATC TGTTTCACTG ATCCATGTGT CTGTTTTTAT GCCAGTACCA TGCTGTTTTG ATNACTATAG CTTTGTAATA AATTTGAAG TCAGGTAGTG TGATNCCTCC AGCTTCATTC TTTTTTGCTCA GGATNGCTTT GGNTATTCAT AGTCTTGTGG TTCCATGTAA ATTTTAGGTT TTTTTTTTTT TTTTTTTTT TTTTTACTAT TTCTGTGAAG AATGTTATTG GTATTTTGAT AAGGATTGTA TTGAATCTGT AAATTGCTTT GGGTAGTCTT GTCATTTAAA AATATTGTTA TAGTTCTTCT AATCCATGAA CATAGAATAC CTCTCCATTT TTTTGGTGTC CTCGAG	60 120 180 240 300 360 416
(2) INFORMATION FOR SEQ ID NO:1261:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 86 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:	
GAATTCGGCC AAAGAGGCCT AGGCAGACAT CCATAAACAT TTTCAAAATG CAGGGTATGT TTTTCAGTGT TAAGGCAACT GTTCTG	60 86
(2) INFORMATION FOR SEQ ID NO:1262:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 332 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:	
GAATTCGGCC AAAGAGGCCT ACTTTTGGTA ATAACATTTT AAAGCAGGAA GTATCTACGG TGTGATCGTG GTACAGCTCT TAGTTCAAGT GTGAAGACAT TTGGTTGTCT TGTATATGAC CTAGAAGAAG GGGCGTCTGC TGGAAAACAA TGCTGTTCTT TTTCTCTTTG TTTTTTGGGA CGGGGTCTTA CTCTGTTGCC CAGGCTGCAG TGCAGTGCCT CAATTTTTCA GTTCAGTGCA GCCTCGACCT CTGGGGCTTA AGCGATCCTC CTGCCTCGGC CTCCCCAGTG ACTGAGACCG CAGGCACACAC CCGCACCTCG AG	60 120 180 240 300 332
(2) INFORMATION FOR SEQ ID NO:1263:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 279 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

GAATTCGGCC	AAAGAGGCCT	AAGCCAGGGT	AGGGACAGCA	GACTGGCAGG	AATGAGTGAC	60
AGTTCTATGC	AAATGGAGTT	ATTATTATTA	TTGTTATTAT	TAATAAGGC	AGGTTTGTAC	120
CAGAACTGCC	CAGTATGGCC	TGTGACTTCT	GCGCAGCAAT	TATTTCTCCA	GGGACAGGGC	180
CTGAAGCTAC	CTCACAGTGA	TGCAAAAAAA	TGGGATTCCC	CACTAACCCC	CACACACACC	240
CCCTTCCTAC	CAAACCACAC	ATCTCTCAGT	CCTCTCGAG			279

- (2) INFORMATION FOR SEQ ID NO:1264:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 629 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

GAATTCGGCC A	AAGAGGCCT	AGGATCACGG	AGGTGGTGCC	TGTGTGTCCC	ACAGGAAGCA	60
AAAGCTGATG C	CCAGTTCCC	AGCATACCTA	AGTAAACTTC	AGGTCCACTC	CCAGCACGTT	120
TCTCGTGATA G	TAAAACTAT	GAAGGAACTC	AGTGTACAAG	GAGCTTCTAC	AAAATAGGCA	180
GAAGACAGTA G	CCAGATGGG	CCAAGGGCCC	CAGCCACCCA	CGCCCCTCCC	TCTCCTTGAA	240
GACCTTCGGT T	CCAACCCCA	CCATCAGCAG	GGCTCTGCTC	AGTTCCTCCT	TATGTGTATC	300
ACCACAGGGC T	CCTGGCTCG	TGTCACGTTC	ACCACCAGAC	CCCACATCAG	GAGTCCCGCC	360
AGGGGTGTGG G	GAGGCAGCG	CTGCCTGGTT	GGCCGTGGAG	CCGTATGGAA	CATGGTGCCT	420
CACAGGCAGT C	TGCTTGGCG	TCCTGGATCC	TGGCTGTATC	CCGCTGGAAA	GGATGTGTGT	480
GGGTCTAAGA T	ATGTATATA	ATAGAAACAT	TTATTCAGAA	GCTTTAGTCA	AGACTTCATT	540
TTTAAGTTCA G	AGTAATAAA	CTCATAGTCT	AAATTTCCTA	ATTTTTCTGT	TTAATTTACA	600
TAAATAAAAT G	AAATGCAAT	TTCCTCGAG				629

- (2) INFORMATION FOR SEQ ID NO:1265:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 426 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

3

GAATTCGGCC AAAGAGG	CCT AGAGGTGCCC	ATTTCAATAA	ATTTTAGCAC	ACTGGATGAT	60
AAAGGAGAAA TGCTTTG	GTT TAAGAGAGGG	AAATCTTTGT	TACCAATACT	ATCGGTGAGT	120
TCACCTAATA CTTCCTC	GTC ATCAAGTTCA	TTGGAGTACG	CATCTTCTTC	ATCCTCATCT	180
CCCGGTTCAG TGGGTTC	ACT TTTGACAGGG	CACTCCCCGT	TTGGGTGTAA	AACGTTGCTT	240
TCTTTTGGCC TTTCACA	GTT GTTCTCTTGG	TCTTTGCTCT	CTGACATCTT	GCTAGACTCA	300
GACGATGAGT GGCTGAG	GGA GACAGAGGTA	ATTGGGGTGT	TCACTACTAA	ACTAGACAGC	360
CCCCCAGAT TCACTTC	AGC CTTTGGCATT	TGGGTAATCC	CCAGCGGCTG	CTCTGCTGAG	420
CTCGAG					426

- (2) INFORMATION FOR SEQ ID NO:1266:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 450 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

GAATTCGGCC	AAAGAGGCCT	ACCGCCCATC	GCGCCGGCGC	GACCCGCAGG	AGCGTAGAGA	60
GCGCGGGACT	AGAGTGCAGA	GCTCCGGGAC	GTGGATCGGA	GCCGGCGCGA	TGGGCGGAGA	120
GCAGGAGGAG						180
CGTGCAGGAG	CTTGTGAACA	CCTTCTTCAG	CTTCCTTCGA	CGCAAAACAG	ACTTTTTCAT	240
TGGAGGAGAA	GAAGGGATGG	CAGAGAAGCT	TATCACACAG	ACTTTCAGCC	ACCACAATCA	300
GCTGGCACAG	AAGACCCGGC	GGGAGAAGAG	AGCCCGGCAG	GAGGCCGAGC	GGCGGGAGAA	360
GGCGGAGCGG	GCGGCCAGAC	TGGCCAAGGA	AGCCAAGTCA	GAGACCTCAG	GGCCCCAGAT	420
CAAGGAGCTA	ACTGATGGAG	AAGACTCGAG				450

- (2) INFORMATION FOR SEQ ID NO:1267:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 459 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

GAATTCGGCC	AAAGAGGCCT	AGCTACTAAG	GCAGGTGCAG	CATCAATGAT	TCACTACATG	60
		GGTACTACTC				120
CTCGTCAATC	TCTTTCGAAG	CCATTCAGTC	CTCAATCTCC	TTTTCCTTGG	CTACCCGTTT	180
GGTGTTTATG	TTCCTCTTTG	CTGTTTTCAT	CAAGATAGTA	GAGCACATCT	TCTTCTCACA	240
		GCACGAGGCA				300
TTGGCCAAAT	CCAAAGACTT	TCTCTCCTTG	TTGCTGGAGT	CGCTAAAAGA	ACAGTTTAAT	360
AATGCCACAC	CCATCCCCAC	CCACAGTTGT	CCCCTATCTC	CAGACCTCAT	TCGCAATGAA	420
GTAGAATGTC	TGAAAGCAGA	TTTCAACCAC	CAACTCGAG			459

- (2) INFORMATION FOR SEQ ID NO:1268:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 432 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

GAATTCGGCC	AAAGAGGCCT	AGAGTTTTCA	TAAGCCCGGC	TGGTGTTTAA	AACGTGTTTT	60
GGCTTTGTTC	ATTTTATGGT	GTTGGTGTTG	GTATTGGTGG	TCATGTACTG	GCATGTAAGA	120
		TCTCTCTGCT				180
		ATATGAGGGC				240
		GCCTCGATCC				300
		CATGATGCGG				360
		GCGCTTCTTG	CTCTTCTGCG	TCCACGGAGA	TGGGCACGCT	420
GGTAACCTCG	AG					432

(2) INFORMATION FOR SEQ ID NO:1269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 510 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

GAATTCGGCC	AAAGAGGCCT	ACCCTGAACT	ACTCCAGTGT	GCACCTGCAC	AACCTCCATG	60
${\tt GTGCCTCTGG}$	AATTGGGTAG	CATGGTGGCC	CTGCTGATGA	GCACCCCAAG	GGGCCATTGG	120
${\tt GGGACCTCTG}$	AGAATCTCTG	CCAGAGCAGT	${\tt TTGGGTGGGA}$	GTCGATTAAG	GAAAGAAGCA	180
GCAAGATCCA	GGACTTTTAA	TCTTAAAAGA	GAGAGAAATG	CTGGCAGATG	AACATTCTGA	240
GGATAAGGAG	CCTGAGTAAT	TGAGCGATTA	GGGATGGAGA	CATACGATTG	AATTCTAGAC	300
CTGCCTCGAG	TAGCCAATCA	AGCTGTGTCT	GGCTGTGCAC	TATCCAGGCC	TCCACATTCT	360
GTGACAAACT	AACAGGGCCG	GCTCCTGTCA	CTCCTGTTCT	CGCCAGCGGG	TTTTACCCTG	420
AAGGTGACTC	AGGCCTTCTC	TTTGCCCTAG	ATCGTGGGGA	TCATCACACG	GCACAACCTC	480
ACCTATGAAT	TTCTGCAGGC	GTAGCTCGAG				510

- (2) INFORMATION FOR SEQ ID NO:1270:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 388 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ. ID NO:1270:

GAATTCGGCC	AAAGAGGCCT	ACGCATCCCC	TGCAGCTCTT	GCCCCCAGAC	GTTTGGTACC	60
AACTCGAAAC	TGCGCTTGCA	CCGGTTAAGG	GTACATGACA	AAACACCTAC	CCACTTCTGT	120
CCACTTTGTG	ACTATAGTGG	CTACCTTCGC	CATGACATCA	CTCGTCATGT	CAACAGCTGC	180
CACCAAGGCA	CCCCAGCCTT	TGCCTGCTCC	CAGTGTGAAG	CCCAGTTCAG	CTCAGAGACA	240
GCACTTAAGC	AGCATGCTCT	GCGCCGACAC	CCCGAGCCTG	CACAGCCTGC	CCCTGGCTCT	300
CCTGCAGAGA	CCACTGAGGG	CCCCCTGCAC	TGTTCCCGCT	GTGGGTTGCT	GTGCCCCAGC	360
CCTGCCAGCT	TACGAGGACG	GCCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:1271:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 407 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

GAATTCGGCC	AAAGAGGCCT	ACAGAACTGT	GCCATATTCT	TAAACATCAT	ACAATATTGC	60
CTTTCAGGCA	TGAAAAGCAA	AGGGAATTAT	TTGTTCATTT	GATAGCGCTT	TAGTAATGTA	120
AGTGGATACA	CTTAGGGCTA	GCCCTCTGGC	TTGTTACCAT	GGTAAGCTAG	GGGAATATAG	180
TTGAGGGGTC	TGCAGCAGAG	CTTGGAGAGG	ATCTGGGATG	TTAAATTCTC	AAGTACTTGA	240
ACTTAGCAAC	AGGACTTGGT	CCCATCCACA	CCCTGCTCTC	CACCCCAGCT	GGAAATAATT	300
AGTGCTGACT	ATGGAGGCAA	AGAGAAACAT	ACTTGTAAGC	TTTTTTTTTTT	GGATTTTCTT	360
TGGGGTTTCC	TTTTTGTCTT	TTCTGAACTG	GAGGGTGAAA	TCTCGAG		407

(2) INFORMATION FOR SEQ ID NO:1272:

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(i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 321 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:
GAATTCGGCC AAAGAGGCCT ACATAAATCA AAAATTTCTG TGAAGATGGG AAATAAGGCC
                                                                     60
AAGATTGCAA AATGTCCTTT AAGAACAAAA ACTGGGCACA TTCTAAAATC AACACAAGAT
ACTTGTATTG GGAGTGAAAA ACTTTTGCAA AAGAAGCCAG TTGGTTCAGA AACATCACAG
                                                                    180
GCAAAAGGTG AAAAAAATGG AATGACTTTT TCATCCACTA AGGATTTATG TAAACAATGT
                                                                    240
ATAGATAAAG ACTGTCTTCA TATCCAGAAA GAGATTTCAC CTGCAACCCC TAATATGCAG
                                                                    300
AAGACTAGAA ACACCCTCGA G
                                                                    321
(2) INFORMATION FOR SEQ ID NO:1273:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 205 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:
GAATTCGGCC AAAGAGGCCT ACGAGAACTT CCTTTTCATC TGAATCTTCG TCAAACTCTC
                                                                     60
TCTCAGAGCC TTCCTCATCT AACACTTTTT CAGAGCCGTC ATCTTCAAAT TCGGAGTTTT
CAGAGTCATT TTCTTCTAAC TCTTTGTCAA GAACATTTTC ATGAAGCTCC TTTTCAGAAC
                                                                    180
CTTCCTCGTC CAAATCTTTC TCGAG
                                                                    205
(2) INFORMATION FOR SEQ ID NO:1274:
      (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 450 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: double
             (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:
GAATTCGGCC AAAGAGGCCT ACTCAATACT GAGGCTGATT GGTCGTTTAG GCCAATTGGG
                                                                     60
TTTGAAAGAA GGATTTCCAT CTGCTGTGAA AAATATTAGT TCGGTTATTG GTATGTTTAT
ACAGCATGCT CACGATGAAG ATATACCATG GGGTATACAG TTAGCAGCCG TGTATGCTCT
                                                                    180
TTGTGACTTG AGTCCCAGCA ATCCAGCAGA AATTTCCAAG ATCCTGGAAG CTTGGCGGAG
                                                                    240
AGAGGCCTCC AAAAGCGTTC CGTCTGCGAT TGTCAGCTGC CTAGAGGAAG TCAGTGCCCT
GAGCACAGAG GAGCTTGGCT GACCTGGGAT GCCACTGAGG CTTGAGAAGT GCCTTGACAC
                                                                    360
420
AGACATAAAA TAGATAAAAG CAGACTCGAG
                                                                    450
(2) INFORMATION FOR SEQ ID NO:1275:
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(i) SEQUENCE CHARACTERISTICS:

(1) SEQUENCE CHARACTERISTICS.	
(A) LENGTH: 255 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) TOPOLOGY: Timear	
( ) NOT BOTTO THE TANK	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:	
GAATTCGGCC AAAGAGGCCT AAAGCAACAG GAAAGGATAA ATTCACAGAG GGAAGAGATA	60
GAAAGACAAC GGAAAATGTT AGCAAAGCGG AAACCTCCTG CCATGGGTCA GGCCCCTCCT	120
GCAACCAATG AGCAGAAACA GCGGAAAAGC AAGACCAATG GAGCTGAAAA TGAAACGTTA	180
ACGTTAGCAG AATACCATGA ACAAGAAGAA ATCTTCAAAC TCAGATTAGG TCATCTTAAA	240
AAGGAGGCTC TCGAG	255
(2) INFORMATION FOR SEQ ID NO:1276:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 367 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:	
GAATTCGGCC AAAGAGGCCT AACAAGATTG ACCGTGAATG GTTCACTGTT GAAACTCTGT	60
GATGGGTACT TGAGAATTTA TTATATTATT ATGCCTATAT TGCAGATATT TGAAGTTTCC	120
CAATAAAATG TTTAAAATAG TGGCAGGGGG CAAGAAGAAA AGGACCACTC AATTTAAAGA	180
AAAAATAATT TTAAAAGACA CAGAGAATAG GAAGAGGGAA AAATTGGTGA GGCAAGAGAA	240
AGGCAGCAGG TGGGGCCATA TCAAGAGTGA TTCTTCAGCA GGTGAGGCGT GATACCACCG	300
CAAAAGTAGA GGGTTGGCTG TAAGATAGGG GGCACAGATG GCTATAATGC AAGGGAAGGC	360
GCTCGAG	367
(2) INFORMATION FOR SEQ ID NO:1277:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 624 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:	
GAATTCGGCC AAAGAGGCCT ACTCAGAAAC AAAGCCAAAA TTAAGTTCAT CATTAAAAAG	60
CCCGAAATGT TTGAGACGCC ACTCAGAAAC AAAGCCAAAA TTAAGTTCAT CATTAAAAAGCCCGAAAA TTAAGTTCAT CATTAAAAAGCCCGAAAAA TTAAGTTCAT CATTAAAAAAGCCCGAAAAA TTAAGGTTCAT CATTAAAAAAGCCCGAAAAA TTAAGTTCAT CATTAAAAAAGCCCGAAAAA TTAAGGTTCAT CATTAAAAAAGCCCAAAAA TTAAGGTTCAT CATTAAAAAAGCCCGAAAAA TTAAGGTTCAT CATTAAAAAAGCCCAAAAAA TTAAGGTTCAT CATTAAAAAAAAAA	120
•	
ATAAATTCAT CACCCAATGT TAATACTACT GCATCAGGTG TTGAAGACCT TAACATCATT	180
CAGGTGACAA TTCCAGATGA TGATAATGAA AGACTCTCGA AAGTTGAAAA AGCTAGACAG	240
CTAAGAGAAC AAGTGAATGA CCTCTTTAGT CGGAAATTTG GTGAAGCTAT TGGTATGGGT	300
TTTCCTGTGA AAGTTCCCTA CAGGAAAATC ACAATTAACC CTGGCTGTGT GGTAGTTGAT	360
GGCATGCCCC CGGGGGTGTC CTTCAAAGCC CCCAGCTACC TGGAAATCAG CTCCATGAGA	420
AGGATCTTAG ACTCTGCCGA GTTTATCAAA TTCACGGTCA TTAGACCATT TCCAGGACTT	480
GTGATTAATA ACCAGCTGGT TGATCAGAGT GAGTCAGAAG GCCCCGTGAT ACAAGAATCA	540
·	600
GCTGAACCAA GCCAGTTGGA AGTTCCAGCC ACAGAAGAAA TAAAAGAGAC TGATGGAAGC	
TCTCAGATCA AGCAGAACCT CGAG	624
502	
JUL	

(2) INFORMATIO	N FOR	SEQ	ID	NO:1278:
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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 286 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

GAATTCGGCC AA	AGAGGCCT ACCCAA	ATCC CATTTAGAT	AATTGAGGTT	CATTTTTCAC	60
ATAGACTTGC AA	TTTTAGA CACCAC	ATTT TTTTTATAG	r AACAGCCTCA	TTTGCCTGTA	120
CAATAACTAA TAA	ATACAGTA TTTCAT	AGGT ACATTGTATO	G TGCACAGGAA	ATTTTTCTTT	180
AAATCTTAAA AG	CCTTTAAT AAACGG	GATA TTTTAATAT	TTAATGTTAC	TACATTTAAA	240
AAATAGTGTT TTO	CTACAAA ATTTTC	TGTA TTCAGTAAT	A CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:1279:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 227 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

GAATTCGGCC	AAAGAGGCCT	ACTCATCATT	AGCTGAAAGT	TTGAGAGCTG	CAGCAGAAGC	60
GGCTGTATCA	CAGACTGGAT	TTAGTTATGA	TGAAAATACT	GGACTGTATT	TTGACCACAG	120
CACTGGTTTC	TATTATGATT	CTGAAAATCA	ACTCTATTAT	GATCCTTCCA	CTGGAATTTA	180
TTACTATTGT	GATGTGGAAA	GTGGTCGTTA	TCAGTTTCAT	TCTCGAG		227

- (2) INFORMATION FOR SEQ ID NO:1280:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 486 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

		ACCCGTGCGC				60
GGGAACTCGA	TCCTGCTGGC	TGCTGTCTCT	ATTCTCTCGG	CCTGTCAGCA	AAGTTATTT1	120
GCTTTGCAAG	TTGGAAAGGC	AAGATTAAAA	TACAAAGTTA	CGCCCCCAGC	AGTCACTGGG	180
TCACCAGAGT	TTGAGAGAGT	ATTTCGGGCA	CAACAAAACT	GTGTGGAGTT	TTATCCTATA	240
TTCATAATTA	CATTGTGGAT	GGCTGGGTGG	TATTTCAACC	AAGTTTTTGC	TACTTGTCTG	300
GGTCTGGTGT	ACATATATGG	CCGTCACCTA	TACTTCTGGG	GATATTCAGA	AGCTGCTAAA	360
		ACTGAGTCTG				420
GCCCTGGGAA	TTGCAAACAG	CTTTCTGGAT	GAATATCTGG	ACCTCAATAT	TGCCAAGAAA	480
CTCGAG						486

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:	
CANDOCCOCO ANACACCOCO ACACAA ANDOCCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	
GAATTCGGCC AAAGAGGCCT AGACAAATTT CCTTTCATTG CTTCCAGCCG TGTTATTTAA AGTAATTAAC CTTAATTTAT AAATTTTTAT ATCAAACTGC CTTTTAACTT TTAGAACTGG	60
CAGGAACAGC CTTATCCCTG GGCTCCTAAT AGTTCTCCAT TTAATCAAAA TTCATCCATC	120
AGGTTCCAGT GTTAATCAT CTTTTAATTG GGAGTTACAT TCTGGTTAAT AGTTTTATAA	180 240
TTCGCCTCCT CTAATAGTTT TTACCACAGG GATCTCGACT CCATTTTTCC TGACTCTATT	300
ATTGCTGGCA TGCGATTTCT GCGGGGATGG CTTAACGCGG CCCTGCCTCT CTGGCCTCTG	360
CTGGTCGCCT CTTTTGTTCT TGGTGGTCTC ATTAATTCCT GAGAAGAGTT ATCCTTCCTC	420
CTCACTCGAG	430
(2) INFORMATION FOR SEQ ID NO:1282:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 333 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:	
GAATTCGGCC AAAGAGGCCT AATCCCCTTC TGCATGTTCC CTTCCTGCAG GTCTGATGGG	
GCCATCCCAC CCTGCTGGGG AGCACAGCTT GCCCTCCCTC CCCTCCTTCT CTTCTGGCGT	60 120
TGCCTGCTGG GTGCCATCGG AGCAGTCCTC ATTACTTCCC ACTTTTGCCC AACTTCTGCT	180
GCTGTGACCA GTCGCATACA CGTGGACACC GTGGGGACTG CCCCTCCATA CAGCTCCTCT	240
GTAAGCTTAG GACCAAGGCT GCCTCTCCAG TCTCCCTGGC CCATGCCTGC CCCGGCATCC	300
TCCGCCCCAG CTACACTGGC CCCCGATCTC GAG	333
(2) INFORMATION FOR SEQ ID NO:1283:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 269 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:	
GAATTCGGCC AAAGAGGCCT AGGACGTTGG TGTTGAGGTT AGCATACGTA TCAAGGACAG	60
TAACTACCAT GGCTCCCGAA GTTTTGCCAA AACCTCGGAT GCGTGGCCTT CTGGCCAGGC	120
GTCTGCGAAA TCATATGGCT GTAGCATTCG TGCTATCCCT GGGGGTTGCA GCTTTGTATA AGTTTCGTGT GGCTGATCAA AGAAAGAAGG CATACGCAGA TTTCTACAGA AACTACGATG	180
TCATGAAAGA TTTTGAGGAT GAGCTCGAG TCATGAAAGA TTTTTGAGGAT GAGCTCGAG	240 269
	265
(2) INFORMATION FOR SEQ ID NO:1284:	
(i) SEQUENCE CHARACTERISTICS:	

- (A) LENGTH: 339 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

GAATTCGGCC A	AAGAGGCCT	AGAGCGTCAA	TTATATCAAT	TTGTCCCAGA	TTTGGATGAG	60
CTGTGAGGAT GT	TAACACAAG	GCTGGAGGAG	GCAGATGAGT	TTTTATCTCT	TCACAGGGGT	120
GGTCGCGGCC AC	GGTGTTTTC	AGAGGTATCG	CTGGGGGCCA	CAGGGTGTCA	ATCAAACTCA	
AAATCCCCGC TC	STCCTTCCT	CTGGTGACTT	TCTGTAGAAC	CTTCATTCCC	ACCACCOMOO	180
AAGACTTCCC TT	CCAACTGT	CTTCCCTTCC	ACATCCTCAA	CTICATICCC	ACCAGGCIGC	240
ACATTCCACA GO	CATCTTCT	ACCACAACCA	ACAIGGIGAA	CICCAAGIGC	ACTTCACCGA	300
······································	JUNICITUI	MCCMGAAGGC	AGGCTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:1285:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 496 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

GAATTCGGNN	AAAGAGGNCT	AGAAATCANA	AAGCATGCCT	GTGCAATTGA	ACAAAGGGCT	60
AAGTTCTAAA	AACATCAGTT	CATCTCCAAG	CGTTGAGAGT	TTGCCTGGAG	GAAGAGAATT	120
CACTGGCTCT	CCACCTTCAT	CTGCTACTAA	AAAAGATTCC	TTTTTTAGCA	ACATCTCACG	180
TTCTCGCTCA	CACAGCAAAA	CTATGGGCAG	AAAAGAATCT	GAAGAAGAAT	TAGAAGCCCA	240
AATTTCCTTC	CTTCAAGGGC	AGTTGAATGA	CCTGGATGCC	ATGTGCAAAT	ACTGTGCAAA	300
GGTGATGGAC	ACTCATCTTG	TAAATATTCA	AGATGTGATA	TTACAAGAAA	ATTTCCAAAA	360
AGAAGATCAA	ATTCTGGTTT	CCCTGGCAGG	ATTAAAACAG	ATCAAAGACA	TTCTAAAACC	420
TTCCCTGCGT	TTTAACCAGA	GCCAGCTAGA	GGCCGAAGAG	AACGAACAGA	TCACCATTGC	480
GGACAACTCA	CTCGAG					496
						170

- (2) INFORMATION FOR SEQ ID NO:1286:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 319 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

CAATTCCCCC TOTAL TOTAL					
GAATTCGGCC TTCATGGCCT	AGCAGAAGCT	AAGAACTGTC	TTAAAATAAA	TTTTTDAAACT	60
AAATAACTTA TAATCCAMAC				111111111111111111111111111111111111111	00
AAATAAGTTA TAATGCATAG	GTTAGCCCAT	TCATTAATGA	TTTTCAGTTT	CAACTCTAAA	120
TATTTCTTAN TCATTACTAC	mmo.s.m.e			Carololina	120
TATTTCTTAA TGATTACTAG	TIGATCAGTG	TAATGAAAAC	ATTGAGTAGA	ТАВАТТАВАТ	180
GCACACTATA AATCTCACAT	3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5				100
GCACAGTATA AATGTGACAT	AAACACTGGT	TTCAATTTGT	CTCAAGAAAA	AAGAAAAAA	240
AAAGGCCCCT GCAATCCCAA	NORGE CO.				270
AAAGGCCCCT GCAATGGCAA	AGAGTGGCCA	CTATTGGGGT	AATTCAAACA	ACCCACTGTA	300
ATACAGGAAA GCACTCGAG					300
THE PART OF THE PERTON OF THE					319

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:	
AAAATGGAGA AGTTACTGGC TGGAGAAGAT GGGACAAGTG AACGAAGGAA AAGCATCAAA ACCTACAGAG AAATTGTTCA AGAAAAAGAG CGGAGAGAGA GAGAGCTGCA TGAAGCATAT AAGAACGCTC GGTCCCAGGA GGAGGCAGAG GGGATCCTTC AACAGTACAT TGAGAGGTTC ACCATCAGTG AGGCTGTCT CGAACGCTTG GAGATGCCAA AAATTCTGGA AAGAAGCCAT TCAACAGAGC CAAAACTCGA G	60 120 180 240 261
(2) INFORMATION FOR SEQ ID NO:1288:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 275 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:	
GAATTCGGCC TTCATGGCCT ACTCTGAAGA TATTTATAGC TCTCTTAGAG GTGTCACTGA AGCAATCCAG AATTTCAGCT TCCGTAGCCA AGAAGATATG AATGAGCCAT TGAAAAGGGA TTCTAAAAAA GATGATGGCG ATTCAATGTG TGGTGGTCCT GGGATGTCTG ACCCAAGAGC AGGAGGTGAT GCTACTGACT CAAGTCAAAC AGCTCTTGAT AATAAAGCTT CATTGCTCCA TTCAATGCCT ACTCACTCCT CTCCACGCTC TCGAG	60 120 180 240 275
(2) INFORMATION FOR SEQ ID NO:1289:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 139 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:	
GCGATTGAAT TCTAGACCTG CCTCGAGAAC GCCGGGGTCC ATCATTAGCA GTCCTCACAT GCGCCGGAGA GCTACATCAA CACGAGAGTG TCCATCTCGC CCACACCAGA CTATGCCCAA CTCATCTTCC CCCCTCGAG	60 120 139
(2) INFORMATION FOR SEQ ID NO:1290:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 358 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

					GCTTTTCTAG	60
CAGCTGGTGT	GTGCAGAGGC	AGATGGCTCT	CTGGTTCCAG	GACTACCTAC	AATATAGAGA	120
					GTAGTGTTAT	180
					TTGACATTTC	240
					GAGTAGTTTC	300
CCAAAGTGAT	TTTGAGTGTG	GAAGAAATGG	TATTGTCCCC	GAACAGCTGG	TGGTCGAG	358

- (2) INFORMATION FOR SEQ ID NO:1291:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 139 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

GAATTCGGCC	TTCATGGCCT	AGAGGATCCT	AATGAAATAC	CTGAAACATA	TATTGGCATT	60
TATCAATGGC	TCAAATCTTC	ATTTATCTCT	GGCCTTAACC	CTGGCTCCTG	AGGCTGCGGC	120
CAGCAGAGCC						139

- (2) INFORMATION FOR SEQ ID NO:1292:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 442 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

GAATTCGGCC	${\tt TTCATGGCCT}$	ACTATCAGGA	AGTGATTCGT	GGAGAGGGGA	TTTTACCTGA	60
TGGTGGAGAA	TACAAACCCC.	CTTCTGATTC	TTTGAAAAGC	AGAGACTATT	ACACGGATTT	120
			GGCACTGGTC			180
			CCAACTGGTC			240
					CCCTGTCAAC	300
GCTTCCTGTG	TTCCACCCTG	TGACTGGGGA	AATCATACCT	CCTTTACACA	CAGACAACTA	360
			GCAGCAGAAC	TTGCCACATC	AGACTCAGAT	420
TCCCCAACAG	CAGACTCTCG	AG				442

- (2) INFORMATION FOR SEQ ID NO:1293:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 231 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

GAATTCGGCC TTCATGGCCT ACATGAATTA TCTGTGAGTT GGTTAAAGGT AATATTGGTT AGCATCAAGA ATAGGAAGCT ATTAGTTTTC AATCAAGAAT AAGCTCAAAT TTGGTCTAAA TCTTAATTTT AAGCTGGGTA ATCATTGATT TACAATTTTT TTCTTGGTGT CACATTTCTT CCAAAACAAT AATCAATGAA GCCTTTCCCA CCCTGTGCCT TTGCTCTCGA G	60 120 180 231
(2) INFORMATION FOR SEQ ID NO:1294:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 355 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:	
GAATTCGGCC TTCATGGCCT ACTCTGCTAA CTTCCTGCCT CTATGTCTTT CCCCACCTAC CTCCTCTCCC CATTCACACT CCTGCGTGAC CTCATCCATT TACCTGCCTT CAATTAGCAT CCATACGTTC CTCCTTTCTC AATATAAGTC CCCAGCTGAG ACTCTGTTTC TGAAAATCCAG ATTTTTATTT CCAATTCTAC TGAACAAACT CAGTCTAAAG CCCAGCCCAT TATCTTCTCC TATAAGCCTG CATCTTTTCT TTTCTTTCTT TCTTTTTTT TTTTTAACAG AGGTTAATGG CATTCAACAT CTACCCAAGC ACCAGGGAGT TAGATTCAGA ACGGATGGAC TCGAG	60 120 180 240 300 355
(2) INFORMATION FOR SEQ ID NO:1295:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 429 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:	
GAATTCGGCC TTCATGGCCT AGGCTAACTG TTATTTGCAT CTTACAGCTC AGAAAACAAG CATGGTGAGA TAAGGAAACT TTACTAAGGT CACATAACTA GTAAGTGGTG GAGCCAGCGT TGAAACTCAG GAAGTCTGTA CACAACTGGG AGGGAAGGCT AATATTTGAA ATGATAGACT CAACATTCAA-TATTTCAGTA TCGATGAGCT CTAAGTTGAT AGGCCTATGAGTA ATTAAGAAAT CATTGGCAGA AGAGTAAGAG AGGCTTTTGG TCAAGTAAGC TGAGTGCATA AGAAAACTCT GGCATTTGAG GTGTCCTTAG CTCCAGATGC TTTGGTAGGG CAGAGTGTAT CCATGGAGGT ACCATGAGCT ACCATGGAGG TAGCTCAGAA AGGAAAGGGA AACCTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:1296:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 406 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:	
CTCGAGCTGT TCTGTAAATA CCTGGTGCTA ACATCCCATG CCGCTCCCTC CTCACGATGC ACCCACCGCC CTGAGGGCCC GTCCTAGGAA TGGATGTGGG GATGGTCGCT TTGTAATGTG	60 120

CTGGTTCTCT TTTTTTT	TTC TTTCCCCTCT	ATGGCCCTTA	AGACTTTCAT	TTTGTTCAGA	180
ACCATGCTGG GCTAGCT	AAA GGGTGGGGAG	AGGGAAGATG	GGCCCCACCA	CGCTCTCAAG	240
AGAACGCACC TGCAATA					300
CAGCCTCTGC GTCCTGG				TGGCGCCGCT	360
TCCTCACATC TGTGCTC	CAT GCCCCTAGGC	CTCTTTGGCC	GAATTC		406

- (2) INFORMATION FOR SEQ ID NO:1297:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 639 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

GAATTCGGCC	AAAGAGGCCT	ACGCCCGCCA	ACACGCCTGG	GTAATTTTTT	GTATTTTTAG	60
TAGAGACGGG	GTTTCACCGT	GTTAGCCAGG	GTGGTCTTGA	TCTCATGATC	TCGTGATCCA	120
CCTGCCTCGG	CCTCCCAAAG	TGCTGCGATT	ACAGGCAAGT	GCCACCGCAC	CCGGTGACAC	180
	AAGCAGAAGC					240
	CTAAGGCCTC					300
	TTAGTAAAAC					360
GCACGGGGCC	ACAGCATAGT	GGATCAGTAC	AACTTTCCTG	GACAGCCTTG	CTACCTGTAC	420
ACTCTTATGG	ACTCAATTCC	ACTTCAATGT	ATTCGTTCTA	GAGGTAAATG	GACATGTGAA	480
CACAGATTCA	CAGGCAAAGA	TGTTTATATG	CACCACTGTC	TTGATGTTCA	AGAAAATGGA	540
ACTGGTTACA	TGCATGTGAT	TAGCTATATA	ATGTAACTGT	ATTCAGCCCC	TAAAAAATGT	600
AGGCCTCTTT	GGCCGATTGA	ATTCTAGACC	TGCCTCGAG			639

- (2) INFORMATION FOR SEQ ID NO:1298:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 606 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

GCGATTGAAT	TCTAGACCTG	CCTCGAGTCC	AACGGCATCG	ACGTGTACCC	CCAGAAGGAA	60
TTTGATGAGG	ACTCGGAGGA	CCGGCTGGTG	AACGAGAAGT	TCCGGGAGAT	GATCCCATTT	120
GCTGTGGTGG	GCAGTGACCA	CGAGTACCAG	GTCAACGGCA	AGAGGATCCT	TGGGAGGAAG	180
ACCAAGTGGG	GTACCATCGA	AGTTGAAAAC	ACCACACACT	GTGAGTTTGC	CTACCTGCGG	240
GACCTTCTCA	TCAGGACGCA	CATGCAGAAC	ATCAAGGACA	TCACCAGCAG	CATCCACTTC	300
GAGGCGTACC	GTGTGAAGCG	CCTCAACGAG	GGCAGCAGCG	CCATGGCCAA	CGGCGTGGAG	360
	CAGAAGCCCC					420
	TTTCCGTCCC					480
	CTCTAAAACG					540
ACCCCACCC	AATCACCCCT	ATTTTTACTC	TTTCTACTTT	CGGAATTGGA	AAGAACGACA	600
CTCGAG						606

- (2) INFORMATION FOR SEQ ID NO:1299:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 267 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

	GAATTCGGCC AAAGAG	GCCT AGGAGTGAT	G TTCATTTTGG	GATTTGCAGG	GTGCATTGGA	60
-	GCGCTACGGG AAAACA	CTTT CCTTCTCAA	G TTTTTTTCTG	TGTTCCTGGG	AATTATTTTC	120
	TTCCTGGAGC TCACTG	CCGG AGTTCTAGC	A TTTGTTTTCA	AAGACTGGAT	CAAAGACCAG	180
-	CTGTATTTCT TTATAA	ACAA CAACATCAG	A GCATATCGGG	ATGACATTGA	TTTGCAAAAC	240
-	CTCATAGACT TCACCC	AGGG ACTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:1300:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 414 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

GAATTCGGCC	AAAGAGGCCT	AGTGTTTTCC	<b>AATCAAGTTA</b>	ATAAATATCT	GTCTTCGTAC	60
CAGGAAAAAT	TCAATATTAT	TTTAAAGGAG	AAAAAATAAG	AATGTATTGG	TAAAATGCTT	120
TCTCTCACTT	CGAAATATCT	TAGTGAACAA	GAACACTGAC	ATAGAATTAA	AATTCTATGA	180
ACAGCCATAA	CCAAAGGAAT	CTCATTTAGT	GAATATTTAT	GTCCAGTAAC	TGCAACCCAC	240
ACTTAGAGCT	ATCCTTTTGC	TTAAAAACAA	AAATTTGGGC	CTTAAGAAGT	GATTAATATC	300
AGGCAAAAAT	AAATTATACT	TTTGTTTATT	TATTCAGGGC	CTTGCTCTGC	TGCCCAGGCT	360
GGACTGCAGT	AGTGCAATCA	TAGCTCACTG	CATCCTTGAA	TTCCTGGGCT	CGAG	414

- (2) INFORMATION FOR SEQ ID NO:1301:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 284 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

GAATTCGGCC AAAGAGGCCT AGTGAAGTT	T ACTGTGATTC	TATGGAACAA	TTTGGACAAG	60
AAGAGTCTTT AGACAGCTTT ACGTCCAAC	A ATGGACCATT	TCAGTATTAC	TTGGGTGGTC	120
ATTCCAGTCA ACCCATGGAA AATTCTGGA	T TTCGTGAAGA	TATTCAAGTA	CCTCCTGGAA	180
ATGGCAACAT TGGGAATATG CAGGTGGTT	G CAGTTGAAGG	AAAAGGTGAA	GTCAAGCATG	240
GAGGAGAAGA TGGCAGGAAT AACAGCGGA	G CACCACAACT	CGAG		284

- (2) INFORMATION FOR SEQ ID NO:1302:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 193 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

GAATTCGATT	GAATTCTAGA	CCTGCCTCGA	GCCTGTGCGA	GAAAAGTGAA	CGCCAGTCTA	60
аааааааа	AAAAATCTAA	AAGAAGCCAA	AAATCCACTT	GTAATGAGAT	TCATAGACCC	120
CTTATTTATA	CAACTCACAT	${\bf ATTTGAATTT}$	TTACATATTG	AATTTTCTTT	TAAAGGGGTG	180
GAGGGGTCTC	GAG					193

- (2) INFORMATION FOR SEQ ID NO:1303:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 305 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

GAATTCGGCC	TTCATGGCCT	AGGGATACAG	CAACTATTTT	ATCAATTGTT	TGTATTTCCC	60
TTTAAGGTAA	CATTTTAAAT	GAAATGTATT	ATATTTTAAT	CTATCCTTTT	CCTTTGTTTT	120
TGTTCTTATT	ATCTCTTCTG	ATATATAACC	AAAAAATGAA	ΔΔΔΔΤΟΤΩΤΑ	CACTTGGTGT	180
TTGATTTACC	TAAGCACCTA	GTTAATTTAA	TCTTTCTAAC	ACTITICCATC	GTTAACTTAA	
CCTTTACTCA	AGTTGGTTTT	TCTTTTCTTC	AAAATCACTT	ACTITIONATO	ACCACTACTC	240
TCGAG		1011111111	AMAMIGACII	ACTIGGIGGA	ACCACTACTC	300
						305

- (2) INFORMATION FOR SEQ ID NO:1304:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 416 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

GCAGCGAGCA	CTATACCACC	3003003300	~			
GCAGCGAGCA	GINIACCAGC	AGCAGCAAGC	GAAAGGAAGA	GTTTGCTGAT	ATGTCAAAAG	60
TTCATTCAGT	GGGAAGCAAT	CCCCTTCTCC	A COMMIC A MILLO	ACA A MAMOR O	G1-G-G-G-G-G-G-G-G-G-G-G-G-G-G-G-G-G-G-	
	999121902211	GGGCTTCTGG	ACTITIONITE	AGAATATCAG	GAGCTCTGGG	120
ATTGGCTGAT	TGACATGGAG	TCCCTTGTGA	TGGACAGCCA	CGACCTGATG	DICTCACACC	180
2002002200	~			CONCCIONIO	AIGICAGAGG	190
AGCAGCAGCA	GCATCTTTAC	AAGCGATACA	GTGTGGAAAT	GTCCATCAGA	CACCTGAAAA	240
ACACCCACCT	COTTROTRAG	0000000				
AGACGGAGCT	GCTTAGTAAG	GITGAAGCIT	TGAAGAAAGG	TGGCGTTTTA	CTACCAAATG	300
ATCTCCTTGA	AAAACTCCAT	TONDOUGH	**********			
crccrrcn	INDIGIONI	ICAMITAMIG	AAAAATGGGA	ACTGCTTGGG	GTATTTGCAT	360
TTTTATTACT	GTTTCTACCT	TATCTCTACA	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	* CMC * * CMC *		
		TUTOTOTACA	111111111111111111111111111111111111111	AGIGAAGTCA	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:1305:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 345 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

GAATTCGGCC TTCATGGCCT ACCAATGTCC TGCACATTGC CAGACTTCCA AACAGGTACA AGTTCCCATC TGTTCTGCAA TAGATGAAAG CAAGTCACAG TTCCCAGGGC TACCAGTGTA ATTTCTCAAG TGGCCAAGTT ACCTGGCTTC ATGGCTTGAC CTGCTGTGTT CTTTTGGAAA TGGAGAATGC CTGAGGGCTG TCTCTAACAG AAGGGTATGT GGCAGATATAT TACAGAATTT ACAAGAAGCA AGGTGCAAAT GAATTACATT GAATTTCATT GTTAAGAAGA GATGATTTAA AATTTGGTAT TTAACAACAT AAACGACTTT GGGGCCCAAC TCGAG  (2) INFORMATION FOR SEO ID NO:1306:	60 120 180 240 300 345
(2) INFORMATION FOR SEQ ID NO. 1306:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 209 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:	
GATTTCTCTC AGCTTTTATT TGTTTGAAAA ATTTTTTAAT TCACCTTCTT TTTTGAAAGA TTTTTACTGA TTATAGAATT CTAAGTAGTT TATTCTTCTA GGACTGTGAA CATATAATTC TACTGTCTTC TGGCATTTAT AGTTTCTTTA TTTTATTTTT TATTGAAAAA CATTTTTTTT GAGACATGGT CTCACTCAGA ATACTCGAG	.60 120 180 209
(2) INFORMATION FOR SEQ ID NO:1307:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 251 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:	
GAATTCGGCC TTCATGGCCT AAGCTTTTGC TTTTTTAATA ACTTGTATAG CTAAAAACTT GACGGTGAAA AGCTCTCAGA TCAAAGCTGA TCCTTCTGTC AGTAATGATT CTAAAAAATAA GCAAGATTTT AATGGGGAAT ATATTTTATT TCATTCTTAT CTCAAACCTA GGTACTGTGG TCGTTTTGAG TTCATTCGA GGCATTTCA ATGTGCCTCA GGCCACATCC AACCTCTCCC CAGAACTCGA G	60 120 180 240 251
(2) INFORMATION FOR SEQ ID NO:1308:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:	
GAATTCGGCC TTCATGGCCT ACCTGACTCT TGAGATACTG ACTGGAAGAT AGACTGTTTT GTTCCACCTG ATTGTATGGG AGAAATTTTT GACCTTAGAA AGTGGAAATG AGGTTGCTAT GGAAACTGGT AATTCTGCTG CCACTCATAA ACTCTTCTGC AGGTGATGGT CTTTTAAGCC GTCCTATTTT TACTCAGGAG CCACATGATG TCATTTTTCC TTTGGATTTA TCAAAATCTG AGGTCATCCT GAATTGTGCT GCTAACGGTT ACCCTTCGCC TCATTATAGG TGGAAGCAAA	60 120 180 240 300

317

ATGGCACAGA ACTCGAG

(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 412 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:	
GAATTCGGCC TTCATGGCCT ACACAGTATC ACTAAAAGAT TTTCATTCGG AAGATCACAT TAGTAAAAAG ACTGAGGAAG TGGTTCTGAA AGATGGAAGA ATTGAAAGAC TAAAGTTAGA GCTTGAAAGG AAAGATGCTG AAATCCAGAA GCTGAAAAAT GTAATCACTC AATGGGAGGC AAAGTATAAAG GAAGTAAAGG CAAGAAATGC ACAATTATTG AAAATGCTTC AGGAAGGTGA AATGAAAGAT AAGGCAGAAA TACTTCTGCA AGTTGATGAA TCACAAAGTA TCAAAAATGA GCTCACTATT CAGGTGACTT CACTTCATGC TGCATTAGAA CAAGAAAGAT CTAAAGTGAA AGTATTACAA GCAGAGTTAG CCAAATACCA GGGTGGCAGA AAAGGGCTCG AG  (2) INFORMATION FOR SEQ ID NO:1310:	120 180 240 300
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 239 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:	
CTCGAGTGTG GTGGTATGTG AATTATATCT CAGTAAAGCC ATCACAGGGC AGAAGAAAAA GAGAAAAAGAA AAAGAAAAACC TTCGAGGAAG TCCAACAAAA AACATGAGGA AGAAAAAGGTG AGAGCCTGAG GATCCACACA GCAGGTACAG CAACTAACTG ACAGAAATTC TAGAGCCAGA CAACAATGAC TAATCAAACT AACCTCAAAA CAAATGATTA GGCCATGAAG GCCGAATTC	120 180
(2) INFORMATION FOR SEQ ID NO:1311:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 278 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:	
GAATTCGGCC TTCATGGCCT ACAAGGAAGC ACAAGGAGAA AATTATGATG AAATGGAGCA AAACAGGTAA GAGAGAGGGT CAGAGAAGTG AATGTGGGCC TTGATGCTGA AGCCATTGGA GGGTTTTCTG TTGAGGAGGA GTATGGGAAT GATATGATCT GACTTATGTT TCAAAAAGTG TACTCTAGCT GCTTTGTGGG AAATATNGGA GGGAGAGAGC AGAATCAAGG AGGCCATTTA AAATGCCATT GCAAATATCC AAGAGAGGCG GACTCGAG  (2) INFORMATION FOR SEQ ID NO:1312:	60 120 180 240 278

(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid

(i) SEQUENCE CHARACTERISTICS:

	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1312:	
GGCATTAAAA CTCACATAGG	TCATGGCCTA ATCACATATG GTAGAGATTT TATACAGAAT TTTAAAATGT AAACTTGTTC CATGGAAAAC TGCTTTCAGA GATTTTTAATA AAGTGTTTCT AACCTAAGCT TCTCAGAGCT TTTAATAGGC TTCTAACAGG CTAATAGTCA CCAAGAAGGG ATATAGTTCA CAGTGTTTTC CACAAATATT TCACCCCAGA	60 120 180 240 247
(2) INFORMA	ATION FOR SEQ ID NO:1313:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 311 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	) MOLECULE TYPE: cDNA	
(xi)	) SEQUENCE DESCRIPTION: SEQ ID NO:1313:	
TTAATTCATT TTTTCATCTT AAAGAAGTTA	TTCATGGCCT AGGGTCTTAG CTTTGGCTCT CCTTGCAAAG TTATTTCTAG ATGCAGAAGG TATAGGGGTT AGTCCTTGCT ATATTATGCT TGGTTATAAT TCCCTTGCGG TACTATATCT ATTGCGCCAG GTTTCCTCTG TCTCAAAAAA CCTTCCAAGAC AGACTTTTAA GATGTAACCA GCACAAAGCA ATGTCAGGGA ATGACAATAA ATGAGTCAGA TGAGCAAGAA GGCCCCAGAA CCCATGCCCC	60 120 180 240 300 311
(2) INFORM	NATION FOR SEQ ID NO:1314:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 261 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	) MOLECULE TYPE: cDNA	
(xi)	) SEQUENCE DESCRIPTION: SEQ ID NO:1314:	
GATCAAGAAG GAGATGGAGA TGGGAGNTGC	C AAACGCCCGC GATACTGTCA GAGATGGAGA AAGGTATGAC AGGAAGAGCA G ACGGGAACAG CACGAGGCAC TGGGAGCTGC AAACGCCCGC GATACTGTCA A AAGGTATGAC AGGAAGAGCA GATCAAGAAG ACGGGAACAG CACGAGGCAC C AAACGCCCGC GATACTGTCA GAGATGGAGA AAGGTATGAC AGGAAGAGCA G ACGAACTCGA G	60 120 180 240 261
(2) INFORM	MATION FOR SEQ ID NO:1315:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 326 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

(D)	\ Т	000	LOG		1 3			
W.	1	OPO	LUG	Υ:	I١	ne	۰.	r

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

CTCCA COMMON NOON CO.					
CTCGACTTGC ACGAGGAGTG	GCAGGATTAT	CTGCAGAGGG	ACCATTGGGA	CACCTACTAA	60
CCCCACCECC MOMENTAGE			caii iddda	CUGCIAGIAN	60
GGCCAGGTGC TCTTTAGGCA	CCCCTTCTTC	CACCAGCTTC	AGGCCTGTCA	CAGCATCAGC	120
TCCTCACAAC CCAAMCOOMC				CHICAGE	120
TGCTGAGAAG CCAATCTTTG	ACGTTAGAAT	CAGAAGGCAA	AAGGCCAGAA	CTGCTGGCAT	180
TTTTATABTT CACAATACCA	COMMONDER			414414	100
TTTTATAATT GAGAATAGCA	GCIIGIAAGI	GTCTGTGATC	CCTTGGGTCT	CTTCTTTTAC	240
TATTGACGCT TCTCTGTTTT	CTTTTTTTTCAC				2.0
THE CONTROL OF THE COUNTY	CITITICAG	AAGGGCTACT	AATGTTGTTG	TTATTAAAAA	300
TACAGTAGGC CTCTTTGGCC	CAATTC			· · · · · · · · · · · · · · ·	500
	OWNIE				326

- (2) INFORMATION FOR SEQ ID NO:1316:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 244 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

GAATTCGGCC	TTCATGGCCT	AACGTCACTC	ACTGTCCTTC	TTAGTATCTA	ATTCTCCTTC	60
ACCTAATAGA	ACAGCAAATT	CTTTGAGTTT	AGGATCCTTA	ATGCAGTGTA	AATATTGCCT	
TTTATCCTTC	TTCTCAGCTA	TOOTOTONAT	TO BE A A TO STORE	ATOCAGIGIA	TGGTGGCTCC	120
CCAAmccccm	CLCTCAGCIA	IGGICICAAI	TCAAATCATG	AGGACCATTG	TGGTGGCTCC	180
CGAGTGGCCT	CACTGTTCCA	CTCCTTCCCC	ACTGCGCTAC	AGTCCATTCC	CCAGTGTCCT	240
COMO						244

- (2) INFORMATION FOR SEQ ID NO:1317:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 149 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

GAATTCGGCC	TTCATGGCCT	AGAAAGGTTT	GCCTGGTAAG	ACTGAACTGT	TCATAGTTCT	60
TTAAATAAGC	TACAATATTT	CCTAATTGTG	TACCCTTGAT	THEACHCART	TCTTGCCCTA	120
GAATGCTGTT	TCTATCATTC	TTCATCGAG		111MCIGITI	ICIIGCCCIA	
		COAG				149

- (2) INFORMATION FOR SEQ ID NO:1318:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 302 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

GAATTCGGCC TTCATGGCCT AGTCAGCAAA GCAAGGGGAG GCAGACCACA GGCCTCATGA CTCTCACTGG AGTGCAATGG GACCCCCATG GGGTGAAAGC AGAGGAGTGA GCTGCTCTGA TGTGAGCACT CACTCTGCTT GCCATATAGT GAGTAGACAG GAGAGACCAG GGCAGAAGTA AGAAGACCCA TCAGAGGCTC CTCAGGAACC CGAGTGGGAG ATGGTGGTGG AACAGGGTTG TAGTAGTGGC AGTAGTGAAA AAATGATCAG GTTTTGGAAA TATTTGGAAG GTCGAACTCG AG	60 120 180 240 300 302
(2) INFORMATION FOR SEQ ID NO:1319:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 219 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:	
GAATTCGGCC TTCATGGCCT AAGAAAAAA GAAAGAAAGA AAAAAGAAAG TACAAGTTTA TAAAGTATTA TAGTGAAAAA TTCGCATTCT GGCTGATTTT AAGCCATTTA AAATTTATAT AAAACAACCT TCCATAAAAA TTTGACAGGT GCCCAGATGT TGCTTTCTCC ATTTATTTTT TGTTTTTTTT TAATCACAGT GGTCTTGAGG CAGGTCGAG	60 120 180 219
(2) INFORMATION FOR SEQ ID NO:1320:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 361 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:	
GAATTCGGCC TTCATGGCCT ACTGAGTTAG GTTTTATTAA TGCAGTTTTT ACAGATGAGG CTACTGTGAC ACAGAGGGCA TAAACTTGTC AAAGACATGC AGCAAACAGG ACAGACAAAT CTGAAGCCAG GTTGTCTAAG CTCAGAATCC ACACCTATAA CCGCTGTACC CCACTGCTTT TGCCAGCAGG AGCTCACGTA CTTAGGACAG ACAATCAGTA CAGTGCTAGG CTCACTGAAG GTGTTGAACA AATGTCTGTT CACTCTTTTT GTTCTCAAAA GTACCAGGAA AGGCCAGAAG AAAAAAACTAC AAGACTTAGA AACTACAATG GATCAGATCA	60 120 180 240 300 360 361
(2) INFORMATION FOR SEQ ID NO:1321:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 66 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:	
GAATTCAAAC GAAAGCCAGC TGAGAATACA GGAAACATGT TTCCAGCCAA ACCCAAAACA	60 66

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:	
GATTGAATTC TAGACCTGCA GCTACAGAAG TCAAGATTCC AAAACCAAGA GGCAGACCCA AAATGGTAAA ACAGCCTGT CCTTCAGAGA GTGACATCAT TACTGAAGAG GACAAAAGTA AGAAAAAAGGG GCAAGAGGAA AAACAACCTA AAAAGCAGCC TAAGAAGGAT GAAGAGGGCC AGAAGGAAGA AGATAAGCCA AGAAAAAGAGC CGGATAAAAA AGAGGGGAAG AAAGAAGTTG AATCAAAAAAG GAAAAATTTA GCTAAAACAG GGGTTACTTC AACCTCCGAT TCTGAAGAAG AAGGAGACGA TCTCGAG	60 120 180 240 300 317
(2) INFORMATION FOR SEQ ID NO:1323:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 106 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:	
GAATTCGGCC TTCATGGCCT ACTGTAAGGA GGAGATGAAA GAATTAGTAG AAAAGGTTTT AAAAAACAGTT ATTATAACTA TATTCCATAT GCTGAAGGCG CTCGAG  (2) INFORMATION FOR SEQ ID NO:1324:	60 106
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 257 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:	
GAATTCGGCC TTCATGGCCT ACTCCTTTAT TTCCTTTGTC TGTAGAATAA AGTCTTAGAA TAATATTCCT GTTAAGGCCC TGCTTATCCC AATACCGTAT CCATACTGAA CTTTCAGTTC TTTATATGCA CTCTACTCTC TGTCTTTCAG ATTTTTGCAG GTATTCCTTT AGAACACTCT TTCTCTTCCA TCTTATCGCC TACTCTTTGG GTTTCTGTTT AAACATTACA TTTCTCGGTG GGGGGGCTTA TCTCGAG	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:1325:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 78 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:	
CTCGAGACCG CAAGCACTTC CCACCTCATC CTTATTTCCT CTATCCCTTT TCATTGTTTT TTTCTCCTTT TTAAATTC	60 78
(2) INFORMATION FOR SEQ ID NO:1326:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 312 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:	
GAATTCGGCC TTCATGGCCT AGAATTGTCC TCTGTGGAAG GGACTTTCTT TTGGCCCTAG GCCCCTTCCT GCCCCTGTCG TCAGCAGAGA GATGGAAAAC TTGATGACTA GCTCCACCCT ACCGCCCCTT TTTGCAGATG AAGACGGTTC CAAGGAGAGT AATGATCTGG CTACCACTGG GTTAAATCAC CCAGAGGTTC CATACAGTAG TGGCGCCACA TCATCCACCA ACAATCCAGA ATTTGTGGAG GATCTCTCTC AAGGTCAGTT GCTTCAGAGT GAGTCTTCAA ATGCAGCAGA AGGCACCTCG AG	60 120 180 240 300 312
(2) INFORMATION FOR SEQ ID NO:1327:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 411 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:	
GCGATTGATT CTAGACCTGC CTCTCCTTCA AGCATTGCAG CAAACAATTG TACTGTGAAT ACGTCATCAA TTGCAACGTC TTCAATGAAG GGTCTTACGA CTACAGGAAA CTCGTCTCTT AATAGCACAT CTAACACTAA AGTATCAGCA GTGCCTACAA ATATGGCTGC CAAGAAAACA TCTACCCCCA AAATAAATTT TGTTGGTGGT AATAAGCTGC AGTCAACAGG AAATAAAGCA GAAGACACAA AAGGAACCGA ATGTGTTAAA AGTACTCCTG TCACTTCTGC TGTGCAGATT CCTGAAGTAA AGCAAGACAC AGTGTCAGAA CCAGTCACAC CTGCATCTCT TGCTGCTTTA CAGAGGTGATG TGCAGCCAGT GAGCCAGT TATGTGGAAG GGATACTCGA G	69 129 189 249 309 369 41
(2) INFORMATION FOR SEQ ID NO:1328:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 286 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	,

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

GAATTCGGCC TTCATGGCCT ACTTTTCCT TGGTCAGATC ACAATGCTCC TATAAATGTT TCACATAACA TGCTTACTTG TGGGTATACC CTCCTTATCT CCTCAGGGGC TAATTTTGGG AAGGGACTAC TGTCCTTACT TTAAAGTTAA ATATAAACTA AATTCCTTCC CTAGTTAGCT CAGCCTACGT GCAGAGATAA GCAAAAGTAG TTAACCTAAA AGATATCACC CTTTGGGGGG TGTCAGAGGC AAAATAGAGT CAGTCATGCT AAGCTCCCCT CTCGAG	60 120 180 240 286
(2) INFORMATION FOR SEQ ID NO:1329:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 340 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:	
GAATTCGGCC TTCATGGCCT AGGGGGATTG AAGATTTTTT GTAGGTGGAA GGCCTGAAGT GCGACTAGAG GGCAATAAAT TCAAGGTGGG AGACTGTCTG CTGATGTTCA TTCCACTGGG CTGTTTATGG ACTGGGCTGT TAGTGCTGGA GTGGCTACCC TGGGCAACTA GTGCATTTGG ACTGGAACTA CTTGGGGATA CAGTAGGCTT GGGAGTTGGG TTGGATTTAG AAATAAGTTT AGTTGATACT GAAGGCTTAG CTGACAGAGA GGGCTTGGGT GAGGCAGAAG GCTTAGGCGA GGGCAGGGGT TTAGGAGATG TGGCAGGTCT AGAATTCGAG	60 120 180 240 300 340
(2) INFORMATION FOR SEQ ID NO:1330:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 297 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:	
GAATTAAAGA GGGCGATATC ATCACACTCA CTAACCAAAT TGATGAGAAC TGGTATGAGG GGATGCTGCA TGGCCATTCA GGCTTCTTCC CCATCAATTA TGTGGAAATT CTGGTTGCCC TGCCCCATTA GGATGTTATG CTGGCTGGCT CGCCTCCTCT TGACCCAGAT AGTTACGGTT AACCACTGCT TTGGCAATGC TGCTTATAAC ACATCCCAAG TGCAGGCCGC AGTGGTCCAC GTCATCCAGC CCCACCAAGT GACTTTGGTT GACCTTGTGG CTCCCACAGG ACTCGAG	60 120 180 240 297
(2) INFORMATION FOR SEQ ID NO:1331:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 355 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:	
CTCGAGTCCG CTGAGCTGAG AAGCACTGCG ACTTTTCCGT GACAGACCAA CGATAGCTAC CATTTTGGCA CCAAGGCTAG AGCGCCGCTT TTTGCCACTG GTGCCCAAGG TGCCCACTGC AGTGTCAGAC TGGCTGCCAT CATTCTTCTC CAGTGAGCAC ATGTCTCCAC TGATGCTGGT GCTTTTTGTC ATGTTCTTCC CTGATATGCC CATTTGTCTG CTTTGCATTT TGGATGTAAA	60 120 180 240

180 240

GACACTGTCA GCCGATGGAT CATTAAAAGT GAGGACAAGA GTAAAAAGGA AAAGACAGAA AATGCATTTT AGATAAAACA TTTGGAGTAT AATTTAGGCC ATGAAGGCCG AATTC	300 355
(2) INFORMATION FOR SEQ ID NO:1332:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 438 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:	
GAATTCGGCC TTCATGTGCG GTGAAGGTCC TGTGATTGTA CAGTTAGCAC ATTTTATATG ACAGTATAAT CTTAAAAAAT AACATAGAAA CAGAAACATT AGAAACGTAA GTCACAGTTT GTGAGTATGT CATTTTTTAG GGAAAAATAA AATATAGTAA CGACTTATAGAA GCCCCAAAAG TTTTATATAA AAATGAAAAA GCTGTTTGGC AGTTAGGACT GACTGTAGCC TTCTGTCAAAA TCAGTCTTGA CAACTGTTAA AAGACATTAT CATCACAAAT AGGGCTGCAT TTCACTCTGT CTGTCAAATA CAATCAATAT ATATGACTTT AAGAAAGTGT GACCATTTTC CCAGAGTGAC ACCAACAAGA TGGTGGAATA GGAATTTTTG TTTAACTTTA CTCACCTCAC	60 120 180 240 300 360 420 438
(2) INFORMATION FOR SEQ ID NO:1333:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 309 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:	
GAATTCTAGC CCCACCCACT TTCTCAGACA TCCCCACCGG AGGATCCCAT CAGTCACAAT CCTCACTAAT TAGACCATTC AAATTCCCCA AAATAAAAAA AGGGAAAGAG GTATAGACTT ATCTTAAGGG TCTTAAGTTC TGGCATTTTT CTATTTAATA ATATATATTG CTATAAAATG GAATTACTAC CAAAATTTAG AAAATCTTTT AGCAGAAGAT ACAGCCCTAA TCTTACCACT CCAGTACAAT CATTATTGAC ATTTATGATG TACTTCGTTA TAGTATCAAA ACAATTCCAG TATGTGAAC	60 120 180 240 300 309
(2) INFORMATION FOR SEQ ID NO:1334:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 243 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:	
GCGATTGAAT TCTAGACCTG CCTCGAGCTG CCGTGTTTTT CATTTTAATT GTGTGACATA AAATGTAAAA TGTACCCTCT AAACCATTTT TTAGTGTCCA GTTTTGTGGT ATTAAGTACA TTCACATTAT TGTGCAACCG TCCCCACCAT CCATTCACAG AACTCTTTCA ACTTGCAAAA CTGAAACTGT ATGCATTAAG CAATAACTAT GCGTTCCTTG TTTCCTCTTG CCCAAACCTTG	60 120 180

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GAG	243
(2) INFORMATION FOR SEQ ID NO:1335:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 280 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:	
GAATTCGGCC TTCATGGCCT AATTCTGGGA AAACTGAGAG AAAAATCTGA GGCCATCCAG AAGGAACTAG AACAGACCAA GCAAAAAACA ATCAGTGCGG TTGGTGAGCA GCTCCTGCCC ACAGTCGAGC ACCTCCAGCT GGAGCTGGAT CAGCTAAAGT CAGAGCTGTC CAGCTGGCGA CACGTGAAGA CCGGCTGTGA GACAGTGGAT GCCGTACAAG AAAGAGTGGA CGTGCAAGTC AGAGAAATGG TGAAACTCCT GTTTTCCGAA ATAGCTCGAG  (2) INFORMATION FOR SEQ ID NO:1336:	120
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 281 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:	
GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGAAT TCGGCCTTCA TGGCCTAGAC TAATCTTACT GTAGAAATGA TGTGAGATTC TTGTTTGACT ATTTTAGAGC AGATTCGGTA TCTAATGGGA TTCCATCTTG ATGTACAGAG CACCTTCTAC ATAATGAATT TTGCATTTCA GATGGATGAA GCCTTTAACA CAGACAGAAT TTTAAGTATT GCATATTTCT GGAAGAAAAG CATTGATCAC ATCCTCCTTA GATATTTAGT AATACCTCGA G	120
(2) INFORMATION FOR SEQ ID NO:1337:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 172 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:	
GAATTCGGCC TTCATGGCCT AATATTTAGG TAAAAAGGTA AACTAGTACA CCTACCAGAA AAGATAAATA TTAATTTATT GCATCTCTGA CATGAGAAAA AAAGCCTTTA TGTTTTACTG TTTTTTTCTA ATTTTTCTTT TTCTTTTTTT TTTTCACATG AATGTTCTCG AG	60 120 172
(2) INFORMATION FOR SEQ ID NO:1338:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 235 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:	
GAATTCGGCC TTCATGGCCT ACTGTATTTC ATAGTGAAGT GTTCATAAAC TAAAGAGTCA TTGATTTGGT TTCCTGGCTA ATTAAAATCT GAATTCCATT TGAAGTTCCA TTGAAATCAT GGTTTTACTC TATAGCAGTG GATGTTTTTT CCCAACCTTT CTGATATTTT TTTCCTTCCT GAGACAGGGT CTTGCTCTGT CACCTGGGAT GGAGTGTAGT TGCACCAAAC TCGAG  (2) INFORMATION FOR SEQ ID NO:1339:	60 120 180 235
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 148 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:	
GAATTCGGCC TTCATGGCCT ACTTGTTTTT AAAGGCATAT GTTGTTTTAT TGTGCTTCAC AGGTACTGTA TCTTTTTTTA CAAATCTAAG TTTTGTGGCA ACTCTGTGTC AAGCAAGGCT ATTGGCCCCA TTTTCCCAAC AAGCACGC	60 120 148
(2) INFORMATION FOR SEQ ID NO:1340:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 257 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:	
GCCTGTGTGA AGTTTTGACT TTAATCTACC AGATCACTCC TTCACCCTCC ATAAAGATGT CTGAACCTGA CACTTCCTCA GGATTTTCGG GAAGTGTGGA GAATGGAACT TTTCTTGAGC TGTTTCCCAC ATCCCTGTCC ACGTCAGTGG ACCCATCCTC AGGCCACCTG TCAAACGTCT ACATCTATGT GTCCATATTC CTCAGCCTTT TAGCGTTTCT GCTTCTGCTT TTAATCATTG CCCCCCCAGAG GCTCGAG	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:1341:	
(i) SEQUENCE CHARACTERISTICS:	

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

GAATTCGGCC TTCATGGCCT ACTATAAAGT ACTCTCGCTG GTATTGTCAG TATGTGTGTT AACAACAATA CTTGGTTGTA TATTTGGGTT GAAACCAAGC TGTGCCAAAG AAGTTAAAAG TTGCAAAAGGT CGCTGTTTCG AGAGAACATT TGGGAACTGT CGCTGTGATG TGAGCTTGGA AACTCGAG GACTTGCACC AAACTCGAG	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:1342:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 268 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:	
GAATTCGGCC TTCATGGCCT AGTCCTTGAC TCTGGAGTTT TACAAAGCAG TCACATTTCA AATAAAAGTC TGGGAAAGCA ACACATCATC GCCAACTTTT AATTTTGCTA AATAAAGGATA TTAGAAAAAG AATAGAAAAT TGCAGTCCCT TACTGTTTAA AGAAAAAACCA AAAGAAGTTA AAAAAAAAAA AACCTCATTA TGTTGTCTTT GTTTTTGTTT TGTTTTTTTT CCTTGGAAAT CAGTGAAAGT TTGGTCAGCC ACCTCGAG	60 120 180 240 268
(2) INFORMATION FOR SEQ ID NO:1343:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 241 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:	
GAATTCGGCC TTCATGGCCT AGCCATTTAA TATACTAAAA CAGTGTTGTA AATTAACTTT GGTACAAATT GCCAGTCATC TCTAGATCAT TTTAAGCATT TTAAGAATAT TTATTATCAA TCTAAGTACA GAAGAATAAC TGCCAGCAGT GATTATTTGC TTTGGATTAG AGTTTTTAAA AATCCACCTC ACTGAAATGG TTATGTTCAT CACAGTTTGC AAGGTTTGTC TGTTTCTCGA G	60 120 180 240 241
(2) INFORMATION FOR SEQ ID NO:1344:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 313 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:	
GAATTCGGCC TTCATGGCCT ACCCATTCCT TCCTTCCTGC CTGGCCTGGG CCCCTCCTGC ACAGATGGCC TAGGTACCCA GCCTGGAGGC CAAGGCTGGA TTCCCAGAGT CTGCCCTGGT GGAGTGGGAA TAGCAGGTTC TCTGCAACTC AGGGGAGCTG CCCTGCAGGG CTTCCCACAT GTGCTCAGGC CCCTGTGCCA GGTCTGGTGA TGCTTCCTCC TTGCCTTTCA GGATCTCCTA TTGCACAGCA GACAAGATGC ACGACAAGGT GTTTGCATAC ATCGCCCAGA GCCAGCACAA	60 120 180 240 300

313

CCAGAGCCTC GAG

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

\-,\ <del></del>	
(A) LENGTH: 327 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:	
GAATTCGGCC TTCATGGCCT AGGCTTCTCT TCTGAATTGA TTGGTAGTGT TGTTATTTTC	60
TTGTTATTCA GTTTAACAAG TACATAATCA ACATCAGTGC TTGGGAAGTC AGGAGTACGA	120
GAGATAAATA AGAAGTATAT GATCTTTTCT CTTATTTTCT CTCAGTATAA GTTGGACCTG	180
TITTTCCCTT CATCTCTTT TCTTCAAGAA CATAATATCG GCTGAAGTGG AATGAGTATT	240
CAAATTGTCC AAAAAAATAT ACAAGTGAGG GAATTAATAA AATTTTTTGT AATTATAAAT	300
ATGTATATAT TGGGGGGCAG TCTCGAG	327
(2) INFORMATION FOR SEQ ID NO:1346:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 189 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
 (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:	
GAATTCGGCC TCATGGCCTA AATCCTTGGA AATACAATGA GACTCATCAG AAACATTTAC ATATTTTGTA GTATAGTTAT GACAGCAGAG GGTGATGCTC CAGAGCTGCC AGAAGAAAGG GAACTGATGA CCAACTGCTC CAACATGTCT CTAAGAAAGG TTCCCGCAGA CTTGACCCCA ACACTCGAG	60 120 180 189
(2) INFORMATION FOR SEQ ID NO:1347:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 262 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:	
011FF00000 FF0000000 100000000000000000	
GAATTCGGCC TTCATGGCCT AGTGGGCTTC AGGAAAGCAA AATATAAATA TTATGGTTAA	60
AGAATTTATA ATTAAGATTT CACCCATAAT TCTTAATACT GTGTTGACAA TCATGGCTGC ATTGTCTCCA AAAACAAAAG AAGATGGATC CAAAGATACG TCTAAGGAAA TGGAAAATCT	120
TTGGGGTATC AAATCGATTA ATGATTATAA CACTTGGTTT CTTGGTGTTG ACACGGCAAC	180 240
AGAAATAACG GAAAAGCTCG AG	262
(2) INFORMATION FOR SEQ ID NO:1348:	
(i) SEQUENCE CHARACTERISTICS:	

- (A) LENGTH: 333 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

GAATTCGGCC TTC2	ATGGCCT ACTA ATCTTA	*****			
	ATGGCCT AGTAATGTTA	AAACAAACGA	AATAAAAATA	GAAGGAAAAA	60
CITTCTGAGT TTCA	VAAAACA ACAGACTAGT	ስርጥርጥአአአርአ	A CTCTTTT A A A	3 C 3 3 mm 3 3 cm	
CTTACCATTO ON OR		ACT CTAAAGA	ACICITIAAA	ACAATTAACT	120
GITAGGATIG CAGI	TTATGAT TGGATATTAT	TTAATTCTGT	TTCTGATGTG	GGGTTCCTCC	180
ACTGTGTTCT GTGT	GCTATT AATATTTACC	`ammoon.o		0001100100	100
	JUNITARIA TARIALI	ATTGCAGAAG	CTTCATTCAG	TGTTGAAAAT	240
GAATGCTTAG TGGA	TCTGTG CCTCTTATGC	<b>ስጥስጥርጥጥክር</b> ክ	A A TOTA TOTAL	Normooms s m	
Charcenan mass		AIAIGIIACA	MATIMICIGG	AGTICCTAAT	300
CAAIGCAGAG TTCC	CCTCCC CTCCGCGCTC	GAG			333
					333

- (2) INFORMATION FOR SEQ ID NO:1349:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 553 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

GAATTCGGCC TTCATGGCCT AGGAAGACAG ATTTCACAGA GAGTGGGTTT CATGTTAAAT 60 GTCTGATTC CTTGTCGGAT GCCCCACAA GGACACTAGG TTTTGTGGGC CAATGTGTTA 120 TGTGTGTATG TAGGCAAGCA GGAGGGGTG GGTGGGCTTC TTTTTTTTTC TATTTTTTC 180 TTTTCTTTTT TGGTTGTGGA AGAACCACGT TAACCCCTCT AATTTCTTTA AAAAGACATA 240 AGGTTTGAAA AGGAGATTT AGGAAGAAGC AAAAGAAAAA AAATGGGATA CATATATTGC 300 ATCTGTAATC CAATCAAGCT GTCACTGAAG ACAAACTTGA TCTCTGTTCT CACCAGTTGA 360 CACACTCATC AGGCTATAGG TCAACTCTAA GTGTGGTGAC AGGTGATGGA CTCTATGCCA 420 ATTCTGATAC TGAATTTCT TTTGCTTATT GAAGCTTCAT TTTGTGTGTT TTAATTATGA 480 AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC 540	CAATTCCCCC	TOTORTOGOOD					
TGTGTGATTC CTTGTCGGAT GCCCCCACAA GGACACTAGG TTTTGTGGGC CAATGTGTTA 120 TGTGTGTATG TAGGCAAGCA GGAGGGGTG GGTGGGCTTC TTTTTTTTTC TATTTTTTC 180 TTTTCTTTTT TGGTTGTGGA AGAACCACGT TAACCCCTCT AATTTCTTTA AAAAGACATA 240 AGGTTTGAAA AGGAGATTT AGGAAGAAGC AAAAGAAAAA AAATGGGATA CATATATTGC 300 ATCTGTAATC CAATCAAGCT GTCACTGAAG ACAAACTTGA TCTCTGTTCT CACCAGTTGA 360 CACACTCATC AGGCTATAGG TCAACTCTAA GTGTGGTGAC AGGTGATGGA CTCTATGCCA 420 ATTCTGATAC TGAATTTCT TTTGCTTATT GAAGCTTCAT TTTGTGTGTT TTAATTATGA 480 AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC 540	OHAT I COOCC	TICATGGCCT	AGGAAGACAG	ATTTCACAGA	GAGTGGGTTT	CATGTTAAAT	60
TGTGTGTATG TAGGCAAGCA GGAGGGGTG GGTGGGCTTC TTTTTTTTC TATTTTTTC 180 TTTTCTTTTT TGGTTGTGA AGAACCACGT TAACCCCTCT AATTTCTTTA AAAAGACATA 240 AGGTTTGAAA AGGAGATTT AGGAAGAAGC AAAAGAAAAA AAATGGGATA CATATATTGC 300 ATCTGTAATC CAATCAAGCT GTCACTGAAG ACAAACTTGA TCTCTGTTCT CACCAGTTGA 360 CACACTCATC AGGCTATAGG TCAACTCTAA GTGTGGTGAC AGGTGATGGA CTCTATGCCA 420 ATTCTGATAC TGAATTTCT TTTGCTTATT GAAGCTTCAT TTTGTGTGT TTAATTATGA 480 AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC 540	GTCTGATTTC	CTTGTCGGAT	GCCCCCACAA	GGACACTAGG	TTTTCTCCCC	Charryman	720
TTTTCTTTT TGGTTGTGGA AGAACCACGT TAACCCCTCT AATTTCTTTA AAAAGACATA 240 AGGTTTGAAA AGGAGATTT AGGAAGAAGC AAAAGAAAAA AAATGGGATA CATATATTGC 300 ATCTGTAATC CAATCAAGCT GTCACTGAAG ACAAACTTGA TCTCTGTTCT CACCAGTTGA 360 CACACTCATC AGGCTATAGG TCAACTCTAA GTGTGGTGAC AGGTGATGGA CTCTATGCCA 420 ATTCTGATAC TGAATTTCT TTTGCTTATT GAAGCTTCAT TTTGTGTGT TTAATTATGA 480 AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC 540	TGTGTGTATG	TACCCAACCA	CCACCCCCC	2000000000		CAMIGIGIA	120
AGGATTTGAAA AGGAGATTT AGGAAGAAGC AAAAGAAAAA AAATGGGATA CATATATTGC 300 ATCTGTAATC CAATCAAGCT GTCACTGAAG ACAAACTTGA TCTCTGTTCT CACCAGTTGA 360 CACACTCATC AGGCTATAGG TCAACTCTAA GTGTGGTGAC AGGTGATGGA CTCTATGCCA 420 ATTCTGATAC TGAATTTCT TTTGCTTATT GAAGGTTCAT TTTGTGTGT TTAATTATGA 480 AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC CCCCATTCTC GAG		INCOCHAGCA	GGHOGGGGTG	GGTGGGCTTC	TITITITTC	TATTTTTTC	180
AGGATTTGAAA AGGAGATTT AGGAAGAAGC AAAAGAAAAA AAATGGGATA CATATATTGC 300 ATCTGTAATC CAATCAAGCT GTCACTGAAG ACAAACTTGA TCTCTGTTCT CACCAGTTGA 360 CACACTCATC AGGCTATAGG TCAACTCTAA GTGTGGTGAC AGGTGATGGA CTCTATGCCA 420 ATTCTGATAC TGAATTTCT TTTGCTTATT GAAGGTTCAT TTTGTGTGT TTAATTATGA 480 AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC CCCCATTCTC GAG	TITTCTTTT	TGGTTGTGGA	AGAACCACGT	TAACCCCTCT	AATTTCTTTA	AAAAGACATA	240
ATCTGTAATC CAATCAAGCT GTCACTGAAG ACAAACTTGA TCTCTGTTCT CACCAGTTGA 360 CACACTCATC AGGCTATAGG TCAACTCTAA GTGTGGTGAC AGGTGATGGA CTCTATGCCA 420 ATTCTGATAC TGAATTTCT TTTGCTTATT GAAGCTTCAT TTTGTGTGT TTAATTATGA 480 AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC CCCCATTCTC GAG	AGGTTTGAAA	AGGAGATTTT	ACCANCANCO	******	1110000000		
CACACTCATC AGGCTATAGG TCAACTCTAA GTGTGGTGAC AGGTGATGGA CTCTATGCCA ATTCTGATAC TGAATTTTCT TTTGCTTATT GAAGCTTCAT TTTGTGTGT TTAATTATGA AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC CCCCATTCTC GAG	ATTOTOTA A TO	G2.20011.111	MOOMMOMOC	<b>АМАНОАЛАЛА</b>	AAATGGGATA	CATATATTGC	300
CACACTCATC AGGCTATAGG TCAACTCTAA GTGTGGTGAC AGGTGATGGA CTCTATGCCA ATTCTGATAC TGAATTTTCT TTTGCTTATT GAAGCTTCAT TTTGTGTGT TTAATTATGA AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC CCCCATTCTC GAG	ATCIGTAATC	CAATCAAGCT	GTCACTGAAG	ACAAACTTGA	TCTCTGTTCT	CACCAGTTGA	360
ATTCTGATAC TGAATTTTCT TTTGCTTATT GAAGCTTCAT TTTGTGTGTT TTAATTATGA AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC CCCCATTCTC GAG  480	CACACTCATC	AGGCTATAGG	TCAACTCTAA	CTCTCCTCAC	A C C C C C C C C C C C C C C C C C C C	CMCTT CO.	
AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC 540	ATTOTO ATAC	MC 3 3 mmm ee	- Caricician	GIGIGGIGAC	AGGIGAIGGA	CTCTATGCCA	420
AAGTATAGTA ACACCTACCA TGCATACCAA AGCAATATCA ATATTTTCAA ATGCATCTTC 540	ATTCIGATAC	IGAATTTTCT	TTTGCTTATT	GAAGCTTCAT	TTTGTGTGTT	TTAATTATGA	480
CCCCATTCTC GAG	AAGTATAGTA	ACACCTACCA	TGCATACCAA	ስርር እስጥስጥር እ	A TO A DESCRIPTION A TA	1000100000	
	CCCCATTCTC	CNC		MOCMMINICA	MIMITICAA	ATGCATCTTC	540
553	ccconficto	GAG					553

- (2) INFORMATION FOR SEQ ID NO:1350:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 246 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

GAATTCGGCC TTCATGGCCT AGGTTTTTGT	TGTTTGTTTT	TAAAGGAGTT	AGACATAGCC	60
TAACAAACTG GAAATTGACA TTTCCATCTA	TOTAL COMMON COM		nonuningec	60
magazio di santi tonchi i i i CCA I CIA	TTTTTCTCCC	TTTTGAAGCT	AAATATGTCT	120
TTGTTATTTT GGTTCCTAGT CCCCATTACT	ACTTATTTTC	TGATAGTTCA	TCCACAGCAA	180
CTTCAGTCAG TTAGCTCACT AGTTCTTATG	CCTACACATT	CCCCC3 Cmmm	TOCOCOTA A A A	
CTCGAG	GCIAGAGAII	CCGCCAGITI	TCCCCTAAAA	240
CICGAG				246

(2) INFORMATION FOR SEQ ID NO:1351:

(A) LENGTH: 231 base pairs

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351: AAAGAAAAA TAAAAAAAAA AAAAAAAAA GGAAGTGTAA TGTCAGACAC ACAAGAAAAG 60 CAAATCAGTG TTGTAAGCTT AAAGTACAAT TTCAAAGGTC ATTACCAACA GCAGGGTTTT 120 TTTTATACTT TAAAAACATT ATGCTACATA TCATTGCCAT TTTCATATTT TGGGGTTTTG 180 CTACTCTTAT ACAATGGAAT CAATGGAAAT GTCATCCAGC CAGATCTCGA G 231 (2) INFORMATION FOR SEQ ID NO:1352: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 260 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352: TGAATTCTAG ACCTGCCTCG AGTTGCTCCC AGGAATAGTC CAAAGGAGCT GCTCTTGCCC 60 CTTTATACAC AAGCGCCAGC AACCAAAACC CTCCCTCCTG GCAATAAGGC CTCACTATAG 120 TTGCCCTCAT GCTTCCTAAG CTCTCTCTTG CTCTAATAAC TCTAATTCTG GGCCAAGCCC 180 AAGAGTGCCA TTCTTTCTTC CTAGCTGGGG ATGGAAAGCT GAGAGGGGCA CAAGGAGGGC 240 AAAAGTATCA CCCTATCGAG 260 (2) INFORMATION FOR SEQ ID NO:1353: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 482 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353: GAATTCGCCT TCATGGCCTA CTTTTCAAGT GAATGATTTG GTGTTTGAAC CTTCTTGATT ACCTTAAGAG GGAAAAATGA AGGAGAGGAG GGAACCATCA TCACATACCT TTACAGTTGT 120 GGAATGTTAG CCCACTATAG TGTTTAACTA AGGAAAATCT AATATAATAC ACTCCCAAGT 180 GATCTGAAAT GATCCGCTAT TCAGAATTCC AGAGAAAGAC ATATCCCTGC CAGAAGGGTG 240 TCCTTCATAA CCAAATTTGG TCTTCAGTCT GGTCGGTGCA TACTCAAACA GGAATCACTT 300 CCCTTAAGGA ACCTAAGGTA TGCAGTTGAG ATCAACTTAT TCCTTTTTGA TTTGTCCCCT 360 TAAAGCATCA ATCAGACGTG AATGCATCTT GTGACTTGGA GTTACTAGTA ATATTGAAAT 420 CTGAAACTTG GGGGATCTTT GAAGACACAT GGGATTAAAA GCTGCATAAT ATACATCTCG 480 482 (2) INFORMATION FOR SEQ ID NO:1354: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

	60
GAATTCGGCC TTCATGGCCT AATACCCAAA ATTGGCATGA CTACTTATAA AATAGTGCCT CCCAAATCCT TGGAAATATC GAAAGACTGG CAATCAGAAA CCATAGAGTA TAAAGATGAT	
CACGACATEC ATSCETTINGS CALLARAGE CARTEAGAAA CCATAGAGTA TAAAGATGAT	120
CAGGACATGC ATGCTTTAGG GAAAAAGCAC ACTCATGAGA ATGTGAAAGA AACTGCCATC	180
CAAACAGAAG ATTCTGCTAT TTCTGAAAGC CCAGAAGAGC CACTGCCAAA CCTTAAACCG	240
AAGCCTAACC TGAGAACAGA GCATCAAGTG CCCAGTTCTG TGAGCTCACC TGATGATGCC	300
ATGGTTAGTC CTCTGAAACC TGCTCCCAAA AATCTCGAG	300
MOSTIAGIC CICIGAAACC IGCICCCAAA AATCTCGAG	339

- (2) INFORMATION FOR SEQ ID NO:1355:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 203 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

GAATTCGGCC TTCATGGCCT A	CTTTTAGAT GCTT	TACATG CATAAATTCA	AATAATACAT	60
TAATAACCTT CCATACATCT T	TCTTTGTGT ACAC	CTTACT ATTTCTCTAA	CATACATTEC	••
TAAAAGTGGA ATTTCTACCC C	ANAMOR TOTAL TOTAL	OTTACT ATTICIGIAA	GATAGATTIC	120
TAAAAGTGGA ATTTCTAGGC C	AAAIGAITT ACAC	TITITI TGTTTGTTTG	TTTTTTTGTT	180
TTTTTGAGAC GGAGTGTCTC G	AG			203

- (2) INFORMATION FOR SEQ ID NO:1356:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 516 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

GAATTCGGCC	TTCATGGCCT	AGGAGAATCA	GGCAGGGAGG	TTGCAGTGAG	CCGAGATGGC	60
AGCAGTACAG	TCTAGCTTCG	GCTCGGCATC	AGAGGGAGAC	CGTGGAAAGA	GACCGACACC	120
GAGACCGTGG	GGAGAAGGAG	AANGAGGGG	AGGGGGAGGG	CCCCACACCC	BOROGORDAN	
TGATGTCTTG	CTGTAGGTAT	TCTTCCCCAT	TTC 3 3 TOTOTO	MOCHON CON	AGAGGGACAA	180
AACATCATTC	ACTOTOTOTO	TATIOCOLAI	TIGAATITI	TCCTCAGCAT	TATTTTTT	240
AAACATTTCTTCT	ACTOTOTOTO	TATACTACAC	TIGGATIGAA	TTTAATATCT	CATGAAGAAA	300
TARCHIICI	ACTTIGAAGC	ATGTGAATTA	GCATGTTTTT	ATAACAGCTT	TATTGAGATA	360
TAATTTACAT	ATATAAATAA	ACCGTTTAAA	GTGTATAAAT	CAGTGGTTTT	TAATGAGATA	420
TAATTTACAT	ATATAAATCA	ACCATTTAAA	GTGTATAAAT	CAGTGGTTTT	TAAAATATTC	480
ACAATGTTGT	ACGACCGTCT	TCTCAGTCAA	CTCGAG			516

- (2) INFORMATION FOR SEQ ID NO:1357:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 405 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

GAATTACTAA	TCAAGAAAAA	ACAAAATCAC	AAATCACTAC	CAAAGCAGTT	CATTGTCAAT	60
AATTTTTTTC	CCTTGTATTT	TTGTTTACTT	TTTGCGAACC	CTGAGCATAC	ATCCAAGTTG	120
CCCTAAATAT	ACGCACACCT	GAGGTTGTCT	TTATAGGAGC	TTTATGGTTG	CAAGTTTTGT	180
GTATAATCTT	TAATCATTTT	GAGTTGATTA	TTGTGTATCT	AGTACCATAA	GAGTCCTGTA	240
TTATTCTTTT	GCATATGGAT	ATCTAGTTTT	GGAAATCTTC	CCCGTTGTGT	CATTTTGGTG	300
GTGTTTTGAA	AAATGTGTTC	ATTCCATATA	AATTTTTGTT	TATTATCGAG	CACATTCATT	360
TTGCTCACTG	GTCTGTGTTT	CTCTGTGTAC	GCCAGTAACC	TCGAG		405

- (2) INFORMATION FOR SEQ ID NO:1358:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 328 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA .
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

CTCGAGTCTG GCTTT	IGTTIC AAAATGATTA	AGATTAAATG	ATGAAATAAT	ATTTTATAGC	60
CACTGCATTG GATAC	CTTGGA TTGTTTTCA	AGCATCTTCT	TATGACTAAA	TCTTCTGTTT	120
CATTCTGTTT TAAAT	CTAAA AAGTAAAATO	ATGGTCACTT	GGAATCTGCT	CTATATTTTA	180
ATTATAGTCT CTTCT	IGTTTA TAAACAATAA	CTTACACATA	TTTTTCATAG	TTTTAAGTAA	240
AGATTAAATA ATGCC	CATCTT AGAAAGGATO	TGTTTAACCT	ATATTATAAA	AGTTAGATAC	300
ACAATTTTAG GCCAT	TGAAGG CCGAATTC				328

- (2) INFORMATION FOR SEQ ID NO:1359:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 250 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
    - ..,
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

CTCGATGGCC	TAAGGCAGTC	TCCTGGAAGC	ATGACATTGA	TGCCCTGGGC	TCACCTCTTT	60
GTTTTGTTTT	CCTTCCACTT	TAGCGGGAAC	CACATCTTCA	AGGGCCGTGC	TGCCGGCATA	120
GCAGTGAATG	AGAACGGCAA	AGGCCTCATC	ACAGGTACGG	ATGGGAACTG	CCTGGCACCT	180
GGCAGCCAGG	CCAAGGTCCC	CTGGCGTCAC	CCCCCAGCTT	CAGGACCTCT	AGGCCATGAA	240
GGCCGAATTC						250

- (2) INFORMATION FOR SEQ ID NO:1360:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 206 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

GAATTCGGCC	TTCATGGCCT	ACGATTCTAT	<b>ጥጥርርጥጥአጥርጥ</b>	CCTTCCACAC	CTATTTAAGA	_
<b>ΑΤ</b> Ο ΑΤΩΤΩΤΩΤ	T. y d.	03.000.000.	TICCTIMICI	GC I I GCAGAG	CTATTTAAGA	60
m chaigici	TATTITICCT	GAGTCCTTTA	TAACCCTATT	CATATTTTCA	ATTGCTGATG	120
CCTCTTTGAG	CTACGAGTTC	TACTTTGTGC	ATAACGTTGA	CCAATTTCTA	CGTTTACTGT	
TTCTCCTTAC	TTCACTCATC	CTCC22		OGMATTICIA	CGITTACTGT	180
- TOTOCTIAC	TICACICATO	CICGAG				206

- (2) INFORMATION FOR SEQ ID NO:1361:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 377 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

GAATTCGGCC TTCATGGCCT CTACAAAGCC TCTGCTGTCT TGGGGAGACT TGGGCAGTGC CACTTGCCTG GCAGGCAGTG GCTGGCTTGG GGAAAATGGA TCTGATGAGG GGTTAACAGG	GTGGTGAGCT TTATAGATGA TGAGGAGATG CTCAGGTCTC	GGGACAGGAG ATAGGGGGAG TCATAAAAAT TAGGTTTGGG	AATGTGGACT GAACACTTCA GTAAGGATGG TGATCAGGGA	TTGGTTTCTG CTTCCAGGAC CACCTTTGGG	60 120 180 240 300
TCTGATGAGG GGTTAACAGG AGTGGGGATA GCTCGAG	CTTTTCTTTG	GTTCTTGGCA	TTTTGGCTGAG	TCCCAGTGAG GGAGTATTGG	300 360 377

- (2) INFORMATION FOR SEQ ID NO:1362:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 264 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

GAATTCGGCC TTCATGGCCT	AGTTAAAGGC	<b>ልልር</b> ሞስምርምርክ	TATTACTCAC		_
AGTCAGCAGA TGAGTGCCAG	TCCACCOOR	MOINIGICA	IATTACTGAG	GCTACAAGTT	60
AGTCAGCAGA TGAGTGCCAG	TCCAGCCTTT	TCTGGTATGT	TATTGTTAGA	AATATTGAGT	120
TCTAATGTTA CATCTGAGGA	AGTATGTAAT	TTGAGAATTG	TAACTTCTAA	GGGATTCACT	180
GCATCATAGC TATGCCTGTA	TGGAGTCTAA	CATATGACCA	ATACCAACCC	ATTA ATTCCACC	
ATTGAATTCT AGACCTGCCT	CONC		ATACCAACCC	ATAATCCAGC	240
	CGAG				264

- (2) INFORMATION FOR SEQ ID NO:1363:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 333 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

GAATTCGGCC TTCATGGCCT ACCCCTCCCC TAGTTCCAGT CCAGGTAAAC AAAAATTGAT TCTATTTTT CAAAACACCA GCCCCTTCAG ATGGCCTGGT TAATCTTCAT TAACATGTTA TCTTCATTAA CATGTTTATC TTCATTAACA TATTTCTCAG TGATAAGAAG GGCCCAGGGT TCAACATCCC ACTTTGCATC CATGCAGACA AGGGCTGTGG GAAGCTGTAA AACTGAAGAG GCGGTGAATC CAGGAGGGAT TCCCCAGATA TCCGTGAGTT GGTGTTTGAC ACGTCTTTCC TTTACTTTAC ACTTCCACTC GAG  (2) INFORMATION FOR SEQ ID NO:1364:	60 120 180 240 300 333
(2) INFORMATION FOR SEQ 1D NO:1364:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 358 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:	
CTCGAGGGGT CATGTTGTTG GGGAGAAAGA GACCACATCA CACACAGAGA GAACAAGTCT GTATTAGTTG CTTTTGCTAC ATAACAAACC ACTCCAAAAT TTAGTGGTTT AGAACAATCA CCTATTTAGT TAATGATTCT CTGGGTTGCA ACTTGGTCTG GGATCAGCTG GGCAGTTCTT TTGCTGGTCT CAGCTGGGTT CAGCTGCCTA TCAGCTAGGG AGCTCTGTTT CAGAGGTTGG TTGGCTATGG GTGGCAGGGA TCAAGGATGA CGGAGCCATG TGTCTCTTTT CCCTTTATTA CCCAGCAGGT TAGCCCAGAT CTTTTCCTTT TCTTTCCTAG GCCATGAAGG CCGAATTC	60 120 180 240 300 358
(2) INFORMATION FOR SEQ ID NO:1365:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:	
GAATTCGGCC TTCATGGCCT ACTTGTTCAG GGTATGGGGC TAGGATGAGA GAGAATNCCA CAGAGTATGA AGGAAGAGTG ATAGATCCAG ATGAGATACA GCTCAGAGTG CCACGCCCC AGAAGAGGA ATCAGGCAAG TACTGTCCCA AGGCAGCTGG AGGGTGAGGG CTGAGTGCCC TGGCTTCCTC ACTTGGGGAG ACCATGGGTC TCTGTAGAAA TTCCAATATA AAGGCAGGGA AATTTGACTG CATGGAGTCT TCAGGTAGAA ATGTTTCTCT TGCCTAAATT CA	60 120 180 240 292
(2) INFORMATION FOR SEQ ID NO:1366:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 335 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:	
GAATTGAGCA AGATACCTGG GTCATGATCT CTGAACAGGG TGAGAAACTT TATAAAATGA TGTGCAGACA AGGAAATCTG ATCAAAGACA GAAAAAGAAA ACTGACTACG TTCCCTAAAT GCTTTCTTGG AAGCGAATTT GTGTCATGGC TGTTGGAAAT TGGAGAGATT CACAGGCCTG	60 120 180

ATAAACATCA	GCACTTGGGA CAAGCATTAT TAGAAAATGG AATCATTCAC CATGTTACTG ATTCAAACCA GAACAGATGT TATATAGATT TCGCTATGAT GATGGAACAT AAATGAGATG CAGGACGTTC TCGAG	240 300 335
(2) INFORM	ATION FOR SEQ ID NO:1367:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 383 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1367:	
GCCTTTCCTC CAGCTCATCG TCAGGCATCA ACGGCTGGGA TGTATGCAGA	TTCATGGCCT ACTTTCTCTG TTTGCCTTGA CCTTTCTTTT TCATGTTAAA AAATGTCTGA TTACCCTTGG CTGCCCGTCA TTTAAGAAAG CGCCACTAGT GAAGCTGTGA GGGAGAGGGC TGCATTTGGT CCTGCCAGGT GGAGGAACAC GTACTAGGAG GTCTTTCCTC TCAGCCCATT GGATTTCCCT AGAGTCCTAC TGAGGCACCT GGGTGCTGAG TAGAGGAAGG GAGTCATGGG TCAGTCACCC TTTTCACACA ACCCCCTCTC TCCAGGACAC GCCTCGCCCC CCACCCTAAG CCCAAATCTC GAG	60 120 180 240 300 360 383
(2) INFORMA	ATION FOR SEQ ID NO:1368:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 347 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1368:	
AGCCTTGATG TACTAAAGAC CACTCTGATT TTTGGAGGGC	GTGACTGCGA TGGATCTCTT TGTTTCTGTT TGTTTCATTT TTGTTTTTGC GAATATGGAA CCTTGCATTA TTTTACCAGC AACCAAAAAG GAAAGACTGC AGAAAGCTAA AAAATAAAGC CTCGATGACT CCTGGTCTCC ATCCTGGATC CCAATGAATA ATATTCTGT GCCGCAAGAA GATGATTATG GGTATCAGTG AAAGATTGTG CCAGCTTCTT CTGTTGCTTT GAAGACTGCA GAACAGGATC GGAAGGATAC ACATACGCAT TGCCAAACTG ACTCGAG	60 120 180 240 300 347
(2) INFORMA	ATION FOR SEQ ID NO:1369:	
(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 243 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1369:	
TGTTAGGAGA AGGGCCTCAA	TTCATGGCCT ACCATTTCT ATGAGCAGAG GAGAGTCACA GGGCATCATG AAGAGGCTGG ACTTTATCTT GTCAGTAATG CTGGATGATA CAATAAGGGT AAAGTAAATG TAAAAATGAT ATTTGGCACA CATTTGGGTG AATAGAGGCT AACCAAGTCA CTATGTATTG GAATAATTCA AGTATAGGCC TGGGATACTC	60 120 180 240

243

GAG

(2) INFORMATION FOR SEQ ID NO:1370:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 256 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:	
GAATTCGCCC TTCATGGCCT AGAGGATTAC TTATTTCTCA GCATTCATCT GGTAACTTAA GCAGCATGAA GCAAGAGTTG CACTTTAAAA AATGACAAGA AAATAGCTAT TCATTTAGTC GACAGAGTAA GGCCCATCTC ATTTCCAGGA TCACTAGTTT CTGCTTATGA CGGGGTGAGC ATCCGCCAGC GCGGTGATTG GGAGGCGCCC CTGTGTCTTT AGGCTGAGGC AGTGCCCATA GCTGCAGTGC CTCGAG	60 120 180 240 256
(2) INFORMATION FOR SEQ ID NO:1371:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 332 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:	-
GAATTCGGCC TTCATGGCCT AGTGTAGCAA GCTTCCCCTT TGGGAGGGAT GTGAGAACAG AAGACTGAGG ATTGTCTCTA ACTCTAGGAT TCTTTGATGA TTGATTGGAT TGGGGTTTTG TGTTGTGTCT AATATTACGG ATGCTAAAAT GCCTGTACTT CCAAGGTGAT AGCCACCAAT AACCATACAC GTACTAGTCA TCCTAGAAGT GTTTTTATTT CTTCTGTTGG TTATCTTCCC TACCCCTAGG GTTGGTGTCT GTTTCCTGCT ACTTCAGGTT GGTTTCCCAC TGGGAGGCTT CTGCTGACAG AAAGCCCCAT GCTTTGCTCG AG	60 120 180 240 300 332
(2) INFORMATION FOR SEQ ID NO:1372:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 275 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:	
CTCGAGGGCA ACTGCAGAAG AAAAGATCAG TGAATCTGAT GACATAGCAG AAGAAACTAT CTAAAGCGAA GAAGACAGGA AAAAAAGCCC CAATGTGAAA TGAACAGATC ACCAGTGAGC TGTGGAACAA CCTATATGGG TTATAGGAGA CCCTAAATGA GAGAACAAGG GACTAAAAGA AGGATTTAAA GAAATAATAG TACAATTTTC TCCAAGTTTC ATGAAAACCG ATTGAATTCT AGACCTGCCT CGAGGCAGGT CTAGAATTCA ATCGC  (2) INFORMATION FOR SEQ ID NO:1373:	60 120 180 240 275

(i) SE	EQUENCE CHARACTERISTICS:  (A) LENGTH: 350 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) M	MOLECULE TYPE: cDNA	
(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:1373:	
CTAAAAAATA CA AGAAGGCTGA GO TCGCGCCATT GO AAAAAGATGA GO AGACCAGCAG CO	TCATGGCCT ACAAGACCAT CCTGGCCAAC ATGGTGAAAC CCTGTCTCTA AAAAAAATT AGCCAGGCAT GGCAGCGTGT GCCTGTAGTC CCAGCTACTC GCAGGAGAC TTGCTTGAAC CCAGGAGGCA GAGGCTGCAG TGAGCCGAGA CACTCCAGC CCGGGCGACT GAAGAGACTC CATCTCAAAA AAAAAAAAAA	60 120 180 240 300 350
(i) SE	EQUENCE CHARACTERISTICS:  (A) LENGTH: 273 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) M	MOLECULE TYPE: cDNA	
(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:1374:	
AAATAGAGAC TA TGAACTTCAA GA AAACGATAAA TA AATACAATGA AA	GGAGACATA TTACCACCAA AAGAACAATA ATTTCCTAGA AGCTGCAAAT ATACACTGC CTTACAGATA ATTTAAAGTA ATTGTTTTAA GGAATCTCAG AAAATACAG AGAATCAGTT CTATGAAATC AGGGAAACAA TAAATCAACA TTAACAGGT TGAAATCACT AAAAGAACCA AACAAATTTT GGGGCTAAAG TGAAATGAA AAATACTCTC GAG  ION FOR SEQ ID NO:1375:	60 120 180 240 273
(i) SE	EQUENCE CHARACTERISTICS:  (A) LENGTH: 332 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) M	MOLECULE TYPE: cDNA	
(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:1375:	
CTGGAGGTGA AG TAGAAGCAAA TI ATCAAAATGT GI CAACAAAGAT TG TGCCTGCAGC TI	AAAGATGCT GGGAAAAAAG TTGTTCCATG TAGACATGAC TGGCATCAGA GTTACCATT TCAGTATATG CTAAAAACTC ACTTCCAGAA CTTAGCCGAG AGCACATTG TTAAATGTGC ATATTGTATT TGAAGGAGAG AAGGAATTTG AAATTATGG GGTGTGATTG ATGTAAAGCG AAGTTATGTA ACTATGACTG GAAATCACT ATGAGAAAAG CTGAACCGAT GCAGTGGGCA AGCCTTGAAC AAAAAAGCAG GAAAAACTCG AG	60 120 180 240 300 332
	ION FOR SEQ ID NO:1376:  EQUENCE CHARACTERISTICS:  (A) LENGTH: 349 base pairs  (B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

GAATTCGGCC	TTCATGGCCT	AGGCTTCAGC	AGCTTCCTAC	GATCAGCCGA	AGAAAGCAGA	60
AGCTCTGGAG	GCTGCCATCG	AGAACCTCAA	TGAAGCCAAG	AACTATTTTG	CAAAGGTTGA	120
CTGCAAAGAG	CGCATCAGGG	ACGTCGTTTA	CTTCCAGGCC	AGACTCTACC	ATACCCTGGG	180
GAAGACCCAG	GAGAGGAACC	GGTGTGCGAT	GCTCTTCCGG	CAGCTGCATC	AGGAGCTGCC	240
CTCTCATGGG	GTACCCTTGA	TAAACCATCT	CTAGAGAGGA	CATCCCTGCT	GGGCTGCTGT	300
GCAGAGTATA	<b>AGATTTTGGA</b>	CTTGTTCATG	TCCCCTCTCA	CCCCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:1377:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 437 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

GAATTCGGCC	TTCATGGCCT	AAATATGTTG	<b>AAATAGGTTA</b>	GAAAAGGAGG	TGAATATTAT	60
GGGCTGTTGT	CATTTGTAAA	TTCTGCAGTA	ACTTCAGCGT	TGAGGGTTTT	TTTTGTTTTT	120
GTTTTTGTTT	TGAGTTTTGC	TTACTGAAAT	CAAAGAGTTG	TTACTCTGTC	TGTGGGTGTT	180
TAAGAGACAG	GATCTCACTC	TGCTGCCCAG	GCTGGAGTGC	AGTGCAGCCA	CGAATGCCTG	240
GGCTCCAGGC	CCTCCTGAGT	AGCTAGGACT	TACAGGCATG	CACCACCACA	CCGATTTTTT	300
TATTTTTTTA	TTTTTTTT	TTTTAGTTTT	TAGAGGTGGT	GGGGGGTCT	CACTGTGTCT	360
GCTTCTGGGC	TCAAATGATC	CTCCTGCCTC	AACCTCCCAA	AGTTCTAGAA	TTACAGAGGT	420
GAGTCACCAC	ACTCGAG		•			437

- (2) INFORMATION FOR SEQ ID NO:1378:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 267 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

GAATTAAAGC	ACTGCCTCTA	TTCAGGCTGC	CGAGGCACTG	CTTTAATTTT	TTGAAAGATT	60
CACCGCGTCT	TCTTGGATTT	CAAGAAAAAT	CCCGTTAAGA	ATTGAGGGGC	TCTCTTCTTC	120
CCCTCCTGAC	GTGAGTGTAA	CTCACTTCCT	GGTATGTCTC	CTTTCCTTTT	GGCCTACATC	180
CTTTGTCTGT	TAGGTGCTTC	CACATCCTTA	TGTCTTAAAT	GGCCAAAATA	CGTCACCCCC	240
ACTGCCAAAA	CAAACAGATC	ACTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:1379:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 305 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

GAATTCGGCC	TTCATGGCCT	AGAGGTGACT	AGAAGCGAAG	ATGGAGGTGG	CGCAGCACCT	60
CATCCCAACT	CATGCCACCT	GGGGAAGCAG	CTTCAGGCCT	TTCTGTTGTA	ACCTCAGCAG	120
AAACTTTGGG	GTTTATCCTT	TATCTTGCAC	ATGCCCCAGG	GAGGTAAAGG	GACTTGCCTA	180
GGTTCATGTA	CAAACTTTCT	GCTTCCAGAG	CAGGACTTTA	TTGGGACACC	ATAAGGTTGA	240
GGCTGGGAGG	TACCCAAGAA	TTCCTGGGGA	TGGTATGTCA	TTGACTGTGG	GTAGAGGGC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:1380:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 206 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

GAATTCGGCC	TTCATGGCCT	AGGCTTGGTT	GCCTCTGAAA	GGAGGGAAAG	TCTCTTGGTA	60
AATTATCTCT	TTTGTGCTGT	TTGCTGTTTC	TCTGCTACCG	TCTTTGCAGT	TCTCCTCTCA	120
CTGGTTGCAG	GCTTTCATAG	TAAGGTTTGG	CGAGAAATGT	TCCAAACATC	ACATTTTGGA	180
TTCTAGGCTG	TCACCCCAGG	CTCGAG				206

- (2) INFORMATION FOR SEQ ID NO:1381:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 496 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

GAATTCGGCC TTCATGGCCT	ACTCCTCGAT	GCTGATTCAT	ATCCTACTGC	CCATGGTTTT	. 60
CTGCGTCTTG CTCATCATGG	TCATGTGCTA	CTTGAAAAGT	CAGTGGATCA	AGGAGACCTG	120
TTATCCTGAC ATCCCTGACC	CTTACAAGAG	CAGCATCCTG	TCATTAATAA	AATTCAAGGA	180
GAACCCTCAC CTAATAATAA	TGAATGTCAG	TGACTGTATC	CCAGATGCTA	TTGAAGTTGT	240
AAGCAAGCCA GAAGGGACAA	AGATACAGTT	CCTAGGCACT	AGGAAGTCAC	TCACAGAAAC	300
CGAGTTGACT AAGCCTAACT	ACCTTTATCT	CCTTCCAACA	GAAAAGAATC	ACTCTGGCCC	360
TGGCCCCTGC ATCTGTTTTG	AGAACTTGAC	CTATAACCAG	GCAGCTTCTG	ACTCTGGCTC	420
TTGTGGCCAT GTTCCAGTAT	CCCCAAAAGC	CCCAAGTATG	CTGGGACTAA	TGACCTCACC	480
TGAAAATGTA CTCGAG					496

- (2) INFORMATION FOR SEQ ID NO:1382:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 280 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

GAAACTAGAC	AAGAAATCTC	AAGCCATGGA	GGAGCTAAAA	GCAGAGCGAG	AAAAACGAAA	60
GAACAGAACA	GCTGAGCTCC	TTGCCAAAAA	ACAGCCATTA	AAAACCAGTG	AGGTCTACTC	120
TGATGATGAA	GAGGAGGAAG	AGGATGACAA	ATCCAGTGAA	AAGTCAGACC	GCTCATCACG	180
AACATCATCG	TCTGATGAAG	AAGAGGAGAA	AGAAGAGATC	CCTCCCAAAT	CCCAACCAGT	240
TTCCTTACCT	GAAGAATTGA	ATCGGGTTCG	ATCTCTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:1383:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 262 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

GAATTCTAGA CCTGCCTCAG	TCTCCCCGTC	ATGCTCCCTC	TGCCCCGCCC	TCAAAAAAAA	60
ААААААААА ААААААААСА	ACAGCACCTG	TCCAGGCTTC	CTTAGGTACA	TCTTCTTTGT	120
ATCCATTGGG AGGCTCTGAG	ACTGGCCCCA	CTTGGTCCTA	AGAATCCCAA	GGTCTTTGGG	180
AGCGTCCAGC ATGTTAATTA	GCGTATCATT	ACATACTGCT	ATCCCTTTCC	ATTTCTTTTT	240
GTTCCATCAC TCTCCTCTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:1384:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 458 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

GAATTCGGCC	TTCATGGCCT	ACAGATTATC	TTACACTGAA	CTGATCAAGT	ACTTTGAAAA	60
TGACTTCGAA	ATTTATCTTG	GTGTCCTTCA	TACTTGCTGC	ACTGAGTCTT	TCAACCACCT	120
TTTCTCTCCA	ACCAGACCAG	CAAAAGGTTC	TACTAGTTTC	TTTTGATGGA	TTCCGTTGGG	180
ATTACTTATA	TAAAGTTCCA	ACGCCCCATT	TTCATTATAT	TATGAAATAT	GGTGTTCACG	240
TGAAGCAAGT	TACTAATGTT	TTTATTACAA	AAACCTACCC	TAACCATTAT	ACTTTGGTAA	300
CTGGCCTCTT	TGCAGAGAAT	CATGGGATTG	TTGCAAATGA	TATGTTTGAT	CCTATTCGGA	360
ACAAATCTTT	CTCCTTGGAT	CACATGAATA	TTTATGATTC	CAAGTTTTGG	GAAGAAGCGA	420
CACCAATATG	GATCACAAAC	CAGATGGCAG	GACTCGAG			458

- (2) INFORMATION FOR SEQ ID NO:1385:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 284 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

GAATTCGGCC	TTCATGGCCT	AAGTTTTCAT	AATCTTTCTA	AGCAAATAAA	TTGAGCATGC	60
AGGTTTTTTT	TGCTTTCAGT	AAGTATGTTA	AAGATATTTA	TTGTACTTTG	GTTTTCTTTT	120
CTTTTTTTT	${\tt TTTTTTTTT}$	TTTGAGACTG	AGTCTCTGTC	ACCCAGGGTG	GAGGGCAGTG	180
GCCCAACCTC	AGCTCACTGC	AACCTCCGCC	TCCCATGTTC	CAGTGATTCT	CCTGCCTCAG	240
TCTCCCGAGT	AGCTGGGATT	ACAGGTGTGA	GCCACCACGC	CCAG		284

- (2) INFORMATION FOR SEQ ID NO:1386:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 275 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

GAATTCGGCC	TTCATGGCCT	AGTAGTTGTT	CCATGCTGTT	GTTTTTTGTT	TTATCTTTCA	60
TTGCCTTTCC	CTCTGCAGTC	AACATTATGA	CCTGGGGACT	CCAGCATCCT	TCAAGCAAGC	120
CATTTCCGAA	GAAGGTGAAA	AGAAGCCAGG	ATGATTGGCA	CCTCCTCCTC	CTCCTCCTCT	180
TCTTCCTCTT	CCCTTGCCCA	GCCCCCTCCT	GTGCGTGTGT	TTCAGACAAC	ACAGGAGCCA	240
GCACAGGAGT	GGAAAATCCT	GTAGCGCAAC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:1387:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 296 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

GAATTCGGCT	TCATGGCCTA	ATTGAATTCT	AGACCTGCCT	CGAGCCTCCA	AAAAGAGTAA	60
ATAAATAAAA	ATAAAATTGC	CTTTAAACAG	AAACACACAT	AAAACAAAGT	TATATATTGA	120
ACCTAACCCT	GTATTTCCTC	TGGGAACAGT	GGTTCAGTAT	TCAATAATTC	AGGATTTGCA	180
GCAGCATAGA	ACTTAATGTA	ATGAGAGTCA	AGTATATATT	TCCCAGAACC	CTAAAACTAC	240
TGCATATGTG	AACATATCTT	ATTCATTGAT	TATGTGGGCA	TATAGTGAAA	CTCGAG	296

- (2) INFORMATION FOR SEQ ID NO:1388:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 548 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

GAATTCGGCC	TTCATGGCCT	ACAACTTGTT	CTAGCTTGTG	ATCCCTCAAA	GTTGGGTCAT	60
ACGTTAGTGC	<b>TAGATACTAG</b>	AAATTTTCAC	TTTTCCACTG	ATCAGAGAGA	CAGACATTAA	120

AAACAAAAAT	AGAAGAAAGG	AAAGCTTTCA	CCCTGCAGCT	TCTTAGCAGG	GAACAATTGT	180
			CATTTTCTTT			240
CTTGCCAGTG	TGACCATGCG	CATTGGTTTA	AAAAGATATT	CTTTCCTAAT	CAGGGCAAGA	300
			GAGGGAAGAA			360
			AGAAAATTCC			420
AAATATTGTC	AATATATATG	AACATATTTG	AAAAACTACA	GTTACAGTAT	ATTTACATTT	480
TTGGAAACTT	TTCTTCAGGG	CCAAGTAACA	TGTTGTATCT	TCCTTTTTGC	TTGTGGGGGC	540
TACTCGAG						548

- (2) INFORMATION FOR SEQ ID NO:1389:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 305 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

GAATTCGGCC TTCATGGC	T AATATGTTCT	TCACAGGGAT	GAGTCCTAAA	TATTTATCTT	60
CAGCCATGAC ATTTTTCTT	TG AATTCCAGAT	TTGCATATCC	AACTGCCAAC	TTGATATCTC	120
ACTTGGAAGA ACATCATCA	AC AAACCTAACT	CATCTGAAGT	TGGCTTCACA	TTCTCCTCCC	180
CTATCACTAA CTGCCTTTC	CC CACAGTATTC	CCCATTTCGG	TACATGGTAC	CACCATTTAT	240
CCAGTTGTTC AGACCTAA	C CCTTCTAATT	ATTCTTTTTC	CTATCGTTAT	CCCACATACC	300
TCGAG					305

- (2) INFORMATION FOR SEQ ID NO:1390:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 292 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

GAATTCGGCC	TTCATGGCCT	ACTGGGTTAT	TATTCTATTC	CGTTGATCTA	GCTAGTTTTA	60
AATTTTCTAC	CTTTTCTACC	TGTTTTTGTT	TAATAGTTTA	CTGTTTTTAT	CTGAACAAAA	120
TTCCTCTTTC	AATAGTTGAT	CCTGCTGAAT	GTCTTCCCGT	AGCATTGGGC	TTCCTCAGGT	180
AACCTGGCAT	TTTGGTTTGA	ATAGAAGGGT	TTTTATTGTC	CTTTTTTTCT	TTTTTTTTTT	240
TGAGATATTT	ATCTTTTCTT	TATTTATTTA	TTCGAGTCGG	AGTCTACTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:1391:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 217 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

GAATTCGGCC TTCATGGCCT AGGCGATCGT ATTAATTCTC AAGAAATTTC CAACAAATAC

CACCTGGTTA ATGTTTTCAT TAAGGGCACA CATTCTTGCT ATTGAGCCAA TGTTGTTGGT GATGGTGATC AAAGTCGCTC TGGCCAGGTC CTCTTTACTG ACAGCCTCTC GCTTCTCCTT GCTCATCATG TTTCCAAAGC TTGAAGCCAC ACTCGAG	120 180 217
(2) INFORMATION FOR SEQ ID NO:1392:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 438 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:	
CGGGAGGCTG AGGCAGGAGA ATCACTTGAA CCCGGGGGGT GGAGATTGCA GTGAGCCGAG ATCAAGACAT TGCATTCCAG CCTGGGCAAG AAGAGGGAAG TTCTGTCTCT AAGAAAAAAA AAAAAAAAAA	60 120 180 240 300 360 420 438
(2) INFORMATION FOR SEQ ID NO:1393:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 272 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:	
GAATTCGGCC TTCATGGCCT AAAACTTCCT AGGAGAAGGC AAGAGAAAGC CACCAGACCA GAGCCGAGGA CTAAACTTTA AGGTCGAAGA CGGCAGAGGG GCAGGTTCTC CCCTGCACAC CCCAAGGCCT CTCCTGCACC CGCGAGGCCT TCCTTGAGCG CCCAGGCCCC CGAAATGCCT GCCCTCCTTC TGACAAAAAGG AGGGGGTAGG ATGTGAAGGG GTAGTGCAAC CAACAATGTT TTTGTAAACA CAACAACAAG GAAATACTCG AG  (2) INFORMATION FOR SEQ ID NO:1394:	60 120 180 240 272
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 311 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:	
GTGAAATTGT CAAATAAAAA TATGAAAACT CAGCTGACAA GAGTAAATGT CCTTAAAGAC AAAACAATTG AAGAGCTCAG GCAATCTTTA GCAAATGTTG AAAGGATGAA AGGAAAGGCA AATGTTGAAA CGATGAAAGA GAAGGCAGTT GTGAAAACAG AAAACTTGAA AACTACATTA GACTCTGCAG AGCAAAAGG	60 120 180

GTCACTTCTG AGCCCCCAAC AGCAAAGAGC GCACCTGAAG AAGTATCAGG ACAAGAACAA GAAGTACTCG A	300 311
(2) INFORMATION FOR SEQ ID NO:1395:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 367 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:	
GAATTCGGCC TTCATGGCCT ACTGTGTGCT TAGTTTTAAA GACAACTTTG AAGTAAACAA TGAAATAAAA GATGTCACTA AAACCTCTGA GGCTCCTGAG CACATTTTGC TGATACAGTC TGTGGGGCTT GAGGAGACCG CATGTATTGT TCTTTCTTTT GTTTTTCTTC TGAGTTCTCA ACTGCGGAGA GCACCTGAAC CCCCTTTCCT TTTTGACCGC AGGCTGCACT TTGGGCCCCA GCCAGCCCTT TTTCTTTTTC TTTTTCTTTT GTGGTTCTTC CCTGGAGCGA CTCTGGGGAG TCCTGGATAT CCCGCCTGCC CCTTCCCCTC AGCCCCATGC TTGTTCCAAC AGTCTCCACA GCTCGAG	60 120 180 240 300 360 367
(2) INFORMATION FOR SEQ ID NO:1396:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 333 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:	
GAATTCGGCC TTCATGGCCT ACTTGGAAAC GAAAGAGGGC CCAACCTACA ACTAAGAAGG GACAAACCTT GAACTAAGTA AGACCTTACA CACCCAGAAA GAACACTGGG CCCTCCTTCT TCAGGGACAA TGCAGTAGCC ACTTGGCTTG TGGAATTTAC TGAAGGCTAT TTCCTGTAAC TTGCTAGTTA ACTTAGTTTT GTATTTCAGG CAGAGGTGCG CTCTGTAATG TTGGGCCTTT GACTTCACAG TACTGGAGAG CTGTTCACAC AGATGTTTAG ACCTTTCTCT TTTCTTCTTT CTCAACAACT CTTATCTCTC GAG	60 120 180 240 300 333
(2) INFORMATION FOR SEQ ID NO:1397:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 356 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:	
GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCGAGAT ACAGCAGCTG CTGCAGAACG TCAAGTCTGA GTTGGAGATG GCCCAGGAAG ACCTGTCCAT GACCCAGAAG GATAAATTTA TGCTCCAGGC AAAAGTGTCG GAGCTGAAGA ACAACATGAA GACCCTGCTC CAGCAGAACC AGCAGCTCAA GCTGGACCTA CGCCGCGGCG CGGCCAAGAC GAGAAAGGAG CCGAAAGGCG AGGCCAGCTC TTCCAACCCT GCCACGCCCA TCAAGATCCC GGACTGCCCA GTTCCCGCCT	60 120 180 240 300

CGCTGCTGGA GGAGCTGCTG AGACCACCGC CCGCCGTGAG CAAGAGCCCC CTCGAG

356

(2) INFORMATION FOR SEQ ID NO:1398: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 447 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398: GAATTCGGCC TTCATGGCCT AATTCTATGA GGTATTATTA TCACTATTTT ACAGATGAGT 60 AAACTAAGGC TCACAGAGAT TAACTGGCAG AACTGAAATT CTCCATATCT TTTTGATTCC 120 AGATTTATTC TCTTAATCAT GATATGATTT TGTCTCATAT AATCCAATAC AATAAATAAG 180 GAGGTCAGGC AGTAGGAGGT GAAGTTGGAG AGACTGGGAG ACCTATCAGG AGGGGTCATT TATGCCTGGC TAGGAGTTTG GACTTTATGC TGAGGCTATG GGAGCACTAT TAAAGTGATT 240 300 CTAGCACTGC AAAGTTATGA TTAGGTTTAT CAGCCAAAGG AAAAAAAAAG ATCTTGGTGG 360 TCACAGTGCA GGTAGATACG ACATAATCGA GAAATGTGAA GAATGCAGAA TCAAGAGTTT 420 GGTGCTGGAC AGAGAGAGGA ACTCGAG 447 (2) INFORMATION FOR SEQ ID NO:1399: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 428 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399: GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACTCTTT TAAATTTTCT GCATTTGCCT 60 GAAAAGCACC CCTGTAAGAA TAGATTTCTC ATGGCTCTAA AAATTATTCC CAAGAATACC TTACTTGGTT CAAAAGCAGA CTGTTTCTCT TCATTTCATC TCAAATCAGA CTTCTGGGCA 180 AGATGTTCTT TAGAGTAAGC AAACCTACAA CCTAAAAATC TCTTCAAGAG GCATCTCTGG 240 TCTTGTGACA AGACCTCTTC AAAAACCCAC AGTAAAACTC CCCTCCCTCC AGTTGGCCAC 300 CAGTCTGCCA CCAAACATGA ACAAATTCTG CTGCTAATCG GTTTCCCTTG TGATCTGGTT 360 CCTGAGGTCT TCGGATCTGT GCAATGAATT ATTTATTGTT TTATTAAACC GACAGTGGTG 420 TGCTCGAG 428 (2) INFORMATION FOR SEQ ID NO:1400: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 276 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400: GAATTCGGCC TTCATGGCCT ACTAGACCTG CCTCAGGGTG TTCTGTGGTT TCAGGTGGAA 60 GGTGGAGGGC CTCGGAGACC AACTGTGAGT TAGGCGGGGT TTAGAATCTG ATGGGAAGAG 120 GGCAGAGACA ACAGGTTCGA AAGAGTCAGG GCTCCTGGGA CCTGGGAAGT AAAGAGTAAA 180

CCTGGGGCAG TGGGTCAGGC CAGTAGTTAC ACTCTTAGGT CACTGTAGTC TGTGTAACCT TCACTGCATC CTTGCCCCAT TCAGCCCGGC CTCGAG	24) 27)
(2) INFORMATION FOR SEQ ID NO:1401:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 316 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:	
GAATTCGGCC TTCATGGCCT AGCCACCGTG CCTGACCTAC TTATTCTTTT TCCTGTTCAG CATCTAGTGT ATGATACGAT TTGCTTATTT GTTTATGTTT CATCATCTGT TCCCCACCCT CAGCCCTGGC CCCCTTGCTG GAACGCAAGC TCCAGGCAAA GCTATTTCAC CGTTGCTGTT TTCCAAGGGC CTCGAACAGT GCCCGGCACA TAGCAAATCC TCAGTGAACA TTAGAGGAAT AAGTGATTCA AGAATAGAGC TGTTAGAAGG TGTTCTGGAG GAAGACGCAT CCGGCTTCAT CCCTGGCACC ATCGAG	60 120 180 240 300 316
(2) INFORMATION FOR SEQ ID NO:1402:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 342 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:	
GAATTCGGCC TTCATGGCCT AAATTCTCCA GCAAAATGAG GATGAAAACC AGGAAAGAAG AAGAAATGAG ATCCATAAAA CAGTGGACCT TACTTAGGAT GTCTCATTCT AGAGTGACAG CCAAAAAGGGT ATCTCACCCT AGAGTGACAG CTATCCAGCA GACTAATTTC AGATGAGAGC ATACTGTCTC GGGAAGAATGT GCATTCAGTG CCATAGATAG TATCACTGAA GAGCTGGGAT GCTTGAGAAG ATTATTTAGT CAAGAAAAAA GAAAGACAAA TCAACAATAT GTCAAAAAAAT TCAGGTCCAA TTATAGAGCA AAAGGGCTCG AG	60 120 180 240 300 342
(2) INFORMATION FOR SEQ ID NO:1403:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 333 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:	
GAATTCGGCC TTCATGGCCT AAGGCTAAAA AGAAGGAAAA AGAAAAGGAA AAAAAGGAGG AGGAGAAAAT GGAAGTGGAT GAGGCAGAGA AAAAGGAGGA AAAAAGGAGGA AAAAAAGAAC CTGAGCCAAA CTTCCAGTTA TTGGATAACC CAGCCCGAGT TATGCCTGCC CAGCTTAAGG TCCTAACCAT GCCGGAGACC TGTAGATACC AGCCTTTCAA ACCACTCTCT ATTGGAGGCA ATGGCCCAAA AATCGAGGGG GAGGTAACTC GAG	60 120 180 240 300 333

#### (2) INFORMATION FOR SEQ ID NO:1404:

- (i) SEQUENCE CHARACTERISTICS:
  - . (A) LENGTH: 422 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

GGGCCCTGGG CCCCAGCCCC CI	AGCCCATCC	GTGGCCCAGG	CACTGGGGG	CTGAGGTCCT	60
CTGAGAAGGG ACACAGGGCC GC	GGGGGCTCT	CTCAGCCCAT	CAGCAGGAGA	GGACTGACTC	120
CAGAAAAATC AGCGTTTGTA CO	CCACTCAGG	CTGCCAAGAC	CTGTGTCCGT	CCTTCCAAGC	180
TCAACCTTCA GAGTTCATGA GO	GCCCCTTGC	CCAGAATGTC	CACAGAGTTC	ATGAGGCCCC	240
TTGCCCGGAA TGTCCACATT TO	GAAACCTCC	CAACACCGAG	CCCCATTTCA	AGTATAACCA	300
GGAGGGAAAA TGGTGCTTGA AA	ATAAGCATG	CCACAAAGGA	AAACCTGCTT	TCTCGAAATG	360
GGCCCTGGCC GCCCAGGCCC TO	GACCTCCCC	GGCCAGGATG	GAACGTTCCA	GAAACCCTCG	420
AG					422

- (2) INFORMATION FOR SEQ ID NO:1405:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 314 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

GAATTCGGCC TTCATGGCCT	ACTECCETTE	3 3 3 000000 3 003	mamma amaa s	G11010000	
	ACTOGGGTCC	MAACIGGAIA	ICIIGGIGGA	GAACATGGGG	60
AGGCTCAGCT TTGGGTCTAA	CAGCAGTGAC	TTCAAGGGCC	TGTTGAAGCC	ACCAATTCTG	120
GGGCAAACAA TCCTTACCCA	CTCCARCARC	mmcccmcmc			
GGGCAAACAA TCCTTACCCA	GIGGAIGAIG	TTCCCTCTGA	AAATTGATAA	CCTTGTGAAG	180
TGGTGGTTTC CCCTCCAGTT	GCCAAAATGG	CCATATCCTC	AACCTCCTTC	TECCCCCACA	240
MMCM3 0MC03 333 03		ouccrc	MIGGICCITC	TOGCCCCACA	240
TTCTACTCCA AAACATTTCC	AATTTTAGGC	TCAGTTGGGG	ACACATTTCT	ATATCTACCT	300
GATGGACACT CGAG					
GNIGGMCNCI CGMG					314

- (2) INFORMATION FOR SEQ ID NO:1406:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 299 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

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GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCGACTGCCC	CAAACCTGAC	60
CCNECORONO	3.000003.000					
CCATCCTCAG	ACCCCCACCC	CCGTCACCGC	TCCTCCCAAT	GATTCCTCCC	TCTGTCAGTC	120
CTCCTCTNCT	TTCCANARCO	magagama ama				
CIGCICIACI	TICCAAATCC	TEGEETGETE	CAAACCTGAC	CCATCCTCAG	ACCCCCACCC	180
CCCTCACCCC	TO CTO COOR BY	03 mmonmoon				
CCGTCACCGC	ICCICCCAAI.	GATTCTTCCT	TCTTTGATCC	TGCCAACTTT	TCCCCAACAG	240
03 000m3 3 ma						230
CACCGTAATC	CTCCCCCAAA	TCATCACAAT	CCTCCACCAT	ACAATCCCCC	CTTCTCCAC	299

(2) INFORMATION FOR SEQ ID NO:1407:

(A) LENGTH: 199 base pairs

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:	
GAATTCTAGA CCTGCCTCTC GCTGGAAATC AGCGTTGTAA GATGGACGCC CTGCTCAGCA	60
GAGCTCATCT TTCTAGAAAG GCACCTGGCC TTGGAAGGCG AGTGAGGAAC TGTCATAAGG	120
ACTITITCTT CCCATGTTGC TTTTCAGGAA AGCTTTCAGG ATGTGGAAAT GATGGTTCAG	180
CTATTGGATG AGGCTCGAG	199
(2) INFORMATION FOR SEQ ID NO:1408:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 220 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) Totoboot. Ifficult	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:	
GAATTCGGCC TTCATGGCCT AGTGATCCAG AAGAATTACC ATTAACTTTA TTTCAGAATT	60
TAGACTICCA AATCAGGTTA ATCCTCCAAT TAAAAGAAAG ATTCAGAGTG AATTTTTTAA	120
AAGGCAAGGC AGTTATATGT TGCTTACAAG AAACTAAACA TAAAGGCACA GATAAGTTGG	180
AAGTAAGAGG GAAAAAGACA TGCGAATACT AAGTATAGAG	220
(2) INFORMATION FOR SEQ ID NO:1409:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 235 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
,,	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:	
GAATTCGGCC TTCATGGCCT AGATAAGCCC TTCAGAAACA CATGCACTGT TAATTCTGTT	6
TTAAATATAA TAAAAACCAT TTCACTTTGA CATTACCTAT TAAGTTTTAC TGAAAGTCAA	12
AAGGCCTACT TACTGTGACT TCCAAAAAAG TATTTTGATA ATATTTTGAA AGAAATAAAT	18
AATTTCCCTT TGCATGAAAT TAAAAGCCAT GATAATAGGG AAAACATTAC TCGAG	23
(2) INFORMATION FOR SEQ ID NO:1410:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 577 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

GAATTCGGCC	TTCATGGCCT	ACCCACGTAA	CGGCTTGGCT	GGGCACCCCC	GCTTGGCTTG	60
GTGGTCCTGG	TTTGGATTGG	CTTTACCCTG	GCATTCCTTT	GCTGGGCTTG	ACCTTTTCTT	120
GCTGGGCTTG	GCATTCCCCT	GGCTGGGCTG	GGTGTTTCCC	CGGTGGGGCG	TGCACTTTCC	180
CTGGGTGGTG	GAGGGGGCGT	${\tt GGGCTCTCCC}$	CGGGTGGTGG	GGGGACGTGG	GATCTCCCCA	240
GTTGGTGGTG	GGGGAGGGGT	CGTGGGCTCT	CCCAGGGTGG	GGTTTTGGCT	GGGATTGACC	300
				TTTGGTGAAA		360
				TGGTGGCTGA		420
AAGCTGGCTG	CCTCCCCTAT	GAAGAAGCCC	TTTGGCTTCA	GGGGCAAGAT	GGGCAAGTGG	480
				ACAACATGGG	TGCTTGGAGA	540
GACCACGACG	ACAGCGCCTT	CACGGAGCCC	ACTCGAG			577

(2) INFORMATION FOR SEQ ID NO:1411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

GAATTCGGCC	TTCATGGCCT	AGGGATGCCT	CTCAGTGACC	CTTATATGTC	AGGTATGAGG	60
CGGATGGGGC	ATCTCTCTAG	TCCTTTCTAG	GGTTTTTACT	CTTCTAGTCC	CTTCAAGGGC	120
TGAGTGCTCT	GACTTTATGT	CTTCCCACGT	AGGCGTTGAC	CCTGCACTAT	CAGATCCTGT	180
GTTGGCCCGG	CGCCTTCGGG	AAAACCGGAG	TTTGGCCATG	AGTCGGCTGG	ATGAGGTCAT	240
	GCAATGTTGC					275

(2) INFORMATION FOR SEQ ID NO:1412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

GAATTCGGCC	TTCATGGCCT	AGTTTTATTT	TGCACTTGGA	AATATGTCAG	AAATCACTTG	60
AAGGCAAATA	AGATCTGGCC	CTCTGCAGAG	TTAAGTGGCT	AACATGCCCT	AGATCTCCAG	120
GCTTAGAGGC	TGCCCCTTTG	GTACCCATGA	TTCTCCAGGC	CTTTCCAGGG	CAACATTGTC	180
CAGCATCTCT	CTCTCTCCTC	CCGCCGTCTT	CCTTTGGAAG	TTTGACTCTC	ATGTGTGGTG	240
CCCGATCCCT	AGGCCACCTG	TGCCGGCCAG	CCCCTGAACA	GATAAATCCT	ACTAAAGGTT	300
AATCCCAAGC	ACAAGCTTTG	GGCTGGTCCT	TCTGGGTTGA	TTGGCTTTCT	CTCTCTCTCT	360
CCTTTTTTGA	GATGGAGTCT	CCTTCTGTCG	CCCAGGCTGG	AGTGCAGTGG	CACAATCTCG	420
ACAATCTTGG	CTCACTGCAA	CCTCTGCCTC	CCGGGTTCAA	GCAATTCTCC	TGCCTCAGCC	480
TCCTGAGTAG	CTGGGATTAC	AGGTGCCCGC	CACTGCTTCT	GGCATACTCG	AG	532

(2) INFORMATION FOR SEQ ID NO:1413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

GAATTCGGCC TTCATGGCCT	AGGCATCCAG	GACAAAAGTT	TGGAAAACAA	AATAATGGAA	60
CTAAATAGTA CTAACCAAAG	TATAGGGTGC	TTTATGATTT	ACAGAACTCT	CTTACAGGCA	120
GTATGTTGTT CAGGCGCCAC	TAGAACCCAC	GTAATGGCAG	AGGCTTCCTG	TTCCATGTTT	180
AAAAACCTTT CCAAGGCTTT	TCATTATTTT	CTTATCTGTG	GTACCCCTAG	CTTCCTGTGC	240
TCTAGACACA CTGGCCTACC	TTCAACTTCC	TTGACCAGTG	TAGCTTACAG	TGTAAGCTTA	300
CCCCCGCCC CCACCCTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:1414:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

GAATTCGGCC TTCATGGC	CT ACATGAACGG	AAGAGTGGAT	TATTTGGTCA	CTGAGGAAGA	60
GATCAATCTT ACCAGAGGG	GC CCTCAGGGCT	GGGCTTCAAC	ATCGTCGGTG	GGACAGATCA	120
GCAGTATGTC TCCAACGA	CA GTGGCATCTA	CGTCAGCCGC	ATCAAAGAAA	ATGGGGCTGC	180
GGCCCTGGAT GGGCGGCT	CC AGGAGGGTGA	TAAGATCCTT	TCGGTAAATG	GCCAAGACCT	240
AAAGAACCTG CTGCACCAC	GG ATGCTGTAGA	CCTCTTTCGT	AATGCAGGCT	ATGCTGTGTC	300
TCTGAGAGTG CAGCACAGG	ST TACAGGTGCA	GAATGGACCT	ATAGGACATC	GAGGTGAAGG	360
GGACCCAAGT GGTATTCC	CA TATTTATGGT	GCTGGTGCCA	GTGTTTGCCC	TCACCATGGT	420
AGCAGCCTGG GCTTTCATO	GA GACACCGGCA	ACTCGAG			457

- (2) INFORMATION FOR SEQ ID NO:1415:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

GAATTCGGCC	TTCATGGCCT	AAAAATATCT	AGTCACTGTT	CTGTTTTACC	CATTCTTTTA	60
AACTTTGTTT	TTCAGTTTCA	GTCAGGCTTC	CAAGAAAACT	GATAACATTT	TGATTGGTTG	120
GTTTCTCTTA	TATCTTTTTC	ATTTCACAGT	ACATTGTGAT	TTAATGATTT	ATCTCTTAAA	180
TCTTTTTCAG	TTCATAGGTT	CCTCCTGTCT	CTTTCTTTTT	CCTTGCACTT	CATTTGTTGC	240
AGAACCTTTG	TCCTGTGGTT	TCGCACAGTC	TGGAGGAATT	GGGGAAAGTG	GCTGTCTAAA	300
CTGGTTCCCT	CCTTCCCATT	ACTGCTGCAA	TCAAGATGTT	AGGGGGCCTA	CAAGCAATAG	360
AAGCATCCTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:1416:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:	
GAATTGGCCT TCATGGCCTA GTCATTTGCT TTTATATCAG ATATCTAATT AATCAAACTT TCTGGTTAAG TGCCTCCAAT TATTAACAAT CCTGCTCAGA GTTAAGATTA GCATCCAAGG ATTTTCCTCC ATATTTCTTT TCAGAGGCAA TGGAATTTAC TAGTTTTTTA GCTCTCAAC TTTGGCTGAT GGTTTAGTG GTGGTTATGC TATCTTCAGT AGTTTTGGGGA TCGCTCGAG	6 12 18 23
(2) INFORMATION FOR SEQ ID NO:1417:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 308 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:	
GAATTCGGCC TTCATGGCCT AAGAAAGGTT AAGTTACTTG CCTGAGGTAA CTTAGCATTG ATAGAATTAG GATTTGAACC TGGGTAGTAT GACTCTTAGG TCCCCATGAG CTGGCACACA GGTTGCCAAT CCACTGATA ACCTTCCCAT CACTGGGTCA GAGAGCCAAG GAGCAGAAGG GGGATAGAAC TTCCCCAGTA CCAAACTAAG GGGCTGAGCT GGGATCGCAA CCACAGGTTC TGTTCCAAAG CTGGGCTCT TTCGACAAGG CCATGCCCGC CTTGTCTCTT ATGCATGCTC CACTCGAG	60 120 180 240 300 308
(2) INFORMATION FOR SEQ ID NO:1418:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 174 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:	
GAATTCGGCC TTCATGGCCT AAACAAACAA AAAAAAATGT TTTATATGCA AAAGTTTTTT GTATCATGCT TGTATAAATC CAGCTTTTTT TGTATCATGC TTGTATTTTT TTTTTCTAGC TGTTATTGCT TTTCTGATAA TAGTACTGAA TTTGGTGTTA TGGCTGGTCT CGAG	60 120 174
(2) INFORMATION FOR SEQ ID NO:1419:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 234 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:	

CILINDOCCO MINOLOGO LINGUISTO	
GAATTCGGCC TTCATGGCCT AATTTTATAT TATTGTTAAA CACTGGGCTG GAATTATTGT	60
TTTGGGAAAA GGCCCATGAG AGTTTTTGCT CTGTGGGTTT TTAAAGGTAA GAATAAATTT	120
CGTGTTTGAG ATGTTTTTGA TGTGCCTGTA ACCAGAATAG AAGTGTCTTA GATTATAACT	180
TTCTCTCAGA TTGAGTAATT CTGTTGTAAT AAGTCAGCAT ATGTTGCCAT CGAG	234
(2) INFORMATION FOR SEQ ID NO:1420:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 157 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:	
•	
GAAAATATTT TTACTTTTAT AATTGATAGT ATTTCTTAAC TCTCAATTAA AAAAAGTTTT	60
TAAGCATTTC TGTGATATAG ATACTATCAT TTCATATTAC ACAATGCTTC TGATGATTTT	120
GCTGTTGTTG TTAGGGACTA CTCGAGGCAG GTCTAGA	157
(2) INFORMATION FOR SEQ ID NO:1421:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 495 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:	
(AI) SEQUENCE DESCRIPTION. SEQ ID NO.1421:	
GAATTCGGCC TTCATGGCCT ACCAGGATGA GAGGGGAAAA AGAAAGCCTC CAGTGACTTC	60
AGTTGCTTTG CCAGTTGTCT TGGGATTGTT TTACACCATC CTTTACTTCC CTTGCTCAGA	120
CCTCTCTGTT TCACCATTGC TCAGGCATTC AGGAAAGTAT CTGCTCACTC CCACTTGGTG	180
AGTCCTCGGC CTTGAGGTTG CTGACTCTCA GGCGTTAGGC AGCTGGATGA CTTCCCGCTT	240
CATGCAGCAA AGGCCAGGGG CTTGCGGGCC TCTGCAGAGT TGTTGCTAGG GAGACTTGTG	300
TCATCATCCA CAACCTTGTT TCTCACTTCC TGGTTGGGCT CATCTCTGAA GAACAGGTCT	360
CCCAGCTTCG CTCCTTATCA CTGCATTGTG AAGAGGAGGA AAAGTGAATC ACGGAGAGAG	420
AAAGGAAAGG ATAGAATCAC AGGCTGCATC TGCACCTGAA AAGTGACCCG CGGAAACTCT ATGGCGGATC TCGAG	480 495
ATGGCGGATC TCGAG	495
(2) INFORMATION FOR SEQ ID NO:1422:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 449 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
•	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:	
GAATTCGGCC TTCATGGCCT AGACAAAAGT AGAATTAGTA AACTACTACA TTGAGTACAC	60
TTTGTGTTAA AATTCATAGG GAAGACTTCT TAAAAACAAG TGAAATTGTT AAACCCCCCC	120
CTAAGCATTA CAGATGGCTT ATAGCTGTCC ACGGGGTTGG TAGAGGTGGG AAAGGGAAGG	180
GTTCTAGGCC AGAATGTTCC TATTTAGAAG ACACTCAAAT TACAGTCTGT GTTATGTATG	240

TATACCATTT ATTCAATGCT ACTGTGTATA TAATGGAAAA CTTAAGTCCA GTTTGAAACA TCTAGTCTTT CTAGGTGTTT AAAAGTGTAC AACAGCCTGT CGCAGTGGCG CATGCCTGTG GTCCCAGCAC TTTGGGAGGC CGAGGCAGGC GGATCACGAG GTCGGGAGAT CGGGACCATC TTGGCCAGCA TGGTGAAACC CCTCTCGAG	300 360 420 445
(2) INFORMATION FOR SEQ ID NO:1423:	***
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 306 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:	
GGGAGTTTAT TATTCATTAA CGAAATTAGC CCTTTTATCT GCCATATAAT TTGCAACAAT TTTATATCAG CTTTTTTATT GTCTTTTGGC TGTTGTTATG AAAGTTATGG CCATGCAGAA ATGTGGGATT TTATGTAGCA CAGTTGTCTC TTTTTTTTT TTTTGAGACG GAGCCTAGCT CTGTCACCCA GGCTGGAGNG CAGTGGCATG ATCTCGGCTC ACNGCAACCT GTGCCTCCCA GGTTCAAGCA ATTCTTCAGT CTCAGCCTCC CAAGTAGCTG GGACTACAGG CGCCCACCCC CTCGAG	60 120 180 240 300 306
(2) INFORMATION FOR SEQ ID NO:1424:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 362 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:	
GAATTCGGCC TTCATGGCCT AGAACTTTGT ACACCATGGA ATGTTCTACT TATTATTTTG TGCTACAATA TGTGCTGTTT CTTTTGTTTG AATTGCAGAT TGTCTACTAT GAAGCAGGGA TTATTCTATG CTGTGCCTG GGGCTGCTGT TTATTATTCT GATGCCTCTG GTGGGGTATT TCTTTTGTAT GTGTCGTTGC TGTAACAAAT GTGGTGGAGA AATGCACCAG CGACAGAAGG AAAATGGGCC CTTCCTGAGG AAATGCTTTG CAATCTCCCT GTTGGTGATT TGTATAATAA TAAGCATTGG CATCTTCTAT GGTTTTGTGG CAAATCACCA GGTAAGAACC CGGATCCTCG AG	60 120 180 240 300 360 362
(2) INFORMATION FOR SEQ ID NO:1425:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 194 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:	
GAATTCGGCC TTCATGGCCT AGTATATCTG AAAAGTACAC TGTGTTTTGA AATTATAAAT TTTCATTCTG AATGAGGTTT CTTTTTTTGA TTTTCTTTAA AAAAAAAAAA	60 120

194

TGAACACCCT CGAG

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 393 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:	
GAATTCGGCC TTCATGGCCT AGCCATGTAT TTTCTAATAT CCCTTGGACT TCATCTTTGA CTCATGTTTT ATTTTGAAGT ATTGGGATTG TTTTTCAGTT ATCTTCTGT TATTATTTCT ATTTAATTCT GTTATGGTCA TACAACATAA TTTAAATTCT TCTAAATTTG TTGAGGATTG TTTTTGTTGC CCAGAATATG ATGAATCTCT CATTGAATGT TGTATGTGCA GTTGAAAAGA ATGTTTATTC TGCTGTTGGT GGGTAAAGTG TCATGAATAT AATTAGGAGA AATTAATGAT AGTGTTAAGG TTTTCTATAT CCTTGCTTTT TTGGTGTACT TATTTTATTG ATTATTGAGA GAGAAGGGTT GAATTATCTA GGTGCAACTC GAG	60 120 180 240 300 360 393
(2) INFORMATION FOR SEQ ID NO:1427:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:	
GCGATTGAAT TCTAGACCTG CCTCGAGCCA CCCCGTTAAT GTGTGTGTTG ACAGTGAAGT CCTTGGGTGG GGCCATGTGT GTGTTTGTGA TGTTCCTTAA GTTGATGCAG CTTCTCGAG	60 119
(2) INFORMATION FOR SEQ ID NO:1428:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 327 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:	
GAAAAAGCAG TAAAAATAGA AATCCATCTT CACCAAGCCT TTAAAGCAAT ATAAATTTAT ACTGAGGTTC CTGCATACTA TAACACACAG AAGGAATTCC TAAAAATGTT CTTTATCCAG CTGTCTACCC AAAGTTCTAT CATCCTGGCA AACTGCTCTC TCCAAAATTC ATCATCTTGG ACTCTCTCTG AAACTCCAAC CCTTCTCTCT TATACCCTGT TCTCCAACAT TCGAATTTGT TTAGTTTGTC TTCTTCCTAA TATAGCTATT TCTGTTTACC ATTTTGAGCT CTGGAACTCT AACCACCTACT TACCACCAAA ACTCGAG (2) INFORMATION FOR SEQ ID NO:1429:	60 120 180 240 300 327
(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 325 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:	
GAATTCGGCC TTCATGGCCT AATCACATAT ACACAATTTA CCCATTTCAA GTGTACACGT AGTGGTTTTA GTATATTAC AGATAGGTGC AACTATCACC ACAGTCAAAT TTAGAACCTT TTCATCAACC CCAAAAGAAA CACCATACCC TTTAGGTATC GCCTCCCTA TACTCCACCT TCCAACTGCT GAGCCCTAAG TTACCACTAA CCTTCCTATC TCTATAGATT TCCTTATTCT GAACTTTTGA ATGGAATTAC AGTATCTGGT CTTTTGTGCC TGTTTTTTTT TGACTAATGT TTCAAGGTTC ATCCAGGCCC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:1430:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 226 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:	
GAATTCGGCC TTCATGGCCT ACCTAAACCT GGCAGAGTAC ATCATGCCTC CGAGAAGAAA CGTCATTCCA CTCCTTTGCC GAGCACTGCT GTACCAAGCC ATACACCTGG CAGCAGCCAG CAGTCCCCGC TCAACAGTCC TCACCCGGGG CCCATCCGGA CAGGCCTGCC TCCTGGGCAC CAGCAGGAAT TTGCCGGACG AGCCAACAGC ACCTCCAACC CTCGAG	60 120 180 226
(2) INFORMATION FOR SEQ ID NO:1431:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 256 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:	
GAATTCGGTT CATGGCCTAG GATTAACAAC TTGGAAAAGG CCTATGATAC TCCTGGTAAA CCTCTTTTGTG CTGCTCTCTG TGGTTTGTGT CCTCTTTAAAT CTAGCTGGAT TTATCCTAGG CTGCCAAGGG GCCCAGTTTG TGTCCAGCGT GCCCAGGTGT GATCTGGTG ACTTAGGTGA AGGCAAGATT TGCTTCTGTT GTGAAGAATT TCAACCAGCC AAGTGCACAG ACAAAGAAAA TGCCTTGAAA CTCGAG	60 120 180 240 256
(2) INFORMATION FOR SEQ ID NO:1432:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 240 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

(ii)	MOLECULE	TYPE: cDNA			
(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:1432:

- (2) INFORMATION FOR SEQ ID NO:1433:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

TCATTCTGAA CAAAAGGGAT TAGAGAAGAA AAATCTCTTG ATATAAGGCT TGAAAGCAAG 60
GGCAGGCAAT CTTGGTTGTG AATATTTTCT GATTTTTCCA GAAATCAAGC AGAAGATTGA 120
GCTGCTGATG TCAGTTAACT CTGAGAAGTC GTCCTCTTCA GAAAGGCCGG AGCCTCAACA 180
GAAAGCTCCT TTAGTTCCTC CTCCTCCACC GCCACCAACCA CTCCTCGAG 229

- (2) INFORMATION FOR SEQ ID NO:1434:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

GAAATTGAAA	CTCAAATCAG	TTAGCTTCAA	ACAAAAACGA	AAGTTAGACC	AAGGGAACGT	60
ATTAGATATG	GAAGTAAAGA	AAAAGAAACA	TGATAAACAA	GAACAGAAAG	GAAGTGTGGG	120
AGCTACATTC	AAATTAGGTG	ACTCTTTGTC	AAACCCAAAC	GAAAGAGCCA	TTGTTAAAGA	180
AAAGATGGTA	TCAAATACTA	AGTCTGTAGA	CACGAAAGCG	AGTTCATCTA	AATTTAGTAG	240
AATTCTAACT	CCTAAGGAGC	ATCTCGAG				268

- (2) INFORMATION FOR SEQ ID NO:1435:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

GAATTCGGCC TTCATGGCCT ACAAGACTGT CTCAAAAAGA AAAGAAACAC AAATATTTGA 60 ACTCCAAATA TTCTTTGTGT GTAGAAAAAT CTAATGGATA ATTAAAACTA GAGCAGAGAG 120

AAAAGCCTAG GAGTTGAGAG ATTTTTAGAT ACGTGACTGA AAAGATTGGA AAAGGCTATC AGTTTTAATG CTTGTGTCTG TCTTTGTGTG GGCCATGGTA TTTTGGAAGA GCACCATGGA GCTCGAG	180 - 240 247
(2) INFORMATION FOR SEQ ID NO:1436:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 258 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:	
GAATTCGGCC TTCATGGCCT ACCTATTTGT GCATCAAGTG GTTATCTAAA TAGTTTGAAA GGATTGATAT ACTACATTAT ACGTCAAAAA TAAATAAATA AAATTAAGAA GACAGGGATT CCAAGATTGT AGCTGACCAA GCTGTCTTGT TTTGCGTACA TCAACACTAT GCTGCTTCCA ATATTCCTAG CCATTCCACA GGTAATGATT TTTCAACAAT CAAGAGAAAG TCATTCTTGT ACTGTAACAT CTCTCGAG	60 120 180 240 258
(2) INFORMATION FOR SEQ ID NO:1437:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 415 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:	
GAATTCGGCC TTCATGGCCT AAATCACTTG GATTGGTTCT CTACTTAAAA CACAAGCTAG CTACCCAGTC TTGTATTTG TATTTTTAAA AAACTAATTT TGTTTTGTAT TTGTGTAAAG CATAGTCATA ATCTATAATC AAACACACTG CATCGAGTTT ATCACTGAAA TTCAGCATCT GCTTTTGTCC TCACTTTGTT ATCTTCTGT CTCATCGATT ACAGGCGTGA GCCACCGCGC CCGGCGGTAT GTTCCTTACC CTTAAGGACA AGAAATACCG TTTGAAAACA TTCTTCTTGA ACATTAACAA ACTTAGAATG GTACATTCAT TTAAGAATTA AAATAGGCAC AAGAGGGATTG AATTTTGGAA ATATGTTGCT TAGAAATTTG GGGGCAATTC TCGAG	60 120 180 240 300 360 415
(2) INFORMATION FOR SEQ ID NO:1438:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:	
GCGATTGAAT TCTAGACCTG CCTCGAAGTG CCAGCAGCAG AGGAGATGAC AGTGACATAT ACAACAGAGG CTGGGGTGGG CACTCCAGGA GCCCTGGAGC GGAAGACCTC AGGGCTAGGA CAGGAGCAAG AGGAAGGGTC AGAGGGCCAG GAGGCAGCCA CTGGGAGTGG CGATGGGAGG CAGGAGACAG GAGCAGCTGA AAAATTCCGA TTAGGATTAT CACGGGAGGG AGAGAGGGAA TTGAGTCCGG AGAGTCTACA GCTCGAG	60 120 180 240 267

(2)	INFORMATION	FOR	SEO	TD	NO - 1439 -
(2)	THE OWNER TON	LON	360	ıυ	NO. ITES

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

GCGATTGAAT	TCTAGACCTG	CCTCGAGTCA	TATCCCTGAG	CAGTAGAGTA	AATTAAATCC	60
TTTCTGAGAG	TCTTAGATGT	TTTTCTATGT	$\mathtt{CTCTTCTTTC}$	TTATTCTCTC	TCTGTTTCTT	120
TCTCTCACTC	ACACACACAC	ACACACACAC	ACACACACCC	CTAAAATTTG	TTCTGAATGG	180
CCCACTAGGG	CTGAATCATT	TAGTGACTTC	ATTGATTACT	ATCCTGAGTT	CTTCTTCCTG	240
CTTCCAGACT	AGTGAAAATA	TTCCAGAAAG	CTTTAATATT	GGAGAAAAGG	CAACGCTCGA	300
G						301

(2) INFORMATION FOR SEQ ID NO:1440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

GAATTCGGCT	TCATGGCCTA	GCATTTGGAA	GTAATTTTTT	AAAACAACAT	TCATATTAAT	60
TTAAGGAGCA	TAACAGATTC	CAGTGAATGT	TATGATTCGC	TATTGTAACA	TTATTCTAGT	120
AAATATGTTG	GAGAAGAACA	GTTCTAGTGA	ATTAACTATG	GTTTTGGAAG	GCAGCTATGC	180
TCACCATCAT	ACCACCAACA	CAACCATGGT	TTTATTTTAT	ATTATTTATT	TTATTTTTGA	240
GACAGAGTCT	C					251

- (2) INFORMATION FOR SEQ ID NO:1441:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

GGAATTGGAA	AGCGTTTCCT	TGCCAACACC	AGAAATCCAG	TCAGATTTCT	TACATAGCAA	60
AGTCGAAGCT	CCTCCTTCAG	AGGTGGCGGA	TACGTTAGTA	ATAATGACTG	CTTCCAAGGG	120
TGTTCGACTC	CCAGAACCCA	AAGATAAGAT	TTTGGAGACA	CCTCAGAAAA	TGACAGAAAA	180
ATCTGAATCA	AAGACACCAG	GAGAAGGGAA	AAAGGAAGAT	AAAAGCAGAA	TGGCAGAACC	240
AATGAAAGGC	TACATGAGAC	CCACCAAGCT	CGAG			274

- (2) INFORMATION FOR SEQ ID NO:1442:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:	
GAATTCGGCC TTCATGGCCT ACCTTTCTCC ATGTTTAACT GGGCTGCTCC CCATTCTCTG CCTCCCTGTC TCCTCAGCCG CCAGAGCCCA GCCCCTCCGA CCAGGCCTCA CCCGCCCCA CCCGACCCTT CCCTGAGGGT CCTTTCCTCA GTACCACTGA CACTTGGAGG CAGGAAACCC AAACCTCCTT AACTAAGGCC TCATTCACCT CGAAAGCAGT GGTGCTTCCC TCTGTTCATC CAGGGCCATA AAGCCACTGT CCCCCTTAACT CGAG	60 120 180 240 274
(2) INFORMATION FOR SEQ ID NO:1443:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 257 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:	
GAATTCGGCC TTCATGGCCT AATTGCGCCA TTGCACTCTA GCCTGGGCGA CGGAGCAAAA CTCCATCTCA AAAAAAAAAA	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:1444:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 258 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:	
GAATTCGGCC TTCATGGCCT AGGAAGCATT AAATTGGGCC ATAGGAAGGA CAAGTCACAT CCAGTTTAGT GATCAATGGT GGTTTGGGAA AGAAATAACA GAATTCTACT CCTACATGAT AGGGAGAGAC TACAGAGGCC ACCTAGACCA ACAAACTCTG CCATCAGGTC CTTGAATCAT TGCTACCATG TCCTGGTGGT GGTTGTAGCA TTGCTAGTGA TATGTAACTC ATTACCTACT TATGCAAACC ATCTCGAG	60 120 180 240 258
(2) INFORMATION FOR SEQ ID NO:1445:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 638 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

${\tt GGATGGCTAC}$	GGCAGGGGGT	GGCTCTGGGG	CTGACCCGGG	AAGTCGGGGT	CTCCTTCGCC	60
TTCTGTCTTT	CTGCGTCCTA	CTAGCAGGTT	TGTGCAGGGG	AAACTCAGTG	GAGAGGAAGA	120
TATATATCCC	CTTAAATAAA	ACAGCTCCCT	GTGTTCGCCT	GCTCAACGCC	ACTCATCAGA	180
TTGGCTGCCA	GTCTTCAATT	AGTGGAGACA	CAGGGGTTAT	CCACGTAGTA	GAGAAAGAGG	240
AGGACCTACA	GTGGGTATTG	ACTGATGGCC	CCAACCCCCC	TTACATGGTT	CTGCTGGAGA	300
GCAAGCATTT	TACCAGGGAT	TTAATGGAGA	AGCTGAAAGG	GAGAACCAGC	CGAATTGCTG	360
GTCTTGCAGT	GTCCTTGACC	AAGCCCAGTC	CTGCCTCAGG	CTTCTCTCCT	AGTGTACAGT	420
GCCCAAATGA	TGGGTTTGGT	GTTTACTCCA	ATTCCNATGG	GCCAGAGTTT	GCTCACTGCA	480
GAGAAATACA	GTGGAATTCG	CTGGGCAATG	GTTTGGCTTA	TGAAGACTTT	AGTTTCCCCA	540
				GCAGTGCTAT	CAAGATCACA	600
ACCTGAGTCA	GAATNGGTCA	GCACCAACCC	GACTCGAG			638

(2) INFORMATION FOR SEQ ID NO:1446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

GCGAGCTCGT GTTTTAAAGG	ACCAAATAGA	AGTTTACCAG	GAGAGAAGTG	ACAGAAGTGC	60
TGTCTAGATA GAGGAAGGGC	ACACACAGAT	GCAAGCATGT	GCAGAAATGA	GCAAACCACT	120
GAGACGCTGC CTTGAGCTCT	GTGTCACACT	GCTATGTTGC	AGCCTGGGAG	GCTGTTCCCA	180
GTTGAGCCCT TCGGAACCAG	CCATGAGATG	GCACGGGTAC	GCGGAAGGGA	GCAGTCTCCA	240
TGGCTGGGTG GTGATGGGGG					269

- (2) INFORMATION FOR SEQ ID NO:1447:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

GGTCTCTCGC	CGCCGGAGGA	AGATGAGGCT	GAAGATTGGA	TTCATCTTAC	CCACTTTCCT	60
GGTGGTGGGA	AGCTTCCTGG	GGCTAGTGGT	CCTCTGGTCT	TCCCTCACCC	CCCCCCCC	
CGACCCAAGC	CCGCTGAGCA	GGATGAGGGA	ACACACACAC	CECTOACC	CGCGGCCGGA	120
CCGAGGCGGC	AATCCACTAC	CTCCTCCCCA	AGACAGAGAI	GICAAIGACC	CCATGCCCAA	180
TCATCTTCAA	CCACMACAAC	CICCIGGGGA	GGACAGATTC	AAACCTGTGG	TACCATGGCC	240
TCATGTTGAA	GGAG TAGAAG	TGGACTTAGA	GTCTATTAGA	AGAATAAACA	AGGCCAAAAA	300
TGAACAAGAG	CACCATGCTG	GAGGAGATTC	CCAGAAAGAT	ATCATACTTC	TCGAG	355

(2) INFORMATION FOR SEQ ID NO:1448:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

GAATTCGGCC TTCAT	GGCCT ATCCTCTGCC	AAGACCAAAA	GGAAAGAAGA	AAAAGGGCCA	60
AAAGCCAAAA TGAAA	CTGAT GGTACTTGTT	TTCACCATTG	GGCTAACTTT	GCTGCTAGGA	120
GTTCAAGCCA TGCCT	GCAAA TCGCCTCTCT	TGCTACAGAA	AGATACTAAA	AGATCACAAC	180
TGTCACAACC TTCCG	GAAGG AGTAGCTGAC	CTGACACAGA	TTGATGTCAA	TGTCCAGGAT	240
CATTTCTGGG ATGGG	AAGGG ATGTGAGATG	ATCTGTTACT	GCAACTTCAG	CGAATTGCTC	300
TGCTGCCCAA AAGAC	GTTTT CTTTGGACCA	AAGATCTCTT	TCGTGATTCC	TTGCAACAAT	360
CTCGAG					366

- (2) INFORMATION FOR SEQ ID NO:1449:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

GATTTCTTAC	CCAAAGCTCT	GGAATTGTAC	ATTTATTTT	TAAAACTCAA	AGAGGGAAAG	60
AGCCTTGTAT	CATATGTGAA	CATTGTATCA	TAGGTAATGT	TGTACAGACC	CTTTTATACA	120
GTGATCTGTC	TTGTTCCTGC	AGCAAAAATC	CTCTATGGAC	ATAGGAGGTG	CTGTGTCCCA	180
TGCCCTCTTG	CCCTGACAGT	GTCCCATGGG	CCCCCTTCTG	CTCCCTGCCC	CCTCCCTGCT	240
ACTGCTGATG	CACTCCCCCC	CCTCGAG				267

- (2) INFORMATION FOR SEQ ID NO:1450:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

GCGATTGAAT	TCTAGACCTG	CCTCGAGACC	TGGGGGGAGA	TTGGGCTCCC	TTTCCTCATG	60
ACATCCTGCC	CTATCAGGAC	TCTGGAGATA	GTGGGAGCGA	CTACCTTTTC	CCAGAAGCTA	120
GTGAAGAATC	AGCAGGCATC	CCGGGAAAGT	CAGAACTTCC	CTACGAAGAG	CTGTGGCTGG	180
AGGAAGGCAA	GCCCAGCCAT	CAGCCTCTCA	CTCGCTCTCT	GAGCGAGAAG	AACAGATGTG	240
ATCAGTTTAG	AGGTTCTGTC	CGATCCAAAT	GTGCGACTTC	TCCTCTTCCC	ATCCCTGGGA	300
CTCTGGGAGC	AGCAGTGAAG	TCTTCAGATA	CTGCCCTACC	TCCACCTCCA	GTGCCTCCCA	360
AATCTGAAGC	CGTCAGAGAA	GAATGCCGGC	TCCTGAACGC	CCCACCTGTT	CCACCCGAA	420
GCGCACTCGA	G					431

- (2) INFORMATION FOR SEQ ID NO:1451:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

GCCTGCCCCC ACCTTACAGG	TCTGGGATGT	ACCTTTCCAT	CTGTTGCTGC	TTTCTTCTAT	60
GGGCCCCTGC CCTCACTCTC	AAGAACCTCA	ACTACTCCGT	GCCGGAGGAG	CAAGGGGCCG	120
GCACGGTGAT CGGGAACATC	GGCAGGGATG	CTCGACTGCA	GCCTGGGCTT	CCGCCTGCAG	180
AGCGCGGCGG CGGAGGGCGC	AGCAAGTCGG	GTAGCTACCG	GGTGCTGGAG	AACTCCGCAC	240
CGCACCTGCT GGACGTGGAC					300
GCGAGTCCCT GTGCCGCCAC					347

- (2) INFORMATION FOR SEQ ID NO:1452:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

GGGGCAGAAG	TTGAATATAC	CGGCAATTTT	GCGAGCACCC	AAGGAGAGAA	AACCAAGTAA	60
AAAAGAAGGA	GGCACACAAA	AGACATCTAC	TCTTCCTGCA	GTACTTTATA	GTTGTGGGAT	120
TTGTAAGAAG	AACCATGATC	AGCATCTTCT	TTTATTGTGT	GATACCTGTA	AACTACATTA	180
CCATCTTGGA	TGTCTGGATC	CTCCTCTTAC	AAGGATGCCA	AGAAAGACCA	AAAACAGTTA	240
TTGGCAGTGC	TCGGAATGTG	ACCAGGCAGG	GAGCAGTGAC	ATGGAAGCAG	ATATGGCCAT	300
GGAAACCCTA	CCAGATGGAA	CCAAAACAAC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:1453:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

GCGATTGAAT	TCTAGACCTG	CCTCGAGATC	CCCATGACTC	CTACATCCTC	TTTTGTGTCT	60
CCGCCACCAC	CCACTGCCTC	ACCTCATTCC	AACCGGACCA	CACCGCCTGA	AGCGGCCCAG	120
AATGGCCAGT	CCCCCATGGC	AGCCCTGATC	TTAGTAGCAG	ACAATGCAGG	GGGCAGTCAT	180
GCCTCAAAAG	ATGCCAACCA	GGTTCACTCC	ACTACCAGGA	GGAATAGCAA	CAGTCCGCCC	240
TCTCCGTCCT	CTATGAACCA	AAGAAGGCTG	GGCCCCAGAG	AGGTGGGGG	CCAGGGAGCA	300
GGCAACACAG	GAGGACTGGA	GCCAGTGCAC	CCTGCCAGCC	TCCCGGACTC	CTCTCTGGCA	360
ACCAGTGCCC	CGCTGTGCTG	CACCCTCTGC	CACGAGCGGC	TGGAGGACAC	CCATTTTGTG	420
CAGTGCCCGT	CCGTCCCTTC	GCACAAGTTC	TGCTTCCCTT	GCTCCAGACA	AAGCATCAAA	480
CAGCAGGGAG	CTAGTGGAGA	GGTCTATTGT	CCCAGTGGGG	AAAAATGCCC	TCTTGTGGGC	540
TCCAATGTCC	CCTGGGCCTT	TATGCAAGGG	GAAATTGCAA	CCATCCTTGC	TGGAGATGTG	600
AAAGTGGAAA	AAGGAGAGCG	ACTCGAG				627

- (2) INFORMATION FOR SEQ ID NO:1454:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

GAACTTTGAC ACCTACACTT	AAATTCTGAG	TCATTAAACA	GGCCTACATT	TATCAACTGT	60
GGAAATATCA GCCAGTTTTT	GCAAACCTCT	TCTTAGGACA	CTAAGTTGTT	TGCAGAAATC	120
ACTAGCATTG ACTGACTCAG	CAACAATGTG	GTTATATTCT	TTGATTAACT	TAGTCCTTTT	180
TCTTGGTCAA GAGTCAGTAG					240
TCCATTACTA CCACCTTGGT					300
TGCTACTCTA CAGACTTGCC	CTGAATGTAA	GAGCAACAAT	TACCTTGTAA	AGTCCAAGTT	360
GGGGCAGGTC ACTCCCAAAC	TCCACAACCT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:1455:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

CAGATGTTCA GA	TATATCTT	GAATTTTCTA	CGAACATCCA	AACTCCTCAT	TCCTGATGAT	60
TTCAAGGACT AC	CACTTTGTT	ATATGAAGAG	GCAAAATATT	TTCAGCTTCA	GCCCATGTTG	120
TTGGAGATGG AA	AGATGGAA	GCAGGACAGA	GAAACTGGTC	GATTTTCAAG	GCCCTGTGAG	180
TGCCTCGTCG TG	CGTGTGGC	CCCAGACCTC	GGAGAAAGGA	TCACGCTAAG	CGGTGACAAA	240
TCCTTGATAG AA	GAAGTATT	TCCAGAGATC	GGCGACGTGA	TGTGTAACTC	TGTCAATGCA	300
GGCTGGAATC AC	GACTCGAC	GCACGTCATC	AGGTTTCCAC	TAAATGGCTA	CTGTCACCTC	360
AACTCAGTCC AG	GTCCTCGA	G				381

- (2) INFORMATION FOR SEQ ID NO:1456:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

GGTGACGCCT	GCTTCACATC	TCTAATGAAC	ACCCTCATGA	CGTCGCTACC	AGCACTAGTG	60
					CCTCATGGCC	120
CGGCTCCTTA	GCACCTCTCC	AGCTCTTCAG	GGAACACCAG	CATCCCGAGG	GTTCTTCGCA	180
		ACAGTCCCAC				240
GCAGTGCTAG	CCCTGTCCCC	TGAGTATGAG	GGCATCTGGG	CCGACCTGCA	GGAGCTCTGG	300
TTCCTCGAG						309

- (2) INFORMATION FOR SEQ ID NO:1457:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

GCACTATTAA	ACAGATACAA	CACAGAATAG	TATGTATAGA	GCATGGTATG	TAGCAGGGGC	60
CTATTCCTGT	CTGAGTGGAC	AAGGAGGCTT	CCTAGAGGAA	GCAACATTTA	AAGCTGAGGG	120
CTGAAGGATG	AATAGGATTT	AACCAAGTAA	AAGTAAGAAA	GGAAGTGGGG	AGCTGGAAAG	180
GGCATTCCAG	GAAGAAGAAA	CTGCATGTGC	AAAGGCCAGG	AGGTCAGAGC	GCACAGTGGA	240
TATGACGATG	TGGCTAGCTG	AGCATGTCTG	TGCAGTGTCA	ACTTTGTTGT	GAACACAGAG	300
GGAGGCTACT	GGGAAATTTT	AAGCAAGAGA	GTTGGAGTAT	GATCACATTT	GCATGTTAGA	360
AAGACACACT	CGAG					374

- (2) INFORMATION FOR SEQ ID NO:1458:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

GAATTCGGCC	TTCATGGCCT	ACATATTTAT	TATGTCAACC	TGTACTTCCC	TTTCCCTCTT	60
CCTCTCCCTC	TTTTCTCTCC	CTCTCCCTCT	CTCTCTCTTC	CTTCCTCCCC	TTCCAGGTAC	120
CCTAGATGAA	CCATGGGAGG	TCCTGGCTAC	ACAGCCATTC	TGTCTGAGAG	AGTCTGAGGA	180
CTCTGAGACC	CAGCCTTTTG	ACACGCACCT	TGAGGCCTAT	GGACCTTGCC	TGTCTCCACC	240
TAGGGCAATA	CCAGGAGACC	AACATCCAGA	GAGCCCAGTT	CACACAGAGC	CAATGGGGAT	300
TCCGGGCAGG	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1459:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

GGAACCACCA	ATTCCGGACA	CACTGGGATT	ACAGTTCCAG	GAAGGATGTT	ACCTTTGACG	60
ATGACAGTGT	TAATCCTGCT	GCTGCTCCCC	ACGGGTCAGG	CTGCCCCAAA	GGATGGAGTC	120
			CTCCTGCCCA			180
			AAGGGACTAG			240
			TACCTCTTTG			300
			TCCATGTTGA			360
			ATCTTGATAG			417

- (2) INFORMATION FOR SEQ ID NO:1460:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

GAAT:	rcggcc	TTCATGGCCT	ACTGAGAAAA	ΔΔΔΔΤCλλλΤ	ርጥን አጥጥጥጥን እ	AATGAAGGTA	
TTTA	ADDCCA	TECEPACAACC	Caccomman	Thurst Chart	CIAATITIAA	AATGAAGGTA	60
22.20	TOTAL CONTRACTOR	100CACAMOG	GAGCCTTATT	TATGGAGCTG	GTGGGAAGCC	AGGATGTTTC	120
CAAT	CCGCTG	CTCTTACAGG	AGCCTGTGCC	TCGCCAGTTC	TGTGCTGCAG	TGGGCAGCCA	100
ACTG	AAGTGC	ATGAGTCAAA	TGCACGAAGC	ACCACA CMCC	1010010010	TOGGCAGCCA	180
_			TOCACOAAGC	AGCAGACTCG	AG		222

- (2) INFORMATION FOR SEQ ID NO:1461:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

GCTGCCTCCA GCATGGTGTT ATTGGGTGCA GACCCTCCCC TCTGGAAAAA	CCTCAGGTGG AAATCCCAAA TCTTTCAACC	AGAGTGGGCA CCAGGATATG	GAAGTTTTTG TGTATGTCTG	CAACACTTTT	TTTTTTAAGTT	60 120 180 240 256
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- (2) INFORMATION FOR SEQ ID NO:1462:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

ACCCAGTGTC GAGGTTAAAA AAAAAACAAA AAACCAAAAAA CCAATGCAGG AATCCAGTGG GTGGAGTGAG GGGATCTGGG ATCCAGTGAT GGGGGCCCCA GGATCCAGGC ATTGTGGTTG TCAGGATCCA GTGGTGAGGT TTGTTGACAT CCAGAATCCA GCAGCTGAGC TTGGAGATCC AGGGCTCGAG 240	ATCTGGG ATCCAGTGAT GGGGGCCCCA GG	CAATGCAGG AATCCAGTGG 120
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- (2) INFORMATION FOR SEQ ID NO:1463:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

	TICATGGCCI AAGITTATAA AAATTTCAGC CAGAAAAACC CAGGTAAGGA	60
TTTTTTTAT	TTTTTTTTA TTTTTTTT TAGACCAGGT GAGAATCCTT TGTTCCACTG	120
AGATTTTAAA	ATTTAGTACA TTCAAAATTG ATATTTCTAC CATTTTCTCA GCCTGCTTGT	180
CTTCTTATCT	TTGCAGCACT GCTTATTGCC ATCACTGCTT ATCTGTTCAC TCAACTTGAA	240
	TGTCCTTGAC CTCATCCCCA CATCTCGAG	279
		2,3
(2) INFORM	ATION FOR SEQ ID NO:1464:	
(5)	SEQUENCE CHARACTERISTICS:	
147		
	(A) LENGTH: 266 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
	GROUPINGS DWG-T	
(XI)	SEQUENCE DESCRIPTION: SEQ ID NO:1464:	
	TTCATGGCCT AGGCCATTTG GTTCTAAACT GCTTGACTAG TTTTAAGCTC	60
ACATAATTCC	TTAAGCTTTC ATATTTTCTT AAATGCAAGG AAATGAATAT AAAAGCACTA	120
	TTCACTGGTA CAAAAATTAC AATGGTCAGT TCCCTTAGGT CATCAAAAAC	180
	AATAGTTCTT GTATTCAACC TGAATGTGCC ACAGGAAAAA AAAAATATTT	240
	CCAGCTCAGC CTCGAG	266
	3.30.13.30	200
(2) INFORM	ATION FOR SEQ ID NO:1465:	
(i)	SEQUENCE CHARACTERISTICS:	
1-7	(A) LENGTH: 259 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: CDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1465:	
GAATTCGGCC	TTCATGGCCT AAACATTTC TGAAAAACGT GATAGAAAGA AGGAGGAGCT	60
	GGGAAATAAA TAATTTGGCA GGAGACTTTT TGAACTAGAT ATCTATTGAA	120
	ACAATGTTCC CCATCCTCTC ATTTCCATTC CCAATTTTAC TTCTCGTCCC	180
	ATTCTTACTT ATGATCGGCG CTATGTCAGT GCCTCTCAGC TGGTCTTCCC	240
AGACCCAGTC		259
(2) INFORMA	ATION FOR SEQ ID NO:1466:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 332 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1466:	
,		
GCGCCTATCA	CAAGCAGATC ATGGGTGGCT TCAAGGAGAC GAAGGAGGCT GAAGATGGCT	60
TCCGCAAGGC	CCAGAAGCCT TGGGCCAAGA AGATGAAGGA GCTGGAGGCA GCCAAGAAGG	120
CCTACCATTT	GGCTTGCAAA GAGGAAAAGC TGGCCATGAC ACGGGAGATG AACAGCAAGA	180
	GGTCACACCT GAGCAGCAAA AGAAGCTGCA GGACAAAGTG GACAAGTGCA	240
	THE	270

AGCAGGATGT CCACACCCCA	GCAGAAGACA CAGGAGAAGT ATGAGAAAGT GCTGGAAGAT GTGGGCAAGA GTACATGGAG AACAAACTCG AG	300 332
(2) INFORM	ATION FOR SEQ ID NO:1467:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 301 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1467:	
GGACATCCTG CCTCCGAATT CGAGAAACAG	TGCTGTCTTC CATGCAAAGT GGAATTTGAC AATCACTGTG CCGTGCCTTG AAAGCCAGCA TGAACACATC CTCTAATCCT GGGACACCGC TTCCGCTCCC CAGAATGACC TCCACCGACA GCAGTACTCC TATATTGATG CCGTCTGTTA CTCCATTGGT TTGCAAAGTT TTTCCCCTAT CTGGTGCTCT TGCACACGCT GCCTGCAGCA ACTTTTGGCT TCACTACCCC AGTACCAGTT CCAGGCTCGA	60 120 180 240 300 - 301
(2) INFORMA	ATION FOR SEQ ID NO:1468:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 436 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1468:	
GTTCTTTCTT CATGTTTCAA TGGGTTGGTT AGTCAGATGT TCGCTGCCCA	TTCATGGCCT AGTGGAAAAT GGGAGGCATG AAATACATCT TTTCGTTGTT TTGCTAGAAG GAGCAAAAC AGAGCAAGTA AAACATTCAG AGACATATTG GACAAGAAGT ACAGAGTGG TGAGAGATG CATCCTTACC TGGAACCTTA TACTGCGTGA ACTGCATCTG CTCAGAGAAT GGGAATGTGC TTTGCAGCCG CCAAATGTTC ATTGCCTTC TCCTGTGCAT ATTCCTCATC TGTGCTGCCC GAAGACTCCT TACCCCCAGT GAACAATAAG GTGACCAGCA AGTCTTGCGA ACAACTTACC AACATGGAGA GCTGTTCGTA GCTGAAGGGC TCTTTCAGAA CTCGAG	60 120 180 240 300 360 420 436
(2) INFORMA	ATION FOR SEQ ID NO:1469:	
(i) :	SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1469:	
AAAAAAAAAC ACAGCACTGT	TTCATGGCCT AGTCTGGGCA ACAGAGCGAG ACCTTGTCTC AAAAAAAAAA	60 120 180 240

GGACAGGAAA CAGTGGTTCA GAGAGATGAA GCACCCTGCC CACCACATGC ACTCGAG

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(2) INFORMATION FOR SEQ ID NO:1470:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:	
GAATTCGGCC TTCATGGCCT AGGACCTATT CTATCAGCAG CATTTGACAC CACTGATTAC TCATTCTGCT CTGGTGTACT TTCTTCAATT GCTTCCAAGA CACCATAAAT TCTTCTGCCT TGCTGGCTGC CTTTGCTGGT TCCTCCTCTT CTCCCTGACC TCTTAATGTT GGAGAACCAC AGGGCTTAGT CCTTGGTCCT CTTCTCTCTT TTCTTTACAC TGTGGTCCTC AGTGAGGGAG ATAGGTAGAT CCACTGTCCC GATCTTAACC CAAAGAAAGA CTTGCTGTCC AGCTACGGGG GCTGTGGTCA GAAGGCAGCC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:1471:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 421 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:	
GAATTCGGCC TTCATGGCCT ACAAAAGGAT GGGAAATGCC TGCATTCCCC TGAAAAGAAT TGCTTATTTC CTATGTCTCT TATCTGCGCT TTTGCTGACT GAGGGGAAGA AACCAGCGAA GCCAAAATGC CCTGCCGTGT GTACTTGTAC CAAAGATAAT GCTTTATGTG AGAATGCCAG ATCCATTCCA CGCACCGTTC CTCCTGATGT TATCTCATTA TCCTTTGTGA GATCTGGTTT TACTGAAATC TCAGAAGGGA GTTTTTTATT CACGCCATCG CTGCAGCTCT TGTTATTCAC ATCGAACTCC TTTGATGTGA TCAGTGATGA TGCTTTTATT GGTCTTCCAC ATCTAGAGTA TTTATTCATA GAAAACAACA ACATCAAGTC AATTTCAAGA CATACTTTCC GGGTACTCGA G	60 120 180 240 300 360 420 421
(2) INFORMATION FOR SEQ ID NO:1472:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 233 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:	
GAATTCGGCC TTCATGGCCT AGTACTCCAT CTCATCCATC TCATGGTAGT TCAGAAATGC CTATATTCCT TCTTAAATTC ACCAGGATTT TTGTTTTTTC TTTCACCCCC TTTTTGCCTT TCTTATTTTC ATCCTTCCAT TTCACTCATT TCCACTCATG TTTAGCAGTT TCTATCCTTT TCTTTCCTGG CGTTTTAGCG TCACACATAG AAACCTATCA CCATCAGCCC TCG	60 120 180 233

(2) INFORMATION FOR SEQ ID NO:1473:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

GCGATTGAAT	TCTAGTTGCC	TACCTACCAA	ACTACCTACT	GAACTTTTTA	ATTTGAAGAT	60
ATTCTTCCTC	CACTACTTOT	mma ma comos			HILLONAGAL	60
	OWCINCILGI	TTATAGTTTA	TTAAATGAAC	TGCTCTATTT	CTAAAAACTT	120
TATTTTTAAA	GTCCTTTCCC	GTTTAGAATG	CCCCATACTC	TTCCTTCTCC	GGTATATATC	
TOTONOCOO	101100100		COOCMINCIC	1100110100	GGTATATATC	180
TCIGNICGIG	ATAACTACCT	ACCGAAAACC	TTTCATGGCT	CCTTGCCAAC	TACAAAATTG	240
CGATATCCTC	GAG					240
	UNO					253

- (2) INFORMATION FOR SEQ ID NO:1474:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

GAATTCGGNC	TTCATGGCCT	ACCGCAAGTT	CCTCCTCTCTCT	mmas acas ac		
722727		ACCOCAAGII	CCICCIGACC	TICAGGGAGC	CTGACTTAGA	60
GAAGAAGTAC	TCCAAGCAGG	TAGACGACCG	ATTTGGTGCC	TATCTCCCCT	CTCCCTCCCT	120
CCTCTTCCTC	TTC3 TCTCC			1A10100C01	GIGCCICGCI	120
CGTCTTCCTC	TICATCIGCT	TIGICCAGAT	CACCATCGTG	CCCCACTCCA	TATTCATGCT	180
CAGCTTCTAC	CTGACCTGTT	CCCTCCTCCT	CACCAMOCANO	cocoooooo		
	oronector.	CCCIGCIGCI	GACCITGGTG	GIGITIGIGI	CTGTGATCTA	240
CTCCTGCGTA	AAGCTCTTCC	CCTCCCCACT	GCAGACCCTC	TCCAGGAAGA	TCCTCCCCTC	300
CAACATCAAC	100100000		Calonecere	ICCAGGAAGA	1CG1GCGG1C	300
CAAGATGAAC	AGCACCCTGG	TTGGGGTGTT	CACCATCACC	CTGGTGTTCC	TGGCGCCTTT	360
TGTCAACATG	TTCACCTCCA	A CTCCCA CCCA			1000000111	300
TGTCAACATG	TICACGIGCA	ACICCAGGGA	CCTGCTGGGC	TGCTTGGCAC	AGGAGCGTCT	420
CGAG						
						424

- (2) INFORMATION FOR SEQ ID NO:1475:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

CACTTAGTTG CAACGTCCCA ATAATACAGG CTGAAGGAAA	TTCCTTCCAG AAGCTATAGT GAGTAAATGT	TGGTTATCAT TGCTCTTGCA GCACTGTTTA	ACTTCTTTTC TTTTGTTCTT TTAATTAAAA	TTGCCATAGT AATTCTTGTA TCCCCGGGAC	TACATGCTAA AGATAAACTA ACGGGATAAA	60 120 180 240
CTGAAGGAAA 1	TCGTGCTTTT	TGAAAAGTAG	GTGTAGCTTG	CCATGCTGCA	ACGGGATAAA TTGTCTTATA	240 300 315

(2) INFORMATION FOR SEQ ID NO:1476:

- Park has been grant of the state of the st

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 321 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:	
GAATTCGGCC TTCATGGCCT AGCCATCATG TTTATTAGAA GGTTGGATTT TGGTGTGTGC TCTAGACAGA TACAGAATAA ATACCTGCGC CTTGAGAACA GGAAGTCCAC GATTCATACA AAGTGCTCAC TACAGGAAGT TGCTGTGTCA AAATCCAGGC AAGGACCCAA CTCCGGGCAG CCCCTCCTCC CTGCTGACCT CAACAAGGGC TGTGCTATTG TTTTTTATTT TATTATTTTA TTTTCTCTTTA TTATTATTAA TATTATTATT ATTTGCTTTT GCTGTGGTCA CTATCATTGG CAAAGTTCCT TTTCCCTCGA G	60 120 180 240 300 321
(2) INFORMATION FOR SEQ ID NO:1477:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 215 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:	
GAATTCGGCC TTCATGGCCT AAGCAAAGCT AAGTGTAAAA CTAAAAAGCA GTTTGTTGCA ACTGGTCATA AAAGTGATTA AATCTAAAGC TGGCATTAAT AAGGAAGCAA GGTAATAAAA CAAAAATATA AACAGCTTTG AGAAAGTACA CCTAATAACA AAATCTTGTA ACACAACAAA TGAAAATCAC AAAAAATATA AGGAGACTCC TCGAG	60 120 180 215
(2) INFORMATION FOR SEQ ID NO:1478:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 291 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:	
GAATTCGGCC TTCATGGCCT AATCGGTCTC CTTTGGAGAG ATCACTAGAA CAGAAAAACA ACCCAGATTA TAACTGGAAT GTTCGGAAAA CATAAAGGAC AGCTCGTAAA GGAGAGAGTA AGAGTCACCA AACACGTGGA TATTTTTGGT CTGATCCTAC AGTAGCCGGT TATCTAGACC AGTAAGTGGA GTTTTGGACA TGCTGCTGCT GTCAACTCAC TGGCTGAAGG AGCACTTCAA GGAATGGGAG GCCTTTCACT GGGTCCAGCT CTGATTCGGA TCACTCTCGA G	60 120 180 240 291
(2) INFORMATION FOR SEQ ID NO:1479:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 514 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

GAATTCGGCC	TTCATGGCCT	AGAGAAAGAA	ATGGCTCGAA	CAGAAAACAG	TGGTCTTGAA	60
AGGCAACGCA	ACAGTAGGTT	ACAAATAGCA	TTAGCTTTTT	CTTTAAAGAA	ATTCATTGTA	120
ACCAGTGAAG	GATAAGATTT	TAAATTAGAA	AAATGGAAAT	CCTATGAATA	AAAAACTAGT	180
AAGCTTGAGA	GCAGAATCAC	TGTGGAAAAA	AAACAGATTG	AAAAATAACT	TGCAGGTATC	240
ATAGACAGGA	AATTGCCACT	AGAGAAAACA	GGAAACTTGT	GATAGATAAA	AATGAAGTAT	300
TTTCATTTGG	AACAAGAGAC	CAACTGAAGA	GAGATCAAGT	GAAGGGGGTT	TATTTTAATG	360
AAACACAAAG	ATTCTTGTGG	AAATCAAAGT	GCCGGAGCCA	GAAACAGGGC	TCAACCTTCA	420
AGATTAGAGC	TGTATTCAAG	TTGTTCAAGT	TGGCTCTCGG	TCCCAAAGCA	ACAGCAATGT	480
CACTAAGGTT	ACAAGTAAAA	GGTAAGCCCT	CGAG			514

- (2) INFORMATION FOR SEQ ID NO:1480:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 194 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

G	AATTCTAGA	CCTGCCCCTC	CACTGCTCCC	CATACCCTGG	CACGATGCGT	TCCTGGTCAC	60
T	GATCACCAT	CATTTTGGGA	AGAGAATCCC	AATCCCTGGC	ACCTGGGTTT	GCCTCATCCA	120
Α	CCATCCTTC	CCTTTCTCAG	CTGCACCCCC	TCTGCAGATC	TGAAGACACA	CCTCACTCTT	180
	CAGGGCCCT						194

- (2) INFORMATION FOR SEQ ID NO:1481:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

GACGCGCCCG	GCCTCCTCTT	TCATTTCAGT	ATACGTAATA	AGAAGTCAGA	AATTACCTTT	60
AACCAAGCCT	GGAAATCTCC	TTATCTAGAT	CATTATATTC	TTTAGGTACA	TTTTTTACTT	120
TCTACATTAC	CACTCACAAC	AATATTGCTA	AATTTTTTCC	TCTAAATAAG	AAGGATTCCC	180
TTTTTCTAAT	AACACTTTCT	TTATTTTTCT	TTAACCTTTC	ACTGAAAGCC	CCCTCAAAAG	240
CTACCTGGCT	TATGCTAACA	GTATGTTTGA	TGTCCTTTCA	ATACTACTCT	GTTTCCATCT	300
GTCTAGCATC	CACCTGCCTC	CCAATCTCAA	AGTCTCCATC	ATATTTTGTC	ACTTTTTACT	360
THE PROPERTY OF A STATE OF THE PARTY OF THE	macmaa				-10111111111	200
TTTTTTGTTA	TGGTGCAACC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:1482:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

```
GAATTCGGCC TTCATGGCCT AGGTTCTGGG ATAGCTGATT GTTGGCCACC CCCGCCCTGG 60
AATGGAAACC CTGTTAGGCC AGGGCCAGG CAGGTGGCCA TGAAGCAAGA CGGCAAAGGC 120
ATTGGAGGAT GTCCCACCTC CACACATACG CCCAGGCATT TCTTGGCTGG GGAATGGTGT 180
TACAGGATCC ACAAGCACAG AGATGGGAAA ACAGTGTGT TGGGGAACAC CAAGAGTTGG 240
GGTTGCCTGG AGGACAGATA GACTCAGGGG GGACATCCAG AGGTAACACT AGGTCCCCAG 300
GTGGGTTCAG AGGCCCCAGC TCTATCCCCT TATTCCCAGC CGGATTAAAG AATAATCTGA 360
GTATGGTTCC CTCGAG 376
```

- (2) INFORMATION FOR SEQ ID NO:1483:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

CAAMMOOOOO	mma> = = = = = =					
GAATTCGGCC	TTCATGGCCT	ATGGATCCAT	CATGGGACAA	TTACTACTTA	TTTACTTTCC	60
TOCOCOMMONO					1111011100	00
ICCGCI I CAG	AAGGTTTTTC	AGACTGAGAG	CCTAAGCATA	CTGGATCTGT	TGTTTCTTTT	120
CCCTCTCTCTCC	mas mas amaa					120
GGGTCTCACC	TCATCAGTGT	GCATAGTGGC	AGGCCTGGTC	AGTAATCTTC	ТСТАСТСТТА	180
TROMBOROS						100
IAGIACAGCA	GCTTTTAGGT	CCACTGATTG	CATTCTTAAT	TTGAGTATTT	AATATTTATT	240
TITLE TOTAL & COMM			·			240
TIATTAACCT	AAGGTTTTCA	TTTGTCACTA	TAGCATGGTC	TCATAATTTT	CAAAAAATCA	300
~~~~~					CHURNICA	300
GAAAACAGTA	GATGTTGGCG	TGGATGCAGT	GAACAGGGTT	ACTCGAG		347
			0	ver cove		34/

- (2) INFORMATION FOR SEQ ID NO:1484:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 709 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

GAATTCGGCC	TTCATGGCCT	ACGAGAATAT	TGTGGAGAAC	TGGTCAGTAG	AAGAACAAGC	60
AATGGAAATG	GATTTGAGTG	TCCTTCAACA	GGTAGAAGAT	CTAGAAAGGA	GAGTTGCATC	120
AGCAAGTTTG	CAAGTGAAGG	GTTGGATGTG	TCCAGAGCCT	GCATCAGAAA	GGGAGGACTT	180
GGTATATTTT	GAACATAAAT	CATTTACTAA	ATTGTGCAAG	GAGCATGATG	GAGAATTTAC	240
TGGCGAAGAC	GAAAGCAGTG	CACATGCACT	AGAACGGAAG	AGTGACAACC	CCCTAGATAT	300
AGCTGTAACC	AGGCTGGCTG	ATTTGGAGCG	GAACATTGAA	AGAAGGTATC	TGAAGAGCCC	360
CTTAAGTACC	ACCATTCAGA	TCAAACTGGA	TAATGTGGGC	ACAGTTACTG	TCCCTGCTCC	420
TGCACCATCC	GTTAGTGGTG	ATGGTGACGG	AATTGAAGAG	GATATTGCTC	CAGGGCTCAG	480
GGTATGGAGA	AGGGCATTAT	CAGAAGCTCG	CAGTGCTGCA	CAGGTAGCTC	TGTGCATTCA	540
GCAATTACAG	AAATCAATAG	CATGGGAAAA	ATCAATTATG	AAAGTTTACT	GCCAAATCTG	600
TCGAAAGGGA	GATAATGAAG	AACTGCTTCT	TCTTTGTGAT	GGCTGTGACA	AAGGCTGTCA	660
TACCTACTGC	CATAGACCCA	AGATTACAAC	AATCCCAGAT	GCTCTCGAG		709

- (2) INFORMATION FOR SEQ ID NO:1485:
  - (i) SEQUENCE CHARACTERISTICS:

<ul><li>(A) LENGTH: 272 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:	
GAATTCGGCC TTCATGGCCT ACTGTTTCAG AACTTCCGTA CCTTTTTCTT GTATGTAGCA CGTATAAATG CAGCTGTCAT GCAGTTCTTT TCTTTTGCTA GAAAATTAGT CAGGAGGTAA GATGAATCTT CCAAAGTTAT GTTAAATTTT GTTTAACTTG ACAAATTAAA CTTTGTTCTT ATTAAACAAA TACGTAAACA AATACTGGAA AAGCAAAGCT TATATTTGGG AGTAAAATGT ATCTTAAAAT GCATGTTCAA CTTTTGCTCG AG	66 120 180 240 273
(2) INFORMATION FOR SEQ ID NO:1486:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 350 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:	
GAATTCGGCC TTCATGGCCT ACCGAGGACG AGGGGAAGAT GTCACGCAAG ATAGAAGGCT TTTTGTTATT ACTTCTCTT GGCTATGAAG CCACATTGGG ATTATCGTCT ACCGAGGATG AAGGCGAGGA CCCCTGGTAC CAAAAAGCAT GCAAGTGCGA TTGCCAAGGA GGACCCAATG CTCTGTGGTC TGCAGGTGCC ACCTCCTTGG ACTGTATACC AGAATGCCCA TATCACAAGC CTCTGGGTTT CGAGTCAGGG GAGGTCACAC CGGACCAGAT CACCTGCTCT AACCCGGAGC AGTATGTGGG CTGGTATTCT TCGTGGACTG CAAACAAGGC CCATCTCGAG	60 120 180 240 300 350
(2) INFORMATION FOR SEQ ID NO:1487:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 276 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:	
GAATTCGGCC TTCATGGCCT AGTACCTGAA GGCCTTCAAG GTGGCCTACA GCCTTAATGG ACACGAATTC GATTCATCC ATGATGTTAA TAAAAAACAC AAGGAGTTTG TGGGTAACTG GAACAAAAAC GCGGTGCATG TCAACCTGTT TGAGACCCCT GTGGAGGCTC AGTACGTGAG ATTGTACCCC ACGAGCTGCC ACACGGCCTG CACTCTGCGC TTTGAGCTAC TGGGCTGTGA GCTGAACGGA TGCGCCAATC CCCTGGGCGT CTCGAG	60 120 180 240 276
(2) INFORMATION FOR SEQ ID NO:1488:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 595 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

GAATTCGGCC	TTCATGGCCT	AGTGGAGATT	ACTTGGCACC	ACTCTCCTTT	CACAGAGCAG	60
AGTCTGAATA	GTCTTCAGAG	ATAGGCCTGT	GGGCCAGATT	GCCATCCCCT	ATGGACCAGA	120
AGCCAAGGAT	CTCTCTAGTG	ATGGTCAGAG	GGCCCAAATG	GCAGGGATAC	CCAGTGATGT	180
CAGGAGGAAT	AGTACAGACA	GAAGGTGCTA	AGCAGACAAT	TCAACTGCCA	TGTTTTGCCA	240
CCCCCTGTGA	GCAGGGATTA	GGTGTTCAGG	CCAGTATCTT	GGGCATGGGG	GAGCCTTTGG	300
CCAGAAGAGG	TATAAAGCTC	AGAAGTTTTT	CAGTCTGATA	ACTATTGATA	TAATTTCCAT	360
AGTGTGAGGG	AGCGGTATGC	TCTACCCTTG	TGTATTTAAG	GCAGGACAGA	CAAATTCACC	420
ATGCCCCTGG	GGCTAGATCG	ATGATATGAC	CAGAAATCAA	AAAGGGAATG	CATTATTATA	480
TGCTGTGTAA	CACTGTTAAG	AGAGGAGGTA	GTTAAGGGAT	GGATAGGCAC	ATACACACC	
AAGGTCTCAG	GAGAAGGGAT	AGAAAGGAAC	TATCTTCACA	AGAACAACAC	MIAGAGAGGG	540
		HOLDWOOTH	INIGITCACA	MUMALAALAC	TCGAG	595

- (2) INFORMATION FOR SEQ ID NO:1489:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 297 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

GAATTCGGCC	TTCATGGCCT	ACAATTTAAT	AGTATAACAA	<b>ATCCCCTAGA</b>	ATAGTAGAGG	60
AGAGAGGAAT	CTTCCCCTGA	TATGTTTTTG	TAATACTTCT	TCCTCCTCTT	CAGTCAATAG	120
GGAAATGTTT	GTTGAAAGAC	TACTTTGCAG	ACATTTAGAA	AGATACAGAG	TAAGTGTAAG	180
ATGTCCCTCC	TTGTCCTTGA	GGAGTCTCTA	GTCAGGCACA	GGTAGGACTA	AATGAAAAAC	240
AACTACAGAA	CTAAGTAGAA	GAGTGTACAA	TAATATGGGG	AATGTGGAAC	ACTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:1490:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 273 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

GAATTCGGCC TTCATGGCCT ACTTACTTTT CCAAAGAATT TTTTCCACCT GGAATAAGAA 60
GAGAGGACTA GTTGAAACAT TTGAGCTGGA GAGGCTTATG GGCAATATGA AGTGGGCCAA 120
ATTCTTGCAA TACACCCTAT TCAATTGAAA GTACAGTGTC TAAGGATAAG AATACTTCTT 180
TAAAGACCAA CAATTGTTTT AATGCAATCT TAATTAGTAA ATGGTTTACA TTTTTTCTAT 240
TGTTATTGGT TTTAAAATTT GCTACCGCTC GAG 273

(2) INFORMATION FOR SEQ ID NO:1491:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 660 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

GAATTCGGCC	TTCATGGCCT	ATTGAATTCT	AGACCTGCCT	CAGGGTAAGG	GAGATTTAAT	60
CTTTTTCTTT	ACTATTTTCT	AGTTTCTATG	AGCATGGATT	ACTTGTGCAA	ATCAAAACAA	120
AACAAACGGA	TGGCTCATCC	GGCAAACATC	CATGGGCAGG	GTTGGTGTCG	GGTGCTGGAC	180
GCAGAGATGA	ATGGAGGGCT	CTGGCCTCAG	CGGCTCACAG	TCTGGTGAGC	ATAGACAGTG	240
CTTTCGATGT	GAGAGCAGAC	CTGAGTGTCG	CCTGGGACTC	CAGGCACAGT	TCTCCCTGCA	300
GCTCACAGCA	CTTACCCTTA	CTGCACCATT	AACTTCTACT	CTAGCTCACT	GCCTCTTAAC	360
TCTGAGCGCC	TTGAAGGCAC	AAAATGAGTC	CCATCTGGGT	CTTTAGCAGC	TGGCAGAAAA	420
CCTAGCTCAA	ACTCATGCTC	TAAAAACCCC	TGCTGAGGGA	GTGGGCGAAT	GCAGGCAGCC	480
CTGGCAGTGG	GATCAAGTTC	AGGGAGTGGC	ACTGGAGGCA	TCACCCCAAG	GCTGAGAAGA	540
CCTTGAACTG	CTGTTCAGGG	TTTTGCTGTC	TCTCCCAAGG	CATGACTCGG	CCCAGGAGGA	600
GATGGGGCAG	ATGCTGCAGA	AGGAGGGTTC	ATGCCCCTCC	ACTGCTGCCC	ATGACTCGAG	660

- (2) INFORMATION FOR SEQ ID NO:1492:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 315 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

GCTGTGCTAT	CTGTTGTCCA	GCATCTGACA	CAGTTGGTTT	TATATTTTGT	CTGGTTTCTA	60
GTTATTAAGC	AGGTTAAGTC	TGGTTCCTGC	TGTTCTATAT	AGCAGGAAGC	AAAGGTTCTC	120
TCATGAATTT	TTAGCATAAT	AACATAAGCG	TGGATTCCAA	AAATTCATTA	CACAGATCCT	180
GGAAATCTGT	TTACTATGTT	TTATACATTC	TGTGAAAGCT	GGAGAATATA	TATTTGTTTT	240
ACTATGTGTA	TCGCAAATAA	AATATCAATT	TCATGTGCCA	GAGAATTGAA	TACATTATCA	300
AAGGGTCAAC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:1493:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 356 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

GGGACAACAA	GCCCATCTGG	ATGCACGCAG	AGGAGCGGGA	GGAAAGCAAG	GATAAGCGCC	60
GGGACAGCGC	CCCCTATGGG	GAATACGGCA	GCTGGTACAA	GGCCTGTAAA	GTAGACAGCC	120
CCACAGTCAA	CACCACCCTG	CGCAGCTTGG	GGGCCCTATA	CCGGCGCCAG	GGCAAGCTGG	180
AAGCCGCGCA	CACACTAGAG	GACTGTGCCA	GCCGTAACCG	CAAGCAGGGT	TTGGACCCCG	240
CAAGCCAGAC	CAAGGTGGTA	GAACTGCTGA	AAGATGGCAG	TGGCAGGCGG	GGAGACCGCC	300
GCAGCAGCCG	AGACATGGCT	GGGGGTGCCG	GGCCTCGGTC	TGAGTCTGAC	CTCGAG	356

- (2) INFORMATION FOR SEQ ID NO:1494:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 366 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

GAATTCGGCC	TTCATGGCCT	AGTAAAGGGA	TTTATAATAA	CATTAAAAAT	TTCGTTAGAT	60
TCCAGCTGAG	CACGAGTATA	GCAGCATTAA	CTTTAATCTC	ATTGGCTACA	TTAATGAACT	120
TTCCTAATCC	TCTCAATGCC	ATGCAGATTT	TGTGGATCAA	TATTATTATG	GATGGACCCC ·	180
CAGCTCAGAG	CCTTGGAGTA	GAACCAGTGG	ATAAAGATGT	CATTCGTAAA	CCTCCTCGCA	240
ACTGGAAAGA						300
TCATTGTTTG						360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:1495:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 258 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

(	SCTCGAGCGT	TGAGGTCAAC	ACTTCCTCCA	GGGAAAAGGA	TTCCATTAAT	AGATTTGAAA	60
7	AGTATTTCAT	AGTCTTTCTC	TGTAAGATCC	AGCCTTACTG	GTACAACTCT	CGCACCTGCA	120
(	GACTCCAAGT	ACTTTACATA	GGACGCAGCA	ATATAGTATC	TTCCATAGTT	TTTCATGACT	180
7	TTATTACGGC	ATTTTTGCAT	TAATATTCCG	ATGATGGGCT	TCTTGGCGGT	GTCGCCGTGG	240
(	GCTCTAGACT	ATCTCGAG					258

- (2) INFORMATION FOR SEQ ID NO:1496:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 437 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

GAATTCGGCT TCATG	GCCTA CTCTCTTTCT	CCATGTTAAA	CCCCTTGGCA	TGAATGAAAG	60
GCTTTCCCCT TTATC					120
AGTAACTTTG CACAT	TTTGC TGTGTGGGCT	GCTGCATCTC	TGCCAAAAGG	TTTATGGGAT	180
TTTTACTCAG GAGAT					240
AGGTACAGAA ACATG	TTGGA GATCTTGAGC	CTCAAGGTGC	TTGCTTCAGA	ATTTTCCTGA	300
TTCTCCCTCT CCAGA	CCTAT TCTGTTCTTG	GGACCCAAGC	TTCTTGGCTC	CAGCCCACTC	360
CCCCACTAGA GGAGC	TGGAA AGTTTGGTGC	TGTGGTCATA	CCAAAGATGG	GCAACACCCA	420
GACTCCTCAC CCTCG	AG				437

- (2) INFORMATION FOR SEQ ID NO:1497:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 516 base pairs
    - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

TGGCCT AGTGCAGGTC	CTGGTGCTTG	ATGGTCGAGG	CCATCTCCTG	60
CATCGT GGCTAAACAG	GTACTGCTGG	GCCGGAAGGT	GGTGGTCGTA	120
CAACAT TTCTGGCAAT	TTCTACAGAA	ACAAGTTGAA	GTACCTGGCT	180
GATGAA CACCAACCCT	TCCCGAGGCC	CCTACCACTT	CCGGGCCCCC	240
				300
TCTCAA GGTGTTTGAC	GGCATCCCAC	CGCCCTACGA	CAAGAAAAAG	360
TGCTGC CCTCAAGGTC	GTGCGTCTGA	AGCCTACAAG	AAAGTTTGCC	420
GGCTCA CGAGGTTGGC	TGGAAGTACC	AGGCAGTGAC	AGCCACCCTG	480
AGAGAA AGCCAAGAAC	CTCGAG			516
	CATCGT GGCTAAACAG CAACAT TTCTGGCAAT GATGAA CACCAACCCT GCGGAC CGTGCGAGGT ICTCAA GGTGTTTGAC IGCTGC CCTCAAGGTC GGCTCA CGAGGTTGGC	CATCGT GGCTAAACAG GTACTGCTGG CAACAT TTCTGGCAAT TTCTACAGAA GATGAA CACCAACCCT TCCCGAGGCC GCGGAC CGTGCGAGGT ATGCTGCCCC ICTCAA GGTGTTTGAC GGCATCCCAC IGCTGC CCTCAAGGTC GTGCGTCTGA	CATCGT GGCTAAACAG GTACTGCTGG GCCGGAAGGT CAACAT TTCTGGCAAT TTCTACAGAA ACAAGTTGAA GATGAA CACCAACCCT TCCCGAGGCC CCTACCACTT GCGGAC CGTGCGAGGT ATGCTGCCCC ACAAAACCAA ICTCAA GGTGTTTGAC GGCATCCCAC CGCCCTACGA IGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG GGCTCA CGAGGTTGGC TGGAAGTACC AGGCAGTGAC	TGGCCT AGTGCAGGTC CTGGTGCTTG ATGGTCGAGG CCATCTCCTG CATCGT GGCTAAACAG GTACTGCTGG GCCGGAAGGT GGTGGTCGTA CAACAT TTCTGGCAAT TTCTACAGAA ACAAGTTGAA GTACCTGGCT GATGAA CACCAACCCT TCCCGAGGCC CCTACCACTT CCGGGCCCCC GCGGAC CGTGCGAGGT ATGCTGCCCC ACAAAACCAA GCGAGGCCAG TCTCAA GGTGTTTGAC GGCATCCCAC CGCCCTACGA CAAGAAAAAG TGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG AAAGTTTGCC GGCTCA CGAGGTTGGC TGGAAGTACC AGGCAGTGAC AGCCACCCTG AGAGAA AGCCAAGAAC CTCGAG

- (2) INFORMATION FCR SEQ ID NO:1498:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 329 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

GCGAGCTCCT	GACCTCAGGT	GATCTACCCG	CCTCAGCCTC	CCAAAGTGTT	AGGATTACAG	60
GCGTGAGCCA	CCGCACCTGG	CACCCCCCC	CTTTTTTTT	AATATAAATG	ATCAGTCTTA	120
ACTCCCTAGG	TTATCAGGTT	GAGGGGGTGG	GGATGAGGCT	GGGGGACAGA	TTGTTTTCCT	180
GGCTTCTAGC	TCGGTGTTCT	TTCTGCCTCT	GTGCACAACA	AGGTATGCGT	GTATTGTGGT	240
					CTGCTGATGC	300
	ACTTGGCGAT					329

- (2) INFORMATION FOR SEQ ID NO:1499:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 430 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

GAATTCGGCC TTCATGGCCT AG	GGAGCGCGG TGGCCACGGA	ACGCTGCCCG	GAGCCGCGCG	60
AGGGAGGACC CGACGCGCGG CG	GTTTACCCA GCGCAGCGTT	CCACCGCTCG	GGTTTGGCTG	120
GATAAAATAA AAAATGGGGA TA				180
CCAATCATTA CTTTCTCCTC TO	STGTCAATC TGCCTCTTCG	AGAAATTCAT	ACTCCTGAAT	240
AGCTCTCCAG ACCCCCAGCT GG	SCCATGTGG TGAGTTCAGG	GCCCAAATCA	AGTAGTACCA	300
GCAATCAGGG AACTCCTATC TO	STTTTGAAT GGATTCACAC	CAGCCACAAG	CCTGGAAAGA	360
TGGTGTCACA ATCTACAGTC AG	GCAGGATT CTCCTGTGGA	GCCCTGGGAA	GGGATCAGCG	420
ATCACTCGAG				430

(2) INFORMATION FOR SEQ ID NO:1500:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

GAATTCGGCC	TTCATGGCCT	AGCCAAGTCT	GGGAAGCCTT	AAGGAAAGGA	GTGCCCGTCG	60
GCGTCTTGGT	CCTCCTGTCC	CTGCTGCAGG	GGCTGGGGCC	TCCGGAGCTG	CTGCGGGCTC	120
CCCTCAGGCT	CTGCTTCGTG	ACCCGTGACC	CATGACCCAC	AGTGCTGGCC	TCCTGTGGGG	180
CCACTATAGC	AGCCACCAGA	AGCCGCGAGG	CCCTCAGGGA	AGCCCAAGGC	CTGCAGAAGC	240
				GCGCCCCTGT		300
TGACCCTTCT	GGAGTGGGG	GCGGCGGCA	GGGCTGCTTT	TCTTAGTCTG	ATACCAAGCA	360
AGGCCTTTTC						375

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEO ID NO:25, SEO ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118. SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145.

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or a complement of said sequence.

2. An isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID

NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID

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NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID
NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID
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NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID
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NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID
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or a complement of said sequence.

3. An isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ

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NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;
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or a complement of said sequence.

4. An isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ

ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

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NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500; or to a complement of said sequence.

- 5. An isolated protein encoded by an isolated polynucleotide of claim 1.
- 6. An isolated protein encoded by an isolated polynucleotide of claim 2.
- 7. An isolated protein encoded by an isolated polynucleotide of claim 3.
- 8. An isolated protein encoded by an isolated polynucleotide of claim 4.

# **PCT**

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	HED I	JNDER THE PATENT COOPERATION TREATY (PCT)
(51) International Patent Classification 6: C12N 15/12, 5/10, C07K 14/47,		(11) International Publication Number: WO 98/45436
C12Q 1/68, A61K 38/17	A3	(43) International Publication Date: 15 October 1998 (15.10.98)
(21) International Application Number: PCT/US (22) International Filing Date: 10 April 1998 ( (30) Priority Data: 08/838,821 10 April 1997 (10.04.97)	10.04.9 U	BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CV, DE, DK, ES, EL, ED, CD, CD, LE, LD, CD, CD, LD, LD, LD, LD, LD, LD, LD, LD, LD, L
<ul> <li>(71) Applicant: GENETICS INSTITUTE, INC. [US/US]; bridgePark Drive, Cambridge, MA 02140 (US).</li> <li>(72) Inventors: JACOBS, Kenneth; 151 Beaumont Aventon, MA 02160 (US). MCCOY, John, M.; 56 Street, Reading, MA 01867 (US). LAVALLIE, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). Lisa, A.; 124 School Street, Acton, MA 01720 (US BERG, David; 2 Orchard Drive, Acton, MA 0177 TREACY, Maurice; 93 Walcott Road, Chestnut F 02167 (US). SPAULDING, Vikki; 11 Meadowbar Billerica, MA 01821 (US). AGOSTINO, Michae Wolcott Avenue, Andover, MA 01810 (US).</li> </ul>	Howar Edward RACII ). MER 20 (US Hill, Mank Roar	LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  Published  With international search report.  Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.  [88] Date of publication of the international search report:
(74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, CambridgePark Drive, Cambridge, MA 02140 (US)	Inc., 8 ).	7
(54) Title: SECRETED EXPRESSED SEQUENCE TAGS		
(57) Abstract	(SEST	5)
Secreted expressed sequence tags (sESTs) isolated from	om a va	riety of human tissue sources are provided.
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Interr nal Application No PCT/US 98/06955

A. CLAS	SIFICATION OF SUBJECT MATTER			71/05 50/00533
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According	to International Patent Classification (IPC) or to both national	alassification	. Inc	
B. FIELD	SSEARCHED	ORES MOREON AND	IPC	
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	ENTS CONSIDERED TO BE RELEVANT			
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A	WO 97 07198 A (GENETICS INST February 1997 see the whole document	ITUT) 27		1-8
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	er documents are listed in the continuation of box C.	X P	atent family members a	are listed in annex.
A" document consider document which is citation other me document later than	which may throw doubts on priority claim(s) or cited to establish the publication date of another or other special reason (as a specified) It referring to an oral disclosure.	oited to invent  "X" docume canno involv' "Y" docume canno docum ments in the i	o understand the prino ion ounderstand the prino ion ent of particular relevant to be considered novel of an inventive step whe ent of particular relevant to considered to invo- ent is combined with o such combination bej	
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ame and mai	ling address of the ISA  European Patent Office, P.B. 5818 Patentiaan 2  NL · 2280 HV Rijswijk  Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016		ORNIG H.	

Intermal Application No
PCT/US 98/06955

Category *	ation) DOCUMENTS CONSIDERED TO BE RELEVANT	
y	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5 536 637 A (JACOBS KENNETH) 16 July 1996 cited in the application see the whole document	. 1-8
A	JACOBS K ET AL: "A NOVEL METHOD FOR ISOLATING EUKARYOTIC CDNA CLONES ENCODING SECRETED PROTEINS" JOURNAL OF CELLULAR BIOCHEMISTRY - SUPPLEMENT, vol. 21A, 10 March 1995, page 19 XP002027246 see abstract	1-8
4	WO 90 14432 A (GENETICS INST) 29 November 1990 see the whole document	1-8
`	WO 96 17925 A (IMMUNEX CORP) 13 June 1996 see the whole document	1-8

page 2 of 2

Ir. .ational application No.

PCT/US 98/06955

Boxi	Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)
This Inter	mational Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1.	Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
	Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
	Claims Nos.: secause they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II	Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
	national Searching Authority found multiple inventions in this international application, as follows:
see	further information sheet
1. A	s all required additional search fees were timely paid by the applicant, this International Search Report covers all earchable claims.
2. A	s all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment I any additional fee.
3. As	s only some of the required additional search fees were timely paid by the applicant, this International Search Report overs only those claims for which fees were paid, specifically claims Nos.:
	o required additional search fees were timely paid by the applicant. Consequently, this International Search Report is stricted to the invention first mentioned in the claims; it is covered by claims Nos.:  ee further information sheet, subject 1.
Remark on	Protest  The additional search fees were accompanied by the applicant's protest.  No protest accompanied the payment of additional search fees.

#### FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. Claims: (1-8) partially

An isolated polynucleotide comprising a nucleotide sequence selected from SEQ ID no.1, consisting of a nucleotide sequence selected from SEQ ID no.1, consisting essentially of a nucleotide sequence selected from SEQ ID no.1; an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence consisting of SEQ ID no.1; an isolated protein encoded by said isolated polynucleotides;

Inventions 2 to 1500. Claims: (1-8) partially

Idem as subject 1 but limited to SEQ ID nos.2 to 1500 respectively clone ID nos. BV34 to BK517. (Invention 2 is limited to SEQ ID. no. 2; Invention 3 is limited to SEQ ID no. 3;.....Invention 1500 is limited to SEQ ID no. 1500);

! mation on patent family members

Internet and Application No
PCT/ US 98/06955

Patent document	Publication		US 98/06955
cited in search report	date	Patent family member(s)	Publication date
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